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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 13, 2004, 19:06:21 ; Search time 516 Seconds

(without alignments)
5258.438 Million cell updates/sec

Title: US-10-044-205A-2

Perfect score: 2889
Sequence: 1 MVDGALDNLNTANTAYIQAR.....NRPTGEGNSKSGVCLLL 553

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-Db=Published Applications NA -QFMT=fastap -SUFFIX=p2n.tmpb -MINMATCH=0.1
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-Fgapop=6 -Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	ID	Description
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1	2889	100.0	1659	14	US-10-044-205A-3	Sequence 3, Appl1
2	2889	100.0	2198	14	US-10-044-205A-1	Sequence 1, Appl1
3	2883	99.8	1662	15	US-10-217-745-1	Sequence 1, Appl1
4	2883	99.8	1662	17	US-10-311-034-45	Sequence 45, Appl1
5	2883	99.8	1662	17	US-10-451-168-49	Sequence 49, Appl1
6	2883	99.8	2249	15	US-10-217-745-5	Sequence 5, Appl1
7	2876	99.6	1662	9	US-09-964-469-1	Sequence 1, Appl1
8	2876	99.6	1662	15	US-10-425-962-1	Sequence 1, Appl1
9	2823	5	97.7	1701	US-10-072-012-273	Sequence 273, Appl1
10	1801	62.3	1062	15	US-10-217-745-3	Sequence 3, Appl1
11	1528	52.9	36651	9	US-09-964-469-3	Sequence 3, Appl1
12	1528	52.9	36651	15	US-10-425-962-3	Sequence 3, Appl1
13	1283.5	44.4	1737	15	US-10-325-430-2	Sequence 2, Appl1
14	1283.5	44.4	2113	15	US-10-325-430-1	Sequence 1, Appl1
15	1252.5	43.4	2467	15	US-10-084-817-110	Sequence 110, Appl1
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17	1252.5	43.4	2519	14	US-10-071-766-13	Sequence 13, Appl1
18	1252.5	43.4	2529	15	US-10-072-036-42	Sequence 42, Appl1
19	1252.5	43.4	2557	9	US-09-972-694-1	Sequence 1, Appl1
20	1252.5	43.4	2557	12	US-10-380-235-7	Sequence 7, Appl1
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22	1245.5	43.1	2519	10	US-09-971-392-72	Sequence 72, Appl1
23	1239	42.9	2848	10	US-09-873-367C-142	Sequence 142, Appl1
24	1239	42.9	2848	16	US-10-159-856-4	Sequence 4, Appl1
25	1235	42.7	2817	16	US-10-388-934-621	Sequence 621, Appl1
26	1233	42.7	2848	9	US-09-851-686-2	Sequence 2, Appl1
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29	725.5	25.1	2362	15	US-10-037-270-273	Sequence 273, Appl1
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33	701	24.3	2070	15	US-10-038-010-47	Sequence 47, Appl1
34	701	24.3	2683	12	US-10-152-319A-1539	Sequence 1539, Appl1
35	701	24.3	3283	16	US-10-191-803-38	Sequence 38, Appl1
36	701	24.3	3283	15	US-10-247-671-3	Sequence 3, Appl1
37	670	23.2	3154	10	US-09-955-999-45	Sequence 45, Appl1
38	663.5	23.0	1411	10	US-09-955-999-14	Sequence 14, Appl1
39	652.5	22.6	2037	13	US-10-087-684-23	Sequence 23, Appl1
40	652.5	22.6	2037	13	US-10-218-779-23	Sequence 23, Appl1
41	652.5	22.6	3073	13	US-10-029-020-11	Sequence 11, Appl1
42	580.5	20.1	1377	16	US-10-264-049-482	Sequence 482, Appl1
43	540	18.7	1679	9	US-09-771-161A-25	Sequence 25, Appl1
44	512	17.7	1416	9	US-09-938-842A-2503	Sequence 2503, Appl1
45	512	17.7	1416	11	US-09-938-842A-2503	Sequence 2503, Appl1

ALIGNMENTS

RESULT 1
US-10-044-205A-3
Sequence 3, Application US/10044205A
Publication No. US20020123464A1
GENERAL INFORMATION:
APPLICANT: KAPTELER-LIBERMAN, Rosana
APPLICANT: BANDAU, Rajasekar
TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Protein
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 10147-52U1
CURRENT APPLICATION NUMBER: US/10/044, 205A
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/242, 428
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: US 60/241, 884
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: US 60/241, 877
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1659
TYPE: DNA

ORGANISM: Homo sapiens
US-10-044-205a-3

Alignment Scores:
Pred. No.: 0 Length: 1659
Score: 2889.00 Matches: 553
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-044-205a-2 (1-553) x US-10-044-205a-3 (1-1659)

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DB 1 ATGGTGGACATGGGGGCTGGACCAACCTGATGCGCAACCGCTTACCTGAGAGCCCG 60
QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
DB 61 AAGCCCTCGGACTGGGACAGCAAGAGCTGCGAGCGGCGGCTAGCTGCTGCTGCTGCC 120
QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
DB 121 GGGCTGCGAGGCTGCGCGAGCTCCGCGAGAGCTGCTGCTGAACTTCCAGAGCTGTGT 180
QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
DB 181 GAGCAGCAGCCCATGCGTGGCGCTCTTCCGTGACCTTCCACCACTGACCGACGCTTC 240
QY 81 ArgLysAlaAlaThrPheLeuGlnAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
DB 241 CGAGAGCGGCAACCTCTCTTGAAGAGCGTGCAAGATGGGAGCTGGCGAGAGAGAGCC 300
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
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QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
DB 361 AACCCTGCAACCTCTCTTCCAGCGCGCGCTGGCGACCAAGTCCCAACAGCCACCACTGAG 420
QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
DB 421 GAAGAGGAGTGGCTGCGAGTACGCTGCCCAAGCTGAGGCTGCTTCTTGAAGAG 480
QY 161 GlnProPheLysAspPheValThrSerAlaPheTyraAspLysPheLeuGlnTrpLysLeu 180
DB 481 CAGCCCTTTAAGGATTTGTCGACCGAGCGCTTCTTACGACAAAGTTTCTGAGTGAAGAAC 540
QY 181 PheGluMetGlnProValSerAspLysTyraPheThrGluPheArgValLeuGlyLysGly 200
DB 541 TTCCAGATGCAACCGAGTGCAGACAGTACTTCACTGAGTTCAGAGTGTGGGAAAGGT 600
QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyraAlaCysLys 220
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QY 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGlyLysMetAlaLeuLeuGlnLys 240
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QY 241 GluLeuLeuGluLysValSerSerProPheIleValSerLeuAlaTyraAlaPheGluSer 260
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QY 281 TyrAsnValGlyThrArgLysLeuAspMetSerArgValIlePheLysSerAlaGlnIle 300
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QY 301 AlaCysGlyMetLeuHisSerLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
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QY 361 IleLeuMetGluLysValSerTyraSerTyraProValAspTrpPheAlaMetGlyCysSer 380
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QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
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RESULT 2
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; Sequence 1, Application US/10044205A
; Publication No. US20020123464A1
; GENERAL INFORMATION:
; APPLICANT: KAPILLER-LIBERMANN, Rosana
; APPLICANT: BANDARU, Rajasekhar
; TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Protein
; TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Protein
; FILE REFERENCE: 10147-52U1
; CURRENT APPLICATION NUMBER: US/10/044,205A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/242,428
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: US 60/241,884
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/241,877
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1

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Qy      361  IleLeuMetGluLysValSerTYrSerTYrProValAspTrpPheAlaMetGlyCysSer 380
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Qy      461  ArgLeuGlnAlaGlyLeuIleGluProProPheValProaspProSerValValTYrAla 480
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Qy      501  AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGlu 520
Db      1791  GATTAAGACGATCTTCAAAAATTGGAGAGGTGCTGTCTTCTTAAGCATGGCAGAGAA 1850
Qy      521  IleIleGlnThrGlyLeuPheGlnGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
Db      1851  ATTATAGAAACGGACGTGTTTGAGAACTGAGATATACCCCAACAGACCTTACGGGTTGAG 1910
Qy      541  GluGluYAsnSerSerLysSerGlyValCysLeuLeuLeu 553
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RESULT 3
US-10-217-745-1
; Sequence 1, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Milgowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20030004328A1el Human G-Coupled Protein Receptor Kinases and
; TITLE OF INVENTION: Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; PRIOR FILING DATE: 2002-08-12
; PRIORITY APPLICATION NUMBER: US/09/802,117
; PRIORITY FILING DATE: 2001-03-08
; NUMBER OF SEQ. ID NOS.: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1

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LENGTH: 1662
 TYPE: DNA
 ORGANISM: homo sapiens
 US-10-217-745-1

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 Score: 2883.00 Matches: 552
 Percent Similarity: 99.82% Conservative: 0
 Best Local Similarity: 99.82% Mismatches: 1
 Query Match: 99.79% Indels: 0
 DB: 15 Gaps: 0

US-10-044-205a-2 (1-553) x US-10-217-745-1 (1-1662)

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 QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPhelHisSerLeuCys 60
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 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
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 Db 541 TTCGAGTGCACACGAGTGCAGACCAAGTCACTTCACTGAGTGTGAGTGTGAGAAAGGT 600
 QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
 Db 601 GGTTTTGGGAGGATGTGTGCGCTGCGAGTGAAGAAACCTGGAGAAAGTGAAGCTGTAG 660
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 QY 241 GlnLeuLeuGlnLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
 Db 721 GAAATCTTGAGAAAGGTACGAGCCCTTTCATGCTCTCTGCGCTTGAAGAGC 780
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 Db 781 AAGGCCCATCTGTGCTTGTGATGAGCCCTGAGATGGAGGAGAACTCAAGTTCACATC 840
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300

Db 841 TACAAGTGGCAAGGGTGGCTGGACATGAGCGGGGTGATCTTTTACTGGGCCACATA 900
 QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
 Db 901 GCGTGTGGAGTCTGACACTCCATGAACCTGAGCATGCTCATTCGGGACATGAGAGCCTAG 960
 QY 321 AsnValLeuLeuAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
 Db 961 AATGTCTTCTGATATACCTCGGCAACTGCAAGGTATCTGAGCTGGGGCTGGCGCTGAG 1020
 QY 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
 Db 1021 ATGAAGGGTGGCAAGCCCATCACCGAGGGCTGGAACCAATGGTTACATGGCTCTGAG 1080
 QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
 Db 1081 ATCTTAATGAAAGAAAGTAAAGTATTCCTATCTGAGCTGTGAGCTGTGCAAGGATGAGC 1140
 QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
 Db 1141 ATTATGAATGGTCTCTGAGCAACACCATTCMAAGATTACAGAGAAAGTCACTGATAA 1200
 QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
 Db 1201 GAGATCTGAAGCAAGAACTCTGCAAGACGAGTCAATTCAGCATGATACTTCACA 1260
 QY 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
 Db 1261 GAGGAAGCAAAAGATTTTGGACGGCTCTTCTTGGCTTAAAGAACAGAGCAACCTTAAGA 1320
 QY 441 SerArgGluLysSerAspAspProArgLysHisPhePheLysThrIleAsnPhePro 460
 Db 1321 AGCAGAGAAAGCTGATATATCCAGAAACATCATTTCTTTAAAGATCAACCTTCTCT 1380
 QY 461 ArgLeuGlnAlaGlyLeuIleGluProPheValProAspProSerValValIleAla 480
 Db 1381 CGCCTGGAAGGTGGCTTAATGAACCCCATTTGTGGCCAGACCTTCAAGTGTATATGCC 1440
 QY 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspLys 500
 Db 1441 AAGACATCGCTGAATATGATATTTCTGAGGTGTGGGGAGTGAATTTGATACAAA 1500
 QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGlu 520
 Db 1501 GATAGCAGATTCTTCAAAACCTTGGACAGGTGCTGTTCTATAGATGCGCAGAGAA 1560
 QY 521 IleIleGluThrGlyLeuPheGlnGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
 Db 1561 ATTATAGAAACGGGAGCTTTTGAAGAACTGATGATGACCCCAAGACCTACGGGTGTGAG 1620
 QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
 Db 1621 GAGGTTAATTCATCCAGTCTGGCGTGTGTTTATTTG 1659

RESULT 4
 US-10-311-034-45
 ; Sequence 45, Application US/10311034
 ; Publication No. US20040023242A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE GENOMICS, INC.
 ; APPLICANT: YUE, Henry
 ; APPLICANT: LAU, Preeti
 ; APPLICANT: BANDMAN, Olga
 ; APPLICANT: BOROMSKY, Mark L.
 ; APPLICANT: AU-YOUNG, Vanice
 ; APPLICANT: LU, Yan
 ; APPLICANT: GANDHI, Ameena R.
 ; APPLICANT: TRIBOULEY, Catherine M.
 ; APPLICANT: CHATLA, Narinder K.
 ; APPLICANT: YAO, Monique G.
 ; APPLICANT: LU, Dyrung Alina M.
 ; APPLICANT: GREENWALD, Sara R.
 ; APPLICANT: RAMKUMAR, Jayalaxmi

APPLICANT: GRIFFIN, Jennifer A.
 APPLICANT: KEARNEY, Liam
 APPLICANT: BURFORD, Neil
 APPLICANT: NGUYEN, Daniel B.
 APPLICANT: TANG, Y. Tom
 APPLICANT: BAUGHN, Mariah R.
 APPLICANT: HE, Ann
 APPLICANT: THORNTON, Michael
 APPLICANT: HAFALIA, April
 APPLICANT: ARVIZU, Chandra S.
 APPLICANT: GURURAJAN, Rajagopal
 APPLICANT: LO, Terence P.
 APPLICANT: KHAH, Farrah A.
 APPLICANT: RECIPON, Shirley A.
 APPLICANT: AZIMZAI, Valda
 APPLICANT: POLICKY, Jennifer L.
 APPLICANT: DING, Li
 APPLICANT: GREYER, Megan
 APPLICANT: ELLIOTT, Vicki S.
 APPLICANT: THANAVELU, Kavitha
 APPLICANT: BATRA, Sajeev
 APPLICANT: ISON, Craig H.
 TITLE OF INVENTION: HUMAN KINASES
 FILE REFERENCE: PI-0125 PCT
 CURRENT APPLICATION NUMBER: US/10/311,034
 PRIOR FILING DATE: 2002-12-10
 PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
 60/228,056
 PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-25
 NUMBER OF SEQ ID NOS: 52
 SOFTWARE: PERL Program
 SEQ ID NO 45
 LENGTH: 1662
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No. US20040023242A1 7477204CB1
 US-10-311-034-45

Alignment Scores:
 Pred. No.: 0 Length: 1662
 Score: 2883.00 Matches: 552
 Percent Similarity: 99.82% Conservative: 0
 Best Local Similarity: 99.82% Mismatches: 1
 Query Match: 99.79% Indels: 0
 DB: 17 Gaps: 0

US-10-044-205a-2 (1-553) x US-10-311-034-45 (1-1662)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
 DB 1 ATGCTGACATGGGAGCCCTCGACACACCTGATCCGACACCGCCTACCTCAGGCCCG 60
 QY 21 LysProSerAspCysAspSerIlyGluLeuGlnArgIleArgIleSerLeuAlaLeuPro 40
 DB 61 AAGCCTCGGACTGGGACGACGAAAGCTGCGCGCGGCGGAGCTGAGCTGGCCCTGCC 120
 QY 41 GlyLeuGlnGlyCysAlaGluLeuAlaGlnIlyLeuSerIleuAsnPhaHisSerLeuCys 60
 DB 121 GGGCTCGAGGGCTGGCGGAGCTCCGCCAAGGCTGTCCCTGACCTTCACAGCCTGTGT 180
 QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
 DB 181 GAGGACGACCCATCGGTGCGCCCTCTTCCTGACTTCCTTACCAACAGTCCCAAGCTTC 240
 QY 81 ArgLysAlaAlaIleThrPheLeuGluAspValGlnAsnIlePheGluLeuAlaGluGlnGlyPro 100
 DB 241 CGCAAGCGCGCACTCTTACGAGGACGCGGAACTGGGAGGTGGCCGAGGAGGCC 300
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120

DB 301 ACCAAGAAGCGCGCTGCGAGGGCTGGTGGCCACTTGGCACTTGGCACTTGGCCCGGCGG 360
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
 DB 361 AACCCGCAACCTTCTTCTGACGCAAGCCGTGGCCCAAGGTCGCAAGGACCAACGCTAG 420
 QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
 DB 421 GAAAGGCAAGTGGCTGAGTACGCTGCGCAAGGCTGGAGGCTGATGGCTTCTTCCGAAAG 480
 QY 161 GlnProPheLysAspPheValIleThrSerAlaPheTyrAspLysPheLeuGlnIlePheLysLeu 180
 DB 481 CAGCCCTTTAAGATTCGTGACCAAGGCTTCTACGCAAGGTTCTGCGAGTGGAACTTC 540
 QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlnLysGly 200
 DB 541 TTGGAGTTCACCACTGTGACAGCAAGTACTTCACTGATTCAGAGTGGGAGAAAGT 600
 QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
 DB 601 GGTTTTGGGAGGTATGTGCGCTCAGGTGAAAAACACTGGAAAGTATGCTCTGTAG 660
 QY 221 LysLeuAspLysIleArgLeuLysLysGlyGlyGlyGlyMetAlaLeuLeuGlnLys 240
 DB 661 AAACCTGACAAAGAGCGGCTGAAAGAAAGGTGGCGGAAAGATGGCTCTTGGAAAAAG 720
 QY 241 GluIleLeuGlnLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGlnSer 260
 DB 721 GAAATCTTGGAGAAAGTACGACAGCCCTTTTCACTTGTCTTGGCTTATGCTTTAGAGC 780
 QY 261 LysThrIleLysCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
 DB 781 AAGACCATCTCTGCTTGTCTATGAGCTGATGAAATGGGGAGACCTCAAGTTCCACATC 840
 QY 281 TyrAsnValAlaGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
 DB 841 TCAACCGTGGGACCGGTGGCTGACATGAGCGGATGATCTTACTCGGCCCAAGTAA 900
 QY 301 AlaCysGlyMetLeuHisIleLeuGlyIleValTyrArgAspMetLysProGlu 320
 DB 901 GCTGTGGAGTGTGACCTTCATGAACTGGCATCGCTTATGGGACATGAAGCTTAG 960
 QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlnAlaValGlu 340
 DB 961 AATGCTCTTGGATGACCTCGGCACTGCAAGGTTATCTGACCTGGGCGTGGCTGGAG 1020
 QY 341 MetLysGlyGlyIleProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
 DB 1021 ATGAAGGTTGGCAAGCCCATCACCAAGGCTGGAAACAAATGGTTACATGGCTCTTAG 1080
 QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTyrPheAlaMetGlyCysSer 380
 DB 1081 ATCTTAATGAAAGGTAAAGTTATCTTATCTTGTGGACGTGGTTTGCATGGAGATGAGC 1140
 QY 381 IleTyrGluMetValAlaGlyThrProPheLysAspTyrIlyGlnLysValSerLys 400
 DB 1141 ATTATGAAATGGTCTGACGAAACACATTCMAAGATTCAAGGAAAGGTGCTGATAA 1200
 QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
 DB 1201 GAGGATCTGAAAGCAAGCACTTCAAGAGGATCAAGTAATTCAGATATTAACCTTCA 1260
 QY 421 GluGlnAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGlnGlnArgLeuGly 440
 DB 1261 GAGGAGCAAAAGATTTTGGAGGCTTCTTGGCTTAAGAAACAGCAAGCAAGCTTAGA 1320
 QY 441 SerArgLysSerAspAspProArgLysHisIlePhePheLysThrIleAsnPhePro 460
 DB 1321 AGCAGAAAGAGCTGATGATCCAGGAAACATCTTCTTAAACGATCAACTTCTCT 1380
 QY 461 ArgLeuGlnAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
 DB 1381 GCGCTGGAAGCTGCTTAATTAAGAACCCCAATTTGTGGCAAGCCCTTCAAGTGGTTATGCC 1440

QY 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
Db 1441 AAGAGCATGCTGGAATGATGATTTCTGTAGGTGCGGGGTGGAATTTGATGACAA 1500
QY 501 AsplGlnPhePheLysAspPheAlaThrGlyAlaValProIleAtrGlnGlu 520
Db 1501 GATAGCATGTTCTTAAAACTTTGGCAGGTGTCTTCTATGACATGGCAGAAAGA 1560
QY 521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
Db 1561 ATTATGAAACCGGACGTTTGGAGAACGATACACCCCAACGACTTACCGGTTTGAG 1620
QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeu 553
Db 1621 GAGGTAATTCATCCAMGCTGGCGTGTGTGTATTG 1659
RESULT 5
US-10-451-168-49
; Sequence 49, Application US/10451168
; Publication No. US20040091969A1
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50039
; CURRENT APPLICATION NUMBER: US/10/451,168
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: PCT/US01/49232
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,710
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/257,048
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/260,482
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/264,922
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/266,797
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/276,988
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/281,535
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/289,622
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-451-168-49
Alignment Scores:
Pred. No.: 0 Length: 1662
Score: 2883.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 17 Gaps: 0
US-10-044-205a-2 (1-553) x US-10-451-168-49 (1-1662)
QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
Db 1 ATGGTGACATGGGGGCGCTCGACAACTGATCGCAACCGCCTTACCTGACAGCCCG 60
QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
Db 61 AAGCCCTCGACTGCGACGCAAGAGCTGCGCGGGCGGCTGAGCTGACCTGACCTG 120

QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
Db 121 GGGCTGACAGGGCTGCGCGAGCTCCGCCAGAGCTGTCCCTGAACCTTCCACAGCTGTGT 180
QY 61 GlnGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
Db 181 GAGCAGACGCCCATCGGTGCGCGCTCTCCGTGACTTCTAGCCACAGTCCCAAGTTC 240
QY 81 ArgGlyAlaAlaThrPheLeuGlnAspValGlnAsnTPGluLeuAlaGluGluPro 100
Db 241 CGCAAGGGCGCAACTTCTTAGAGAGAGTGCAGACATGGAGCTGGCGCAAGAGGAGCC 300
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
Db 301 ACCAAGACACGCCCTGAGGGGCTGTGGCCACTTGTGGATGTCCTTGGCCCGGG 360
QY 361 AACCCGCAACCTTCTCCTCAGCCAGGCGTGGCCACCAAGTCCCAAGCAGCACTGAG 420
QY 141 GlnGlnArgValAlaAlaValThrLeuArgValAlaGluAlaMetAlaPheLeuGln 160
Db 421 GAAGAGCAGTGTGCTGAGTACGCTGTGCCAGAGCTGAGCCATGCTTCTTGCAGAG 480
QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
Db 481 CAGCCCTTTAAGATTTCTGTGACAGCGCTTCTACGACAGTTTCTGACAGGAACTC 540
QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
Db 541 TTCGAGATGCAACAGTGCAGACAGTACTCAGTTCAAGAGTGGTGGGAAAGT 600
QY 201 GlyPheGlyGluValGlyAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
Db 601 GGTGTTGGGAGGATATGTCGCTCCAGGTAAACCTCGGAAAGATGATGCTGTAG 660
QY 221 LysLeuAspLysLysArgLeuLysAlaLysGlyGlyLysMetAlaLeuLeuGlnLys 240
Db 661 AATCGGACAGAGAGCGGCTGAGAGAAAGATGCTGCTTGGGAAAG 720
QY 241 GluIleLeuGlnLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGlnSer 260
Db 721 GAATCTTGGAGAGGCTCAGACGCCCTTTCATGTCCTCGGCGCTTATGCTTGAAGC 780
QY 261 LysThrHisLeuCysValLeuValMetSerLeuMetAsnGlyLysAspLeuLysPheHisIle 280
Db 781 AAGACCATCTCTGCTGTGTATGATGAGCTGTATGAGGGAGAGCTCAAGTTTCAATC 840
QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
Db 841 TACAACTGGGAGCGGCTGCTGAGCATGAGCGGGGTATCTTTATCTGGCCAGATA 900
QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
Db 901 GCCTGTGGATGCTGCACCTCATGAACTCGGCATGCTGTATGGGACAGAGGCTTGA 960
QY 321 AsnValLeuLeuAspSerLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaGlu 340
Db 961 AATGTGCTTCTGATATACCTCGGCACTGACAGGTATCTGACCTCGGGGCTGCGCTGAG 1020
QY 341 MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
Db 1021 ATGAAAGGTGGCAAGGCCATCACCCAGAGGGCTGGAAACCAATGTTATCATGCTCTGAG 1080
QY 361 IleLeuMetGluLysValSerLysTyrProValAspTrpPheAlaMetGlyCysSer 380
Db 1081 ATCTTAATGAGAAAGGTAAAGTATTTCTATCTGAGCTGTGCACTGTGCAAGGATGCGC 1140
QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGlnLysValSerLys 400
Db 1141 ATTATTAATGTTCTCTGAGACAGCACTTCAAAAGATTACAGAGAAAGCTGACGTAA 1200
QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420

Db 1201 GAGATCTGAAACAAAGAACTCGCAAGACGAGGTCAAAATCCACATGATTAATCTTCAACA 1260
QY 421 GUGUUAUAlayAspIleCysArgLeuPheLeuAlaIysProGluGlnArgLeuGly 440
Db 1261 GAGGAAGCAAAAGATATTTGACAGCTCTTTCTTGCTTAAGAAACGACGAAAGCTTTAGGA 1320
QY 441 SerArgGluIysSerAspAspProArgIysHisPhePheIysThrIleAsnPro 460
Db 1321 AGCAGAGAAAGTGTGATGATCCAGAAACATCATTTCTTTAAACATCAATCTTCCCT 1380
QY 461 ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValValTyrAla 480
Db 1381 CGCTGGAAGCTGGCTTAATGAAACCCCATTTGTGCCAAGCCCTTGAGTGCTTATGACC 1440
QY 481 LysAspIleAlaGluIleAspAspPheSerGluValArgIleValGluPheAspAspLys 500
Db 1441 AAGAGATCGCTGAATGATGATTTCTGTGAGGTTGCGGGGGTGGAAATTGATGACAA 1500
QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGlu 520
Db 1501 GATAGCAGTCTTCAAAAACCTTTGCGACAGGTGCTGTTCTATAGCATGGCAGGAAGA 1560
QY 521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
Db 1561 ATTATGAAACGGGACTGTTTGAGAACTGATGACCCCAACAGACCTACGGGTGGAG 1620
QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeu 553
Db 1621 GAGGTAATTCATCCAGCTGCGGTGTTTGTATTG 1659

RESULT 6

US-10-217-745-5
; Sequence 5, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20030004328A1 Human G-Coupled Protein Receptor Kinases and
; TITLE OF INVENTION: Polynucleotides
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 2249
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-745-5

Alignment Scores:

Pred. No.: 0 Length: 2249
Score: 2883.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
DB: 15 Gaps: 0

US-10-044-205A-2 (1-553) X US-10-217-745-5 (1-2249)

QY 1 MetValAspMetGlyAlaLeuAspAsnIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
Db 354 ATGATGACATGAGGAGCCCTGGAACAATCCGCAACCGCCCTACCTGCAAGCCCG 413
QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
Db 414 AAGCCCTCGAATGAGACGAAAGCTGCAAGCGCGCGCGGCGTGAAGCTTGGCCCTGCCC 473

QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
Db 474 GGGCTGCAAGGGCTGCGCGAGACTCCGCAAGAGCTGTGCTTGAATCTTCCACAGCTGTGT 533
QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
Db 534 GAGCAGAGCCCATGCTGCGCGCTCTTCCGTGATCTTCAAGCCACATGCGCCACGCTC 593
QY 81 ArgIysAlaIleThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluIlePro 100
Db 594 CGCAAGCGGCAACCTTCTTGAAGAGAGTGCAGAACTGGAGAGCTGCGCCAGAGAGAGACC 653
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
Db 654 ACCAAAGACAGCGCGCTGCAAGGCGCTGTCGACCTTGTGCAAGTCTGCGCCCTCCGCG 713
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
Db 714 AACCCGCAACCTTCTTCAAGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 773
QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
Db 774 GAAGAGCAGTGGCTGCAAGTGCAGCTGCGCAAGCTGAGGCGCATGCTTCTTGGCAAG 833
QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
Db 834 CAGCCCTTTAAGGATTCGTGACAGGCGCTTCTCAAGCAAGTTCTGCAAGTGGAACTC 893
QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuLysGly 200
Db 894 TTCAGAGATGCAACAGTGCAGCAACATCTTCACTGATGTCAGACAGTGTGGGAAAGT 953
QY 201 GlyPheGlyGluValCysAlaValAlaGlnValLysAsnTrpGlyLysMetTyrAlaCysLys 220
Db 954 GGTTTGGGAGGATATGTCCTGCTCAGAGTGAAGAAACATCGGAAGATGThTGCCTGTAG 1013
QY 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGlyGlyMetAlaLeuLeuGluLys 240
Db 1014 AAATCGGCAAGAAAGGCGCTGAAGAAAGGTTGGCGAAGATGCGCTTCTTGGAAAG 1073
QY 241 GluIleLeuGlnLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
Db 1074 GAAATCTTGGAGAGAGGTGAGAGCGCTTCAATGCTCTCTCGGCGCATGCTTTAGAGC 1133
QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyLysAspLeuLysPheHisIle 280
Db 1134 AAGACCATCTTCTGCTTGTCTATAGCTGATGATGGGGAGACCTCAAGTTCACATC 1193
QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
Db 1194 TCAACCTGGGCGAGCGGTGCGCTGACATAGCGCGGTGATCTTTACTGCGCCAGATA 1253
QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
Db 1254 GCGTGTGAGTGTGACCTTCATGAACCTGCGATCGTATCGGAGCAAGAGCTTAG 1313
QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
Db 1314 AATGCTCTTGGAGTACCTCGCAACTGCAAGTTATCTGACCTGGGGCTGGCGCTGAG 1373
QY 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
Db 1374 ATGAAGGATGGCAAGCCATCAACCAAGAGGCTGGAACCAATGATTACATGCTCTAG 1433
QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
Db 1434 ATCCAAATGAAAGGTAAGTTATCTCATCTGAGACTGTTGCAAGGAGGAGAGC 1493
QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
Db 1494 ATTATGAAATGTTGCTGCGACGAACCATTCAAAGTTATCAAGAGAAAGTCTGATAA 1553
QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420

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Db      1554 GAGGATCTGAGCAAGAACTCTGCAAGACGAGTCAAAATTCAGAGATGATTAATTCACG 1613
QY      421 GUGUUAUUAUyAsp11eCySaRgleuPheleuAluYslySProGluGlnArgLeuGly 440
Db      1614 GAGGAGCAAAAGAAATTTGGAGCTCTTCTTGCTAGAGAAACAGAGCAAGCTTAGCA 1673
QY      441 SerArgGluUySerAspAspProArgLysHsiSphPheUyThrI1AsnPhaPro 460
Db      1674 AGCAGGAAAAGTCTGATGATCCAGGAAACATCTTTCTTAAACATCACTTCTCT 1733
QY      461 ArgLeuGluAlaGlyLeuIleGluProPropheValProAspProSerValIyAla 480
Db      1734 CGCTGGAGAGCTGACCTTAATTGAACCCCATTTGGCCAGACCCCTTGAGTTTATGCC 1793
QY      481 LysAsp11eAlaGluI1leAspAspPheSerGlyValArgGlyAlaGluPhaAspLys 500
Db      1794 AAAGCATGCTGGAATTTGATTTCTCTGAGGTCGGGGGGTGGAAATTTGATGACAA 1853
QY      501 AspLysGlnPhePheLysAsnPhaAlaThrGlyAlaValProI1eAlaTrpGlnGlu 520
Db      1854 GATAGCATTTCTTAAACCTTGGCAGAGGTGCTGTTCTTATGACATGGCAGAGAA 1913
QY      521 I1eIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCyseGlu 540
Db      1914 ATTATGAAACGGAGCTGTTGAGGAAGTGAATGCCCAAGACCTTACGGGTTTGAG 1973
QY      541 GluGlyAsnSerSerLysSerGlyValCysLeuLeu 553
Db      1974 GAGGTAATTCATCCAACTGCGCTGTGTGTATTG 2012

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RESULT 7

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US-09-964-469-1
; Sequence 1, Application US/09964469
; Patent No. US2002034803A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636DIY
; CURRENT APPLICATION NUMBER: US/09/964,469
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-09-964-469-1

```

Alignment Scores:

```

Pred. No.: 0 Length: 1662
Score: 2876.00 Matches: 551
Percent Similarity: 99.64% Conservative: 0
Best Local Similarity: 99.64% Mismatches: 2
Query Match: 99.55% Indels: 0
DB: 9 Gaps: 0

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US-10-044-205A-2 (1-553) x US-09-964-469-1 (1-1662)

```

QY      1 MetValAspMetGlyAlaLeuAspAsnLeuI1eAlaAsnThrAlaTyLeuGlnAlaArg 20
Db      1 ATGGTGGACATGGGGCCCTGACAACTGATCGCAACCGCCCTACCTGAGCCCGG 60
QY      21 LysProSerAspCyAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
Db      61 AAGCCTCGGACTGGACAGCAAGAGCTGACGGCGGGCGGTAGCTTGGCCCTGCCCC 120

```

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QY      41 GlyLeuGlnGlyCysAlaGluLeuArgGlnTyLeuSerLeuAsnPhaSerLeuCys 60
Db      121 GGGCTGCAAGGGCTGCCGAGCTCCGACAGACTGTCTCTGAACCTTCCACAGCTGTGT 180
QY      61 GUGUUGlnProI1eGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
Db      181 GAGCAGCAGCCCATTCGGTGGCCGCTCTTCCGTGACTTCTTACAGCAGAGGCCCATC 240
QY      81 ArgLysAlaAlaThrPheLeuGlnAspValGlnAsnTrpGluLeuAlaGlnGluPro 100
Db      241 CGCAAGCGGCAACTTCTTACAGAGAGCTGACAGACTGAGAGCTGCGCAGAGAGAGCC 300
QY      101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
Db      301 ACCAAGACAGCCGCTGACGGGCTGTGGCCACTTGTGGAGTGGCCCTTCCCGGGG 360
QY      121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
Db      361 AACCCGCAACCTTCTCTCAGCCAGGCGCTGCGCCACCAAGTCCCAAGCAGCCACAG 420
QY      141 GUGUArgValAlaAlaValaThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
Db      421 GAAGAGCGAGTGGCTGCACTGACCTGCGCAAGGCTGAGGCGCATGCTTTCTTGAAG 480
QY      161 GlnProPheLysAspPheValThrSerAlaPheTyAspLysPheLeuGlnTrpLysLeu 180
Db      481 CAGCCCTTTAAGATTTTGTGACCAAGGCTTCTTACAGCAAGTTTCTGCAAGTGAATC 540
QY      181 PheGluMetGlnProValSerAspLysTyPheThrGluPheArgValLeuGlyLysGly 200
Db      541 TTCAGATGCAACCAAGTGCAGACAACTACTTCACTGAGTTCAAGAGTGGCGGAAAGT 600
QY      201 GlyPheGlyValAlaValAlaGlnValLysAsnThrGlyLysMetTyAlaCysLys 220
Db      601 GGTGTTGGGAGGTATGTGCGCTGCAAGTAAACACTGGAGAAAGATGTATGCTGTAG 660
QY      221 LysLeuAspLysLysArgLeuLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
Db      661 AATCGGACAAAGAGGGCTGACAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY      241 GUGULeuGlnLysValSerSerProPheI1eAlaSerLeuAlaTyAlaPheGlnSer 260
Db      721 GAATCTTGGAGAGGTGACGAGCGCTTTCATGTCTCTGCGCTTATGCTTTCAGAGC 780
QY      261 LysThrHisLeuGlySerValMetSerLeuMetAsnGlyLysAspLeuLysPheHisLe 280
Db      781 AAGACCAATCTCTGCTGTGTATGAGCTGTATGAGAGAGAGAGAGAGAGAGAGAGATC 840
QY      281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValI1ePheTySerAlaGlnIle 300
Db      841 TACCAAGTGGGCAAGGCTGTGCTGGAATGAGCCGSGTGAATCTTTATCTGGCCAGATA 900
QY      301 AlaCysGlyMetLeuHisLeuHisGlnLeuGlyI1eValTyAlaArgAspMetLysProGlu 320
Db      901 GCGTGTGGAGTCTGACCTCCATGAACCTGCGCATGCTATCGGACAGAGAGAGCTGAG 960
QY      321 AsnValLeuLeuAspLysPheGlyAsnCyAspArgLeuSerAspLeuGlyLeuAlaGlu 340
Db      961 AATGTGCTCTGATATACCTTGGCAACTGCGAGGTTTCTGACTGGGGGCTGGCGCTGAG 1020
QY      341 MetLysGlyLysPheProI1eThrGlnArgAlaGlyThrAsnGlyTyMetAlaProGlu 360
Db      1021 ATGAAAGGTGGCAAGCCCATCCACCAAGAGGCGTGGAAACATGTTATCAATGAGCTCTAG 1080
QY      361 I1eLeuMetGluLysValSerTySerTyProValAspTrpPheAlaMetGlyCysSer 380
Db      1081 ATCTTAATGGGAAAGGTATGATTCTTATCTTATCTGAGACTGTTTGCATGGAGAGCAGC 1140
QY      381 I1eTyGlnMetValAlaGlyArgThrProPheLysAspTyLysGlnLysValSerLys 400
Db      1141 ATTATTAATAGGTGTCTGAGAGACCAATTCATCAAGATTAACAGAGAAAGGTCTGATTA 1200
QY      401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPhaThr 420

```

Db 1201 GAGGATCTGAAGCAAAAGACTGCAAGACAGAGGTCAAAATTCACAGATTAATCTTCACA 1260
 QY 421 GUGUUAUAlAspIleCysArgLeuPheLeuAlaIysIleProGluGlnArgLeuGly 440
 Db 1261 GAGGAAAGCAAAAGATATTTCAGAGCTCTTCTGGCTTAAGAAACCGAGAACCTTTAGGA 1320
 QY 441 SerArgGluIleSerAspAspProArgIleHisIlePhePheLeuThrIleAsnPro 460
 Db 1321 AGCAGAGAAAGAGTCTGATGATCCAGAGAAACATCATTTCTTAAGATCAATCTTCT 1380
 QY 461 ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValIleTyrAla 480
 Db 1381 CGCTGGAGAGCTGGCTTAATTAAGACCCCATTTTGGACAGACCTTCAGGCTTTATGCC 1440
 QY 481 LysAspIleAlaGluIleAspAspPheSerGluValArgIleValGluPheAspAspLys 500
 Db 1441 AAGACATCTGCTGAATTAATTAATTTCTCTGAGGTTGGGAGGTGGAATTTGATGACAA 1500
 QY 501 AspLysGlnPhePheLeuAsnPheAlaThrGlyAlaValProIleAlaIleProGlnGlu 520
 Db 1501 GATAGCAGTCTTCAAAACCTTGCGACAGGTGCTGTTCTTAATGATGGCAGAGAA 1560
 QY 521 IleIleGluThrGlyLeuPheGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
 Db 1561 ATTATGAAACGAGACTGTTTGAAGACTGATGACCCCAACAGACCTTACGAGGTGTGAG 1620
 QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeu 553
 Db 1621 GAGGATATCTCAAGCTGAGCTGCTGTTGTTGTTATG 1659

RESULT 8

US-10-425-962-1
 ; Sequence 1, Application US/10425962
 ; Publication No. US20030180786A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GUEGLER, Karl et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; FILE REFERENCE: C1000636D1V2
 ; CURRENT APPLICATION NUMBER: US/10/425,962
 ; CURRENT FILING DATE: 2003-04-30
 ; PRIOR APPLICATION NUMBER: 09/964,469
 ; PRIOR FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: 09/738,894
 ; PRIOR FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: 60/208,331
 ; PRIOR FILING DATE: 2000-06-01
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1662
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-425-962-1

Alignment Scores:

Pred. No.: 0 Length: 1662
 Score: 2876.00 Matches: 551
 Percent Similarity: 99.64% Conservative: 0
 Best Local Similarity: 99.64% Mismatches: 2
 Query Match: 99.55% Indels: 0
 DB: 15 Gaps: 0

US-10-044-205a-2 (1-553) x US-10-425-962-1 (1-1662)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
 Db 1 ATGTGTGACATGAGGAGGCTGTCGACAACTGATCCGCAACGCGCTTACCTGCGAGGCGCG 60
 QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40

Db 61 AAGCCTCGGACTGCGACAGCAAAAGCTGACAGCGCGCGCGCTGATGCTGCGCTGCC 120
 QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnIleLysLeuSerLeuAsnPheIleSerLeuCys 60
 Db 121 GGGCTGAGGGGCTGGCGGAGAGCTCCCGAGAGCTGTCTTGAATCTTCACAGCTGTGT 180
 QY 61 GlnGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
 Db 181 GAGCAGAGCCATCGGTGCGCGCTCTTCGCTGACTTCCAGCCACAGTGGCCACGCTTC 240
 QY 81 ArgIleAlaIleThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGlyPro 100
 Db 241 CGCAAGCGGCAACCTTCTTAAGAGAGCGTGAAGAACTGGAGCTGGAGAGAGAGAGCC 300
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 Db 301 ACCAAACACGCGCGCTGAGAGGCTGTGGCTCACTTGTGAGTCCCTGCGCGG 360
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
 Db 361 AACCCTGCAACCTTCTCAGCCAGGCGGTGGCCACCAAGTGCACAGACACCACTGAG 420
 QY 141 GlnGluArgValAlaAlaValThrLeuArgIleValAlaMetAlaPheLeuGlnGlu 160
 Db 421 GAAGAGGAGTGTGAGTGAAGCTGGCCAAAGCTGAGGCTGAGGCTTCTTGAAGAG 480
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
 Db 481 CAGCCCTTAAGATTTGTGTACACGCGCTTCTTACCAAGATTTCTGAGAGGAAATC 540
 QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
 Db 541 TTCAGATGCAACAGTGTGACAGAGTCACTTCACTGAGTTCAGAGTGTGGGAGAGGT 600
 QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
 Db 601 GATTTTGGAGGTATGTCGCTGCGTCAAGTGAAGAAACATGGAGATGATGCTGTGAAG 660
 QY 221 LysLeuAspLysIleArgLeuLysIleLysGlyGlyGluLysMetAlaLeuLeuGlyLys 240
 Db 661 AAACCTGCAACAGAGCGGCTGAAGAGAAAGTGGCCAGAGAGTGTCTCTTGGAAAG 720
 QY 241 GlnIleLeuGlnLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
 Db 721 GAAATCTTGAAGAGAGTCAAGAGCCCTTCAATGTCTCTGCGCTATGCTCTTGAAGC 780
 QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyLysPheIleGlyLe 280
 Db 781 AAGACCATCTGCTGCTGTATGAGCTGATGAATGGGAGAGACTCAAGTTCACATC 840
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
 Db 841 TACACGTGGGACCGCGTGGCTTGACATGAGCCGGGAGTCTTAACTCGGCCACAGTA 900
 QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
 Db 901 GCGTGTGAGTGTGCTCACTTCATGAATCGGACATGCTATGCGGACATGAAGCCTGAG 960
 QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaGlu 340
 Db 961 AATGTGCTTGTGATGAGCTTGTGAGCTCACTGAGTATGATGAGCTGGAGCTGGAG 1020
 QY 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
 Db 1021 ATGAAGGTGGCAAGCCATCAACCAAGAGGCTGGAACCATGGTTACATGCTCTGAG 1080
 QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
 Db 1081 ATCTTAATGGGAAAGTATGATTAATCTTCTGAGCTGCTGCTTGCATGGAGATGACG 1140
 QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
 Db 1141 ATTATGAATGTGCTGAGACAGACCACTTCAAGATTCAAGAGAAAGTCACTGA 1200

QY 401 GluAspLeuValGlnArgThrLeuGlnAspGluValIleAspPheGlnHisAspAsnProThr 420
 Db 1201 GAGGATCTGACCAAGAAAGCTGCGACGAGCGGGCAAAATTCAGATGATTAATCTTACA 1260
 QY 421 GluGluAlaIleAspIleCysArgLeuPheLeuAlaIleValSerProGluGlnArgLeuGly 440
 Db 1261 GAGGAAGCAAAAGATATTGGAGGCTCTTCTGGCTAAGAAACGAGCAACGCTTAAGGA 1320
 QY 441 SerArgGluIleSerAspAspProAlaGlyHisHisPhePheThrIleAsnPro 460
 Db 1321 AGCAGGAAAGTCTGATGATCCAGAGAAACATATTCTTAAACATCAACTTCTCT 1380
 QY 461 ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValIleValAla 480
 Db 1381 CGCCTGGAAGCTGGCTGATTAATGAAACCCCATTTGGCCAGACCTTCCAGTGTATGCT 1440
 QY 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
 Db 1441 AAAGACATCGTGAATATTGATGATTTCTCTGAGGCTCGGGGGGTGGAAATTTGATGACAAA 1500
 QY 501 AspLysGlnPhePheLysAsnProAlaThrGlyAlaValProIleAlaIlePheGlnGlu 520
 Db 1501 GATPACCAATCTTCAAAAACCTTTCGACAGGCTCTTCTTCAATGACATGCGAAGAA 1560
 QY 521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
 Db 1561 ATATGAGAAACGAGACCTGTTTGAGAACGATGATACCCCAACGACCTACGGGTGTGAG 1620
 QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeu 553
 Db 1621 GAGGTAATTCATCCAGTCTGGCGTGTGTATTGTTATTG 1659

RESULT 9

US-10-072-012-273

Sequence 273, Application US/10072012

Publication No. US20040033493A1

GENERAL INFORMATION:

APPLICANT: Tcherev, Valizar
 APPLICANT: Spytek, Kimberly
 APPLICANT: Zernusen, Bryan
 APPLICANT: Patuturajan, Meera
 APPLICANT: Shinkets, Richard
 APPLICANT: Li, Li
 APPLICANT: Gangoli, Esha
 APPLICANT: Padigam, Muralidhara
 APPLICANT: Anderson, David W.
 APPLICANT: Rastelli, Luca
 APPLICANT: Miller, Charles E.
 APPLICANT: Gerlach, Valerie
 APPLICANT: Taupier Jr, Raymond J.
 APPLICANT: Gusev, Vladimir Y.
 APPLICANT: Colman, Steven D.
 APPLICANT: Wolenc, Adam R.
 APPLICANT: Pena, Carol E. A
 APPLICANT: Furtak, Katarzyna
 APPLICANT: Grose, William M.
 APPLICANT: Alsobrook II, John P.
 APPLICANT: Lepley, Denise M.
 APPLICANT: Rieger, Daniel K.
 APPLICANT: Burgess, Catherine E.
 TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 FILE REFERENCE: 21402-258
 CURRENT APPLICATION NUMBER: US/10/072,012
 PRIOR APPLICATION NUMBER: 60/265,102
 PRIOR FILING DATE: 2001-01-31
 PRIOR APPLICATION NUMBER: 60/265,514
 PRIOR FILING DATE: 2001-01-31
 PRIOR APPLICATION NUMBER: 60/265,517
 PRIOR FILING DATE: 2001-01-31
 PRIOR APPLICATION NUMBER: 60/265,412
 PRIOR FILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265,395
 PRIOR FILING DATE: 2001-01-31
 PRIOR APPLICATION NUMBER: 60/266,406
 PRIOR FILING DATE: 2001-02-02
 PRIOR APPLICATION NUMBER: 60/266,767
 PRIOR FILING DATE: 2001-02-05
 PRIOR APPLICATION NUMBER: 60/267,057
 PRIOR FILING DATE: 2001-02-07
 PRIOR APPLICATION NUMBER: 60/266,975
 PRIOR FILING DATE: 2001-02-07
 PRIOR APPLICATION NUMBER: 60/267,459
 PRIOR FILING DATE: 2001-02-08
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 1391
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO 273
 LENGTH: 1701
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-072-012-273

Alignment Scores:
 Pred. No.: 0 Length: 1701
 Score: 2823.50 Matches: 547
 Percent Similarity: 98.568 Conservative: 0
 Best Local Similarity: 98.568 Mismatches: 1
 Query Match: 97.738 Indels: 7
 Gaps: 3

US-10-044-205a-2 (1-553) x US-10-072-012-273 (1-1701)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaThrLeuGlnAlaArg 20
 Db 19 ATGTTGACATGAGGGGCTCTGACACCTGATGCGCAACCTGCTTCTGAGGCTCCG 78
 QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
 Db 79 AAGCCTCGAGTCTGAGAGCAAGCAAGAGCTGACGCGCGGCGGTGACCTGCGCC 138
 QY 41 GlyLeuGlnIleCysAlaGluLeuArgGlnLysLeuSerLeuAsnProHisSerLeuCys 60
 Db 139 GGGCTGAGGGGCTGCGCGAGCTCCGCGAAGCTGTCCCTGAACTTCCACAGCTGTGT 198
 QY 61 GlnGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
 Db 199 GAGCAGGAGCCCATGCTGCTGCGCCCTCTTCTGCTGCTTCTGCTGCTGCTGCTGCT 238
 QY 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluPro 100
 Db 259 CGCAAGCGGCAACCTTCTCTAGAGAGAGTGAAGACTGGAGCTGGCGAGGAGGAGCC 318
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 Db 319 ACCAAAGACGCGCTGCGAGGGCTGTGGCCACTTGTGGAGTGCCTTCCCTCCGCGG 378
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrGlu 140
 Db 379 AACCGCAACCTTCTCTGACGAGCGCTGGCCACCAAGTCCCAAGACACCACTGAG 438
 QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGln 160
 Db 439 GAAAGCGAGTGGCTGACGAGTCCGCAAGGCTGAGGCTGCTTCTTCAAGAG 498
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyraPheLysPheLeuGlnTrpLysLeu 180
 Db 499 CAGCCCTTAAGGATTTGTATCCAGCGGCTTCTTACCAAGATTTCTGAGGAGAACTC 558
 QY 181 PheGluMetGlnProValSerAspLysTyraPheThrGlnPheArgValLeuGlyLysGly 200
 Db 558 TTGAGATGACACAGTGTGAGACAGTACTTCACTGAGTTCAAGTGTGAGGAGAAAGT 618
 QY 201 GlyPheGlyGluValCysAlaValAlaGlnValIleAsnThrGlyLysMetTyraLys 220

Publication No. US2003004328A1
GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Wilganski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.
TITLE OF INVENTION: No. US2003004328A1 Human G-Coupled Protein Receptor Kinases and
TITLE OF INVENTION: Polynucleotides
TITLE OF INVENTION: Encoding the Same
FILE REFERENCE: LEX-0147-USA
CURRENT APPLICATION NUMBER: US/10/217,745
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: US/09/802,117
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1062
TYPE: DNA
ORGANISM: homo sapiens
US-10-217-745-3

Alignment Scores:
Pred. No.: 2,44e-215 Length: 1062
Score: 1801.00 Matches: 349
Percent Similarity: 99.71% Conservative: 0
Best Local Similarity: 99.71% Mismatches: 1
Query Match: 62.34% Indels: 0
DB: Gaps: 0

US-10-044-205A-2 (1-553) x US-10-217-745-3 (1-1062)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
Db 1 ArgGtGACATGGGGGCGCTGGACACCTGATGCCACACCGGCTTCTGGACGGCCGG 60
QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
Db 61 AAGCCCTGGACCTGGACACGACAGAAAGCTGCACGGCGGGCGGCGTACCTGGCCCTGCCC 120
QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnProHisSerLeuCys 60
Db 121 GGGCTGACAGGGCTGCGCGGAGCTCGGCACAAAGCTCTCCCTGAATCCACACCCCTGT 180
QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrAlaProThrPhe 80
Db 181 GAGCGACAGCCCATCGGTGCGCGCTCTCCGTGACTTCTTACGCCACAGTCCACGCTTC 240
QY 81 ArgLysAlaAlaThrPheLeuGlnAspValGlnAsnTrpGluLeuAlaGluGlnGlyPro 100
Db 241 CCGAAGCGGCGAACCTTCTTAAGSACGTGCACAAATCGGGAAGCTGGCGAGGAGACCC 300
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
Db 301 ACCAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTGTGGCAGTGGCCCTCGCCGGGG 360
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
Db 361 AACCCGCAACCTTCTCAGCCAGGCGGTGGCCACCAAGTGGCAGACGACCACTAGG 420
QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
Db 421 GAAGGCGAAGTGGCTGCATGACGTGGCCCAAGGCTGAAGGCGATCTTGGCAAGAG 480
QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
Db 481 CAGCCCTTAAAGATTTCGTGACCAAGCCCTTCCACGACAAATTTCTGCAGTGGAAATCC 540
QY 181 PheGluMetGlnProValSerAspLysTrpPheThrGluPheArgValLeuGlyLysGly 200
Db 541 TTCGAGAGCAACCAAGTGCACAAAGTACTTCACTGAAGTTCAAGGTGCTGGGAAAGGT 600
QY 201 GlyPheGlyGluValCysAlaValGlnAlaValLysAsnThrGlyLysMetTyrAlaCysLys 220

Db 601 GGTITGGGAGGTATGTCCGTCACAGTGAACAAACATCGGAGATGATGCTGTAAAG 660
 QY 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGlyLysMetAlaLeuLeuGlnLys 240
 Db 661 AAATGGACAAAGAACCGCTGAAAGAAAGAGTGGCAAGAAAGTGGCTCTCTTGGAAAG 720
 QY 241 GlnLysLeuGlnLysValSerSerProPheLeuSerLeuAlaTyrAlaPheGlnSer 260
 Db 721 GAAATCTTGGAGAGAGTACAGAGCCCTTCATTGCTCTCTGCGCAATGACCTTGGAGAG 780
 QY 261 LysThrHisLeuCysLeuValMetSerLeuMetLysGlnLysLysLeuPheHisLeu 280
 Db 781 AAGACCATCTCTGCTTGTGATGACCTCGATGATGAGGAGAACCTCAAGTTCACATC 840
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValLysPheTyrSerAlaGlnLeu 300
 Db 841 TACACGTGGGCAACCGCTGGCAATGAGCCGGTGTATCTTTTACTCGACCGCAATG 900
 QY 301 AlaCysGlyMetLeuHisLeuHisGlnLeuGlyLysValTyrArgAspMetLysProGln 320
 Db 901 GCGTGGGATGCTGCAACCTTCATGAATCGGCACTGCTATCGGAGACATGAGCCCTGAG 960
 QY 321 AsnValLeuLeuAspAspLeuGlyLysCysArgLeuSerAspLeuGlyLeuAlaValGln 340
 Db 961 AATGTCCTTCTGAGATGACCTCGCAACCTGCAAGTTATCTGACCTGGGCGCTGGCTGGAG 1020
 QY 341 MetLysGlyGlyLysProLeuThrGlnArg 350
 Db 1021 ATGAAGGTCGCAAGCCCATCACCCAGAG 1050

RESULT 11

US-09-964-469-3
 ; Sequence 3, Application US/09964469
 ; Patent No. US20020034803A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GUEGLER, Karl et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; FILE REFERENCE: CLO00636D1V
 ; CURRENT APPLICATION NUMBER: US/09/964,469
 ; CURRENT FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: 60/208,331
 ; PRIOR FILING DATE: 2000-06-01
 ; PRIOR APPLICATION NUMBER: 09/738,894
 ; PRIOR FILING DATE: 2000-12-18
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 36651
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(36651)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-964-469-3

Alignment Scores:

Pred. No.: 1,32e-178 Length: 36651
 Score: 1528.00 Matches: 349
 Percent Similarity: 41.40% Conservative: 0
 Best Local Similarity: 41.40% Mismatches: 1
 Query Match: 52.89% Indels: 493
 Gaps: 1

US-10-044-205A-2 (1-553) x US-09-964-469-3 (1-36651)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuLeuAlaAsnThrAlaTyrLeuGlnAlaArg 20
 Db 2076 ATGTCGACATGAGGAGGCGCTGAGACAACTGATGCGCAACACCGCTTACTGCGAGCGCGG 2135
 QY 21 LysProSerAspCysAspSerLysGlnLeuGlnArgArgArgSerLeuAlaLeuPro 40

Db 2136 AAGCCCTCGACCTGCGACAGCAAGAAAGACTCAGCCGCGGCTGACCTGCGCTGCC 2195
 QY 41 GlyLeuGlnGlyCysAlaGlnLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
 Db 2196 GGGCTGCAAGGCTGCGCGGAGCTCGCCAGAAAGCTGCTCCGAACTTCCACAGCCCTGTGT 2255
 QY 61 GlnGlnGlnProLysArgLeuPheArgAspPheLeuAlaThrValLysProPhe 80
 Db 2256 GAGCAGAGCCCATCGGTGCGCGCTTCTCCGTAATCTTCTAGCCACAGTGCACGTTTC 2315
 QY 81 ArgLysAlaAlaThrPheLeuGlnAspValGlnAsnTrpGlnLeuAlaGlnGlnPro 100
 Db 2316 CGCAAGGGCGCAACCTTCCCTAGAGAGAGTCAAGAACTGGAGCTGCGCCAGAGAGAGCC 2375
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 Db 2376 ACCAAAGACAGCGCGCTGCGAGGCTGTGCGCACCTTGTGCAAGTGCCTGCCCGGGG 2435
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGln 140
 Db 2436 AACCCGCAACCTTCTCTGACGAGGCGGTGGCCACCAAGTCCCAAGACGACACCTAG 2495
 QY 141 GlnGlnArgValAlaAlaValThrLeuArgLysAlaGlnAlaMetAlaPheLeuGlnGln 160
 Db 2496 GAAAGCGAGTGGCTGCGACGTACGCTGCGCCAGGCTGAGGCCAAGGCTTTCTTGCAGAG 2555
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
 Db 2556 CAGCCCTTTAAGGATTTGTCGACAGCGCTTCTACGACAAAGTTTCTGCAAGTTCGAGGAAATC 2615
 QY 181 PheGlnMetGlnProValSerAspLysTyrPheThrGlnPheArgValLeuLysGly 200
 Db 2616 TTCCAGATGCAACCGTGTGACAGAACTTCTTCACTGAGTTCAAGATGCTGGGAAAGGT 2675
 QY 201 GlyPheGlyGln 204
 Db 2676 GGTITTTGGAGGTAAGTGTCTCCAGTAGCAGGCTGAAGGTGAAGCATGAGCATGA 2735
 QY 204 204
 Db 2736 AAGGGGTAATGTGCTTCTTTTAAATCGATTAAGTAATTCAGAC 2795
 QY 204 204
 Db 2796 CATATGAGAGATTTCTAGCCCGCTCTCCAGCCCTTCTTTGTGTGCCATGTGT 2855
 QY 204 204
 Db 2856 TGAATTAACACAAATGCGATGAGAGACAAAGCAAAATTTATCTTGGCAAGACTCT 2915
 QY 204 204
 Db 2916 GTCATGGTCTCATTAAGAAAGTGTGATGATCTCTGACACTTCAAGAGATGATAGCA 2975
 QY 204 204
 Db 2976 TGTGTGACAGAGATCTCCGTTCCCTTAATTGTGATTAAGAGCACTTAAGAAAA 3035
 QY 204 204
 Db 3036 TGATATTTTAAGAAAAATCTAATAGTAGCTGGGTGTGTGACATGGCTGTATCCAGCT 3095
 QY 204 204
 Db 3096 ACTTGGAGGCTGAAGCAGAGAAATCACTTAGCTGGAGGTGAGAGTTGAGTAGGCC 3155
 QY 204 204
 Db 3156 AAGATGTGCACTGCACTCCAGCTGGGTGACAGAGCAAGACTCAAAAAAAAAAAAAA 3215
 QY 204 204

[illegible]

Db	3336	CTGTGATTTAAATACATACATTAACGTGTTTAAATGTACATGACGTGGACCTTGACA	3339
Oy	204	-----	204
Db	3339	AATGCATGTGTGGTAAGACACACTGCATCTGGATCCAGACACTGCATCACCCTGT	3455
Oy	204	-----	204
Db	3455	GCCATTAAATAGTGCCTCCCATCCCTCTCTCCAGCCCTGACACACATAGTCCCG	3515
Oy	204	-----	204
Db	3515	TTTCTGCTCTAGGGATTTGGCATTTGGGGTGTTCACACAAATGTACCTTTGTGT	3575
Oy	204	-----	204
Db	3575	CTGGCTTCCTTACCTATTAGATGTGTTTGGGGTTCATTACACATGTAGCATGTGCA	3635
Oy	204	-----	204
Db	3635	TACTCATTCCTTTTATGTGGCTGTAAATTCATCGTATGTAGTACTACATTTCTAG	3695
Oy	204	-----	204
Db	3695	TAGCATTGATGTGTGTATGACACTTGGGGTGTTTTACCTTTTGGCATTTGTATGG	3755
Oy	204	-----	204
Db	3755	TGTGCTATTATGACACAGATATTGTGTGATCCTGTGTTTCAATTCCTTGGATTAT	3815
Oy	204	-----	204
Db	3815	GCCAGAGATGGAAATCTGTAGGGCATATGTGTACTATGTTAACTTTTCAAGAGACA	3875
Oy	204	-----	204
Db	3875	CCAACTTTCCACATTTTTTATTTCCACACAGAAATGCTTAAAGTTTGGATTTCCACA	3935
Oy	204	-----	204
Db	3935	TCTTCGCAACCTTGATATTTTCTGTATTTTGTAAAGGCTGCTAGTAGAGTGA	3995
Oy	204	-----	204
Db	3995	AGGAGTATGACATGTATGTGCCACTTTTCTTGAGAACTTTTATTACACTTACTC	4055
Oy	204	-----	204
Db	4055	CTTTCCTCAATGCCCAACATCTTTCCACACCACCTCCTCTTATCATCTCACCTCTCG	4115
Oy	205	-----ValCysAla	208
Db	4115	CAGTACCATTACTTCTTACCTCTTCTCTCTTTCTTCTCTTCAAGGTATGTCCGT	4175
Oy	208	IginValIlysAsnthrgIyIysMetYTrAlaCysIyIysLeuAspIyIysArgLeuIy	228
Db	4175	CGAGTGAAGAAACCTGGGAGATGTATGTCTGTGAAGAACTGGAAAGAGCGGCTGA	4235
Oy	228	sIyIyIysGIyGIyIyIysMetAlaLeuLeuGIyIyIysIleLeuGIyIyIysIser	248
Db	4235	GAGAAAGGTGGCAGAAAGATGGCTCTTTGGAAAGGAANTCTTGAGAGAGTCACGAC	4295
Oy	248	rProPheIleValIserLeuAlaYTrAlaPheGIuIserIyIysThrHisIleuCysIleuVal	268
Db	4295	CCCTTCATATGTCTCTGTGGCTTATGGCTTGTAGAGAGAAACCAATCTGTCCCTGTGAT	4355
Oy	268	tSerIleuMetAsnGIyGIyAspLeuIyPheHisIleYrAsnValGIyThrArgIyIy	288
Db	4355	GAGCTGATGATGTGGGGAGACCTTCAGTTCCACATCTTCAAGATGTGGGCAAGGCTGGCT	4415
Oy	288	uAspMetSerArgValIlePheYrSerAlaGlnIleAlaCysGIyMetLeuHisIleuHis	308

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Db      4416 GACATGAGCCGGGTGATCTTTTACTGCGCCAGATAGCCTGTGGAGTGTGACCTCCCA 4475
Qy      308 sctluenclyllevaityrargaspmetlvsprogluamvalleuenuaspbleugl 328
Db      4476 TGAAGTGGATCTCTTATCGGACATGAAAGCTGGAATGTCTTGTGATACCTGG 4555
Qy      328 yAencysargleuseraspbleuglyleualavalglumetlvsclglylvsprolleth 348
Db      4536 CAAGTCAGAGTTATTCACCTCGGGGCTGCGCTGTGAGATGAAAGGGTGGCAAGCCCATCAC 4595
Qy      348 rglmarg 350
Db      4596 CCAGAGG 4602

RESULT 13
US-10-325-430-2
/ Sequence 2, Application US/10325430
/ Publication No. US20030153525A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc
/ APPLICANT: Siles-Santiago, Imaculada
/ APPLICANT: Rosenfeld, Julie Beth
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
/ TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
/ FILE REFERENCE: MP101-294P1RNM
/ CURRENT APPLICATION NUMBER: US/10/325,430
/ PRIOR FILING DATE: 2002-12-19
/ PRIOR APPLICATION NUMBER: US 60/341,953
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 1737
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)...(1737)
US-10-325-430-2

Alignment Scores:
Pred. No.: 4.67e-150 Length: 1737
Score: 1283.50 Matches: 255
Percent Similarity: 65.49% Conservative: 96
Best Local Similarity: 47.57% Mismatches: 162
Query Match: 44.43% Indels: 23
DB: 15 Gaps: 8

US-10-044-205A-2 (1-553) x US-10-325-430-2 (1-1737)
Qy      7 leuaspantleuilealaenhrhalarleuclnlaalarglysproser---aspys 25
Db      7 CTGGAGAACATCGTGGCCAACTGCTGCTGTAAGCCGTCAGAGATATGGCAAA 66
Qy      26 AspserlysgluenargargargserleualaleuProglyleuglnglyys 45
Db      67 AAAAGTGTCTGAGTAAATAAGAAAGAGATACGACACCTGCTGTCAGCAGTGC 126
Qy      46 AlagluuarglngllyleuSerleuanshehiserleucysglnglnglnprolle 65
Db      127 AGTACCTTAGCATTCCTTCAAAAGATATAGCAGCTTTGTGACAGCAACGATA 186
Qy      66 glyargargleupheargaspheleualathrvalProthpharglysalalathr 85
Db      187 GGAAGACGTCTCTCAGGCACTCTGTGTATACCAAAACCCACTTAAAGAGGCCACTTGA 246
Qy      86 PheleugluaspvalglnaenhrghluenualagluclnglyProthlyasp----- 103
Db      247 TTCTTGATGACAGTGTGCGAATATGAAAGTTCGATGATAGAGACCGAAGTATGGGA 306
Qy      104 ---SeraleuenglnglyleuvalalathrcysalaserlaProalProglyanpro 122

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Db      307 CTGTCAATCTTATGATTAATCTTCAATGATTAAGTGGACCCCTTTTACGAAATACCT 366
Qy      123 GlnProPheleuserglnalavalalathrlyscysglnalalathrThrgluclnglu 142
Db      367 CCGAGT-----GTTGTGACAGATGTATGATTTGGAGACTAGAGAGAAC 411
Qy      143 ArgvalalavalThrleuarlysalal-----GluAlMetala 156
Db      412 -----CCTTCACAAAAGCCTTTGAGGATGACTAGAGTTGCCCATTAC 456
Qy      157 PheleuglnglnglnProthelysaephelvalThrserlahehyrAspdyephelu 176
Db      457 TACCTAAGAGGGGAAACCAATTTGAAGATTCAGAAAGCTCAATATTTTCTCCAGTTTGA 516
Qy      177 GlntrpLyseuPheglumetGlnProvalSeraspysrlyrPhehrclupharval 196
Db      517 CAATGAAATGCTGTGAAAGGCAACCCGTAACAAAGACACATTTAGCATTTACAGATT 576
Qy      197 leuuglylysglylyphegllylvalcysalavalglnvallyshantThrglyyMet 216
Db      577 CTAGAAAAGGCGGATTTGGAGAGTTTGCCTGTCAAGTGCAGCCACAGAGAAATG 636
Qy      217 TyrAlaCyslylyleuaspysrlyargleuylslyslglylylyMetala 236
Db      637 TATGCTGCAAAAAGCTACAAAAAAGAAATAAAGAAAGGAGAGAGCTATGAGCT 696
Qy      237 leuengllylysgluileuengllylyValSerSerProthelleyalserleualatyr 256
Db      697 CTAAATGAGAAAGAAATTTGCGAAGAAAGCAAGTAGATTGCTATTAAGTTAGCTTAC 756
Qy      257 AlaPhegluserlysrhnsleucysleuvalMetserleuMetasnlyglylyAspleu 276
Db      757 GCTATGAAACCAAGATGCTGTGCTGTGCTCAATTTGATGATGAGGAGGATTTTG 816
Qy      277 lysPhehislleuYAsnvalglyThrarglyleuasphehrargvalillePheTyr 296
Db      817 AAGTTTACATTTTAAACCTGGGCAATCCCGCTTTATATAGAGAGACCGGTTTCTAT 876
Qy      297 SeralaglnlealaCysglyMetleuhsleuhsleuhsleuclnglylleyalTyrArgasp 316
Db      877 GCTGACAGCTGTGTGGGCTTGGAGATTTACAGAGGAGAAAGATTTCTATACAGAGAC 936
Qy      317 MetlyProgluasnvalleuenuaspbleuglyyAencysargleuseraspbleugly 336
Db      937 TTGAAGCTGAGATATATCTCTGATGATCGTGACACATCCGCAATTCAGACCTGGT 996
Qy      337 leuualavalglumetlysglylyysprollethrharglialythransglyTyr 356
Db      997 TTGGCCACAGAGATCCAGAAAGACAGAGGTTTCAGAGAGAGTTGAAACGTGGCTAC 1056
Qy      357 MetAlaProgluileuMetgllyysValSerlyrSerlyrProvalAspTirPheala 376
Db      1057 ATGGACCTGAACTGTCAATATATGAA---AAGTATACGTTTATGTCGATTTGGTGGGA 1113
Qy      377 MetglyCysseriletyrglumetvalalaglyarghrProthelysaspTyrlysglu 396
Db      1114 CTGGGCTGTGATCTATGAAATGATTCAGGACATTCCTCATTCATAAAATACCAAGAG 1173
Qy      397 lysvalserlysgluaspbleuysglnarghrleuhsleuhsleuhsleuhsleuhsleu 416
Db      1174 AAAGTCAATGAGAGAGAGTGCATCAAAAGATCAAGAAATGATCCAGAGAGATTTCT--- 1230
Qy      417 AspasnphethrghluclualalyaspilleCysargleupheleualalylyspProglu 436
Db      1231 GAGAAATTTCAAGAGATGCCAAATCTATCTCAGAGATTTACACCAAGATCCAGAC 1290
Qy      437 Glnargleuglyserarg---GluysSeraspaspProalglyshisshisPhehels 455
Db      1291 AAGCGGCTGGGCTGAGGGGCGAGAGGCGCTGGGCTGGAAGCAGACCCCGTGTCAAG 1350
Qy      456 ThrileasnphethrargleugluaglyleuileglnuprothphelvalProaspPro 475
Db      1351 GACATCAATTCAGAGGCTGAGAGCAAAACATGCTGAGGCCCTTTCTGCTGATCT 1410

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QY 476 SerValValTyrAlaLysAspIleAlaGlnIleAspAspSerGluValArgGlyVal 495
 Db 1411 CARGCGTTACTGTAGAGAGCTCTCGATATCCAGCATGTTCCGGCGGTAAAGGATC 1470
 QY 496 GluPheAspAspLysAspLysGlnPhePheLysAsnAlaThrGlyAlaValProIle 515
 Db 1471 TACCTGACACCGCATGTAAGACTTCTATGCTCGGTTTCTACCGGCTGTCTCCATC 1530
 QY 516 AlaTrpGlnGluGlnIleIleGlnThrGlyLeuPheGlnIleuAsn 531
 Db 1531 CCCTGGCAGATGAGATGATCGATCCGGTGTTCCTCAAGACATCAAC 1578

RESULT 14

US-10-325-430-1
 ; Sequence 1, Application US/10325430
 ; Publication No. US20030153525X1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc
 ; APPLICANT: Siles-Santiago, Immaculada
 ; APPLICANT: Rosenfeld, Julie Beth
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
 ; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
 ; FILE REFERENCE: MP101-294P1RNM
 ; CURRENT APPLICATION NUMBER: US/10/325,430
 ; PRIOR FILING DATE: 2002-12-19
 ; PRIOR APPLICATION NUMBER: US 60/341,953
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 2113
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 US-10-325-430-1

Alignment Scores:

Pred. No.: 6,41e-150 Length: 2113
 Score: 1283.50 Matches: 255
 Percent Similarity: 65.49% Conservative: 96
 Best Local Similarity: 47.57% Mismatches: 162
 Query Match: 44.43% Indels: 23
 DB: 15 Gaps: 8

US-10-044-205A-2 (1-553) x US-10-325-430-1 (1-2113)

QY 7 LeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArgLysProSer---AspCys 25
 Db 261 CTCGAGACATCTGGGCAATCTCGCTGCTGAAACCGGTCAAGAGATATGCGACA 320
 QY 26 AspSerLysGlnLeuArgArgArgSerLeuAlaLeuProGlyLeuGlnGlyCys 45
 Db 321 AAAAGTGTCTGATGTAATAAATGAGAGATCTGACACTGCTCTGACCCAGTGC 380
 QY 46 AlaGlnLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCysGlnGlnGlnProIle 65
 Db 381 AGTAGCTTAGACATTCATTGAAAGATTATAGCAGCTTGTGGAACAGCAACGATA 440
 QY 66 GlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThr 85
 Db 441 GGAAGACGTCTCTTCAAGGAGTTCGTGTATCCAAACCACTTAAAGAGCATTGAA 500
 QY 86 PheLeuGlnAspValGlnAsnTrpGlnLeuAlaGlnIleGlyProThrLysAsp----- 103
 Db 501 TTCTTGAGTACAGTGGAGAGATATAGAGTCCGATGATGAGAGACCAAGATGTTGGA 560
 QY 104 ---SerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGlyAsnPro 122
 Db 561 CTGTCAATCTTATAGATATCTTCAATGATATAGTGGAGCCCTTTACCGAAATACCT 620
 QY 123 GlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlnGlnGlu 142

Db 621 CCAGAT-----GTTGACAGAAATGATGATTGGAGCTGAGAGAGAGAC 665
 QY 143 ArgValAlaAlaValThrLeuArgLysAla-----GluAlaMetAla 156
 Db 666 -----CCTTCCAAAAAGCCTTTGAGGAATGACTAGAGTTCCCATAC 710
 QY 157 PheLeuGlnGlnIleProPheLysAspPheValThrSerAlaPheTyrAspPheLeu 176
 Db 711 TACCTAAGAGGGAACATTTGAAAGATACCAAGAAACCTATATTTTCTCAGTTT 770
 QY 177 GlnTrpLysLeuPheGlnMetGlnProValSerAspLysTyrPheThrGlnPheArgVal 196
 Db 771 CAATGAAATGCTGGAAAGCAACCCGTACAAAGAACATTTAGACATTACAGACTT 830
 QY 197 LeuGlyLysGlyLysPheGlyGlyValCysAlaValGlnValLysAsnThrGlyLysMet 216
 Db 831 CTAGGAAAGCGGATTTGGAGAGGTTTGGGCTGTCAAGGCGAGCGACAGAAAAATG 890
 QY 217 TyrAlaCysLysLysLeuAspLysLysArgLeuLysLysGlyGlyGlyMetAla 236
 Db 891 TATGCTGCAAAAAGCTCAAAAAAAGATTAAGAGAGAAAGGTAGACTGTGCT 950
 QY 237 LeuLeuGlnLysGlnIleLeuGlnLysValSerSerProPheIleValSerLeuAlaTyr 256
 Db 951 CTAATGAGAAAGAAATCTCGAAGAAAGTGCAAGTATCGAGTATGTTACCTAC 1010
 QY 257 AlaPheGlnSerLysThrHisLeuCysLeuValMetSerLeuMetSerGlnLysLeu 276
 Db 1011 GCTTATGAAACCAAGATGCTGTGTGTGCTGCTACCATTAAGATGAGAGGATTTG 1070
 QY 277 LysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyr 296
 Db 1071 AAGTTTCACTTATACACTGCGGCAATCCCGCTTGTATAGCAGAGACCGTTTCTAT 1130
 QY 297 SerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGlnLeuGlyIleValIlyrArgAsp 316
 Db 1131 GCTGCAAGCTGTGTGTGGGCTTGGAAGATTATACAGAGAAAGAAATTATATACAGAGAC 1190
 QY 317 MetLysProGlnAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerLysGln 336
 Db 1191 TTGAAGCTTGAATATTTCTCTTGAAGATCGTGACACATCGGATTTCAACCTCGGT 1250
 QY 337 LeuAlaValGlnMetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyr 356
 Db 1251 TTGGCCACAGAGATCCCAAGAGAGCAGAGGTTCCAGAGAAAGTGGAACTCGGCTAC 1310
 QY 357 MetAlaProGlnIleLeuMetGlnLysValSerTyrSerTyrProValAspTrpPheAla 376
 Db 1311 ATGGCACTGAAGTTGCAATATATGAA---AAGTATACGTTTATGCCATTTGGTGGGA 1367
 QY 377 MetGlyCysSerIleTyrGlnMetValAlaGlyArgThrProPheLysAspTyrLysGln 396
 Db 1367 CTGGCTGTGTGATCTATGAAATATATTCAGGAGCACTTCCATTCAAAAAATCAAGAG 1427
 QY 397 LysValSerLysGlnAspLeuLysGlnArgThrLeuGlnSerGlnValLysPheGlnHis 416
 Db 1428 AAAGTCAAAATGGAGAGAGTGCATCAAAAGATCAAGATATATACAGAGAGATTC--- 1484
 QY 417 AsnAsnPheThrGlnGlnAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGln 436
 Db 1485 GAGAGATTTCAAGAGATGCCAAATCTATCTCAGAGATTTATCTCCAAAGAAATCAAG 1544
 QY 437 GlnArgLeuGlySerArg---GlnLysSerAspAspProArgLysHisPheLys 455
 Db 1545 AAGCGGCTGGGCTGACAGGAGGAGAGCGGCTGGGAGTGAAGACAGACCCGTTTCAAG 1604
 QY 456 ThrIleAsnPheProArgLeuGlnAlaGlyLeuIleGlnProPheValProAspPro 475
 Db 1605 GACATCAACTTCAGAGAGGCTGAGAGCAACATGTCGAGAGCCCTTTCTGCTGATCT 1664
 QY 476 SerValValTyrAlaLysAspIleAlaGlnIleAspAspPheSerGlnValArgGlyVal 495
 Db 1665 CATCCGTTACTGTAGAGAGCTGAGATATGAGCAGTTCCTGCGGCTGAAAGGATC 1724

QY 496 GluPheAspAspLysAspLysGlnPhePheLysAsnPheAlaThrGluValAlaProIle 515
 DB 1725 TACCTGACACCCGACATGAAGACTTATGCTCGGTTCGACCGGGGTGTCTTCATC 1784
 QY 516 AlaTyrGlnGlnGlnIleIleGluThrGlyLeuPheGluGluLeuAsn 531
 DB 1785 CCTGGCAGATGATGATGATGATCGGGGTGTTCAAGACATCAAC 1832
 RESULT 15
 US-10-084-817-110
 / Sequence 110, Application US/10084817
 / Publication No. US20030119009A1
 / GENERAL INFORMATION:
 / APPLICANT: Susan Stuart
 / APPLICANT: Ted G. Nuchtern
 / APPLICANT: Sharon E. Pion
 / APPLICANT: Jason M. Shohet
 / TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
 / FILE REFERENCE: PA-0046 US
 / CURRENT APPLICATION NUMBER: US/10/084,817
 / PRIOR FILING DATE: 2002-02-25
 / PRIOR APPLICATION NUMBER: 60/270,784
 / NUMBER OF SEQ ID NOS: 365
 / SOFTWARE: PERL Program
 / SEQ ID NO 110
 / LENGTH: 2467
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: misc feature
 / OTHER INFORMATION: Incyte ID No. US20030119009A1 875668CB1
 US-10-084-817-110
 Alignment Scores:
 Pred. No.: 6,38e-146 Length: 2467
 Score: 1252.50 Matches: 259
 Percent Similarity: 63.07% Conservative: 103
 Best Local Similarity: 45.12% Mismatches: 162
 Query Match: 43.35% Indels: 50
 Gaps: 11
 US-10-044-205A-2 (1-553) X US-10-084-817-110 (1-2467)
 QY 7 LeuAspPheLeuIleAlaAsnThrAlaTyrIleGlnAlaArgLysProSerAspCysAsp 26
 DB 134 CTGGAACACATCGGCGCAACAGGTCTTGTGAAGCCAGGAGGAGGCGGAGGAGAG 193
 QY 27 SerLysGluLeuGlnArgArg--ArgArgSerLeuAlaLeuProGlyLeuGlnGlyCys 45
 DB 194 CGGAAAGGAGAAAGCAAGAAAGTGAAGAAATCTGAAGTCTCCCTCACTTACCGAGTGT 253
 QY 46 AlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCysGluGlnGlnProIle 65
 DB 254 GAAGACTCTCCAGAGGACCATAGACAGAGATTAAGCATGTTATGTGCAAGACGCAATC 313
 QY 66 GlyArgArgLeuPheArgPheLeuAlaThrValProThrPheArgLysAlaAlaThr 85
 DB 314 GGGAGGCTGCTTTTCGCGAGTGTGAAACGAGGCTGGGCTGAGTGTTCATTGAC 373
 QY 86 PheLeuGluAspValGlnAsnTyrGlu-----LeuAlaGluGlnGly 99
 DB 374 TTCTTGACTCCGTCGAGCAATATGAAATGACTCCAGATGAGAAATCTGGAGAGAAAGG 433
 QY 100 ProThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaPro 119
 DB 434 -----AAGAAATTATGACCAAGTACCTC-----ACCCA 463
 QY 120 GlyAsnPro-----GlnProPheLeuSerGlnAlaValAlaThr 132
 DB 464 AAGTCCCTGTTTCATAGCCCAAGTTGCGCAAGACTGTCTCCAGACGAGGAGAAAG 523

QY 133 LysCysGlnAlaAlaThrThrGluGlnLysValAlaAlaValAlaThrLeuAlaGlyAla 152
 DB 524 CTCTCAAGAAAGCCGTCGCAAGACCTTTTCTGCTCGTGCACACTGTCTCAGAG-- 580
 QY 153 GluAlaMetAlaPheLeuGlnGlnGlnProPheLysAspPheValThrSerAlaPheTyr 172
 DB 581 -----TACCTGAGGGAGAACCATTTCCAGCAATATCTGACAGCATGTTTTT 628
 QY 173 AspLysPheLeuGlnTyrLysLeuPheGluMetGlnProValSerAspLysTyrPheThr 192
 DB 629 GACCGCTTCTCCAGCTGGAAGTGTGTGAAGAGCAACCGGTGACCAAAACATTTCAAG 688
 QY 193 GluPheArgValLeuGlyLysGlyLysGlyPheGlyGlyValCysAlaValGlnValLysAsn 212
 DB 689 CAGTATCAGTGTCTAGAGAAAGGGGGCTTCGGGGAGCTGTGCTCCGACAGTTCGGGCC 748
 QY 213 ThrGlyLysMetTyrAlaCysLysLysLeuAspLysLysArgLeuLysLysGlyLys 232
 DB 749 ACGGTTAAAGTATGCTCCGCAAGCGCTTGAGAGAGAGAGATCAAAAGAGAGAAAGG 808
 QY 233 GluLysMetAlaLeuLeuGlnLysGlnIleLeuGlnLysValSerSerProPheIleVal 252
 DB 809 GAGTCCATGGCCCTCATAGAGAGAGATCCTCGAGAGAGTCAACAGTCAGTTGTGTCTC 868
 QY 253 SerLeuAlaTyrAlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsn 272
 DB 869 AACCTGGCTTATGCTTACGAGACCAAGATGACCTGTGCTGTCTCATCATCATATAT 928
 QY 273 GlyGlyAspLeuLysPheHisGlyTyrAsnValGlyThrArgLysLeuAspMetSerArg 292
 DB 929 GGGGGTGAATGATGATTCACATCTTACACATGAGGCAACCTTGCTTGAGAGAGAGCGG 988
 QY 293 ValIlePheTyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIle 312
 DB 989 GCTGTGTTTATGCGGAGAGATCCTGCGGCTTAGAGACCTCCACCGAGAGAACACC 1048
 QY 313 ValTyrArgAspMetLysProGluAsnValLeuLeuAspLeuGlyLysCysArgLeu 332
 DB 1049 GTCTACCGAGATCTGAACCTGAAACATCTGTATGATATATATATGCAATTAAGATC 1108
 QY 333 SerLysPheGlyLeuAlaValAlaGluMetLysGlyLysProIleThrGluArgAlaGly 352
 DB 1109 TCAGACTGGGCTGTGCTGTGAAGATCCCGAGAGAACCTGATCCGGCGCGGTGGGC 1168
 QY 353 ThrAsnGlyTyrMetAlaProGlnIleLeuMetGlnLysValSerTyrProVal 372
 DB 1169 ACTGTGCTACATGCTCCAGAGGTCTGAAACCAACAG--AGTACGGGCTGAGCCCC 1225
 QY 373 AspTyrPheAlaMetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLys 392
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 QY 433 LysLysProGlnGlnArgLeuGlySerArgLysLys--SerAspAspProArgLysHis 451
 DB 1403 AAAGATCGAAGAGAGGCTGGCTGCGAGGAGGAGGAGGCTGCAAGGTCGCAAGGAC 1462
 QY 452 HisPhePheLysThrIleAsnPheProArgLeuGlnAlaGlyLeuIleGluProPhe 471
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Search completed: August 13, 2004, 21:21:52
 Job time : 573 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 13, 2004, 17:28:46 ; Search time 4223 Seconds

(without alignments)
5675.751 Million cell updates/sec

Title: US-10-044-205A-2

Perfect score: 2889

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 segs, 2167151695 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2889	100.0	2198	6	AX797552 Sequence
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4	2883	99.8	1662	6	AX252439 Sequence
5	2883	99.8	1662	6	AX642968 Sequence
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7	2883	99.8	1799	9	AR439409 Sequence
8	2883	99.8	2249	6	AR225819 Sequence
9	2883	99.8	2249	6	AX252443 Sequence
10	2883	99.8	3186	6	AX710216 Sequence
11	2883	99.8	3186	6	AF282269 Homo sapi
12	2876	99.6	1662	6	AR263766 Sequence
13	2876	99.6	1662	6	AR343544 Sequence
14	2876	99.6	1662	6	AX357902 Sequence
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17	2823.5	97.7	1701	6	AX921933 Sequence
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24	1700	58.8	2954	5	AB009568 Oryzias 1
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 DEFINITION Sequence 3 from Patent WO02095032.
 ACCESSION AX797554
 VERSION AX797554.1 GI:37518056
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 Kapeller-Liebermann, R. and Bandaru, R.
 TITLE Method and compositions of human proteins and uses thereof
 JOURNAL Patent: WO 02095032-A 3 28-NOV-2002;
 MILENITUM PHARMACEUTICALS, INC. (US)
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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 AX797552

LOCUS AX797552 2198 bp DNA linear PAT 04-OCT-2003
 DEFINITION Sequence 1 from Patent WO02095032.
 ACCESSION AX797552
 VERSION AX797552.1 GI:37518055
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 Kapeller-Libermann, R. and Bandaru, R.
 AUTHORS
 TITLE Method and compositions of human proteins and uses thereof
 JOURNAL Patent: WO 02095032-A 1 28-NOV-2002;
 MILENITUM PHARMACEUTICALS, INC. (US)

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US-10-044-205a-2 (1-553) x AX797552 (1-2198)

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RESULT 3
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DEFINITION Sequence 1 from patent US 6444456.
 ACCESSION AR225817
 VERSION AR225817.1 GI:27263947
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1662)
 AUTHORS Walke, D.W., Milgowski, N.L. and Turner, C.A. Jr.
 TITLE Human G-coupled protein receptor kinases and polynucleotides encoding the same
 JOURNAL Patent: US 6444456-A 1 03-SEP-2002;
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ORIGIN

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US-10-044-205A-2 (1-553) x AR225817 (1-1662)

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 ACCESSION AX252439
 VERSION AX252439.1 GI:15985733

KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Walke, D.W., Wilganowski, N.L. and Turner, C.A.
Human g-coupled protein receptor kinases and polynucleotides
encoding the same
Patent: WO 0168869-A 1 20-SEP-2001;
Lexicon Genetics Incorporated (US)
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/organism="Homo sapiens"
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FEATURES
source

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Alignment Scores:
Pred. No.: 2,45e-250 Length: 1662
Score: 2883.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
Gaps: 0

US-10-044-205a-2 (1-553) x AK525439 (1-1662)

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QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
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DEFINITION Sequence 45 from Patent MO01096547.
ACCESSION AX642968
VERSION AX642968.1 GI:28550117

KEYWORDS
SOURCE

ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS

1 Yue, H., Lal, P., Bandman, O., Borowsky, M., Au-Young, J., Lu, Y.,
Gandhi, A.R., Tribouley, C.M., Wallis, N., Yao, M.G., Lu, D.A.,
Greenwald, S.R., Ramkumar, J., Griffin, J.A., Kearney, L., Burford, N.,
Nguyen, D.B., Tang, Y.T., Baughn, M.R., He, A., Thornton, M.,
Hafalla, A., Patterson, C., Gururajan, R., Lo, T.P., Khan, F.,
Reichman, S.A., Azimzai, Y., Policky, J.L., Ding, L., Grether, M.,
Elliot, V.S., Thangavelu, K., Batra, S. and Ison, C.H.
Human kinases
Patent: WO 01096547-A 45 20-DEC-2001;

TITLE
JOURNAL

Human kinases
Incyte Genomics, Inc. (US)

FEATURES

Location/Qualifiers
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Alignment Scores:

Pred. No.: 2,456-250 Length: 1662
Score: 2883.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
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US-10-044-205A-2 (1-553) x AX642968 (1-1662)

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DB 61 AACCTCTGGAGCTGGACACCAAGAGCTGACAGGGGGGGCGGCGTGGCTGGCCCTG 120
QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnIysLeuSerIysAsnPheHisSerLeuCys 60
DB 121 GGGCTGCAAGGGCTGGGGAGCTCCGCCAAGAGCTGCTCCGAACTTCCACAGCTGT 180
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 VERSION WO 02103020-A/10.
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 ORGANISM Homo sapiens
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 REFERENCE 1 (bases 1 to 1761)
 AUTHORS Koyama, N., Tanida, S. and Yamamoto, K.
 TITLE A novel gene relating to disease and use thereof
 JOURNAL Patent: WO 02103020-A 10 27-DEC-2002;
 TAKEDA CHEMICAL INDUSTRIES LTD, NOBUYUKI KOYAMA, SEIICHI TANIDA, KOJI
 YAMAMOTO
 COMMENT OS Homo sapiens (human)
 PN WO 02103020-A/10
 PD 27-DEC-2002
 PR 14-JUN-2002 WO 2002JP005942
 PR 15-JUN-2001 JP OIP 182654
 PI NOBUYUKI KOYAMA, SEIICHI TANIDA, KOJI YAMAMOTO
 PC C12N15/54, C12N9/12, G01N33/50, G01N33/15, C07K16/40, A61K39/395 CC
 A novel gene relating to disease and use thereof FH Key
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 Pred. No.: 2.64e-250 Length: 1761
 Score: 2883.00 Matches: 552
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 Best Local Similarity: 99.82% Mismatches: 1
 Query Match: 99.79% Indels: 0
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LOCUS Homo sapiens G-protein-coupled receptor kinase 7 (GRK7) mRNA,
DEFINITION GRK7-S allele, complete cds.
ACCESSION AF439409.1 GI:17933258
VERSION AF439409.1 GI:17933258
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1799)
AUTHORS Chen, C.K., Zhang, K., Church-Koplich, D., Huang, W., Zhang, H.,
Chen, Y.J., Frederick, J.M. and Baehr, W.
TITLE Characterization of human GRK7 as a potential cone opsin kinase
JOURNAL Mol. Vis. 7, 305-313 (2001)
MEDLINE 21626361
PubMed 11754336
REFERENCE 2 (bases 1 to 1799)
AUTHORS Baehr, W. and Chen, C.-K.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2001) Ophthalmology, University of Utah, 15
North/2030 East, Salt Lake City, UT 84112, USA
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ALIGNMENT SCORES:

Pred. No.: 2.71e-250 Length: 1799
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Percent Similarity: 99.82% Conservative: 0
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LOCUS AR225819
DEFINITION Sequence 5 from patent US 644456.
ACCESSION AR225819
VERSION AR225819.1 GI:27263949
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2249)
AUTHORS Malke,D.W., Wiganowski,N.L. and Turner,C.A. Jr.
TITLE Human G-coupled protein receptor kinases and polynucleotides
encoding the same
JOURNAL Patent: US 644456-A 5 03-SEP-2002;
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Pred. No.: 3.62e-250 Length: 2249
Score: 2883.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
Gaps: 0
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 ACCESSION AX252443
 VERSION AX252443.1 GI:15965735
 KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1
 Walke, D.W., Wilganowski, N.L. and Turner, C.A.
 Human g-coupled protein receptor kinases and polynucleotides
 encoding the same

JOURNAL Patent: WO 0168869-A 5 20-SEP-2001;
 Lexicon Genetics Incorporated (US)

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Pred. No.: 3.62e-250 Length: 2249
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 Best Local Similarity: 99.82% Mismatches: 1
 Query Match: 99.79% Indels: 0
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US-10-044-205A-2 (1-553) X AX252443 (1-2249)

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 VERSION AX710216.1 GI:29786804
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 REFERENCE 1
 AUTHORS Xia, Y.
 TITLES Regulation of human g protein-couple receptor kinase
 JOURNAL Patent: WO 03018615-A 4 06-MAR-2003;
 Bayer Aktiengesellschaft (DE)
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 Weis, E.R., Ducceschi, M.H., Horner, T.J., Li, A., Craft, C.M. and Osawa, S.
 TITLE Species-specific differences in expression of G-protein-coupled receptor kinase (GRK) 7 and GRK1 in mammalian cone photoreceptor cells: implications for cone cell phototransduction
 JOURNAL J. Neurosci. 21 (23), 9175-9184 (2001)
 MEDLINE 11717351
 PUBMED 21574315
 REFERENCE 2 (bases 1 to 3186)
 AUTHORS Osawa, S. and Weis, E.R.
 TITLE Direct Submission
 JOURNAL Submitted (24-JUN-2000) Cell Biology and Anatomy, University of North Carolina, CB#7090, 108 Taylor Hall, Chapel Hill, NC 27599-7090, USA

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ACCESSION  AR263766
VERSION     AR263766.1  GI:28075747
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
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REFERENCE 1 (bases 1 to 1662)
 AUTHORS Guegler, K., Beasley, E. M. and Di Francesco, V.
 TITLE Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof
 JOURNAL Patent: US 6331423-A, 18-DEC-2001;
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ORIGIN

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 ACCESSION AX357902
 VERSION AX357902.1 GI:18674690
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 Guegler, K., di Francesco, V. and Beasley, E. M.
 TITLE Isolated human kinase proteins, nucleic acid molecules encoding
 human kinase proteins, and uses thereof
 JOURNAL Patent: WO 0192496-A 1 06-DEC-2001;

Apiera Corporation Robert A. Millman Assistant Secretary (US)
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 QY 321 AsnValLeuLeuAspAspLeuGlyAsnGlySerArgSerLysLeuAlaValGlu 340
 Db 961 AATGCTCTTCTGATGACCTGGCACTGCAAGTTATCTGACCTGGGCTGGCGGAG 1020
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 QY 361 IleLeuMetGluLysValSerLysSerLysProValAspTrpPheAlaMetGlyCysSer 380
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 LOCUS AX166511
 DEFINITION Sequence 2 from Patent WO0138503.
 ACCESSION AX166511
 VERSION AX166511.1 GI:14546856
 KEYWORDS
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Plozman, G.D., Whyte, D., Manning, G.S., Sudarsanam, S.S., Martinez, R.,
 Flanagan, P. and Clary, D.S.
 TITLE Novel human protein kinases and protein kinase-like enzymes
 JOURNAL Patent: WO 0138503-A 2 31-MAY-2001;

FEATURES
 source
 Sugen, Inc. (US)
 Location/Qualifiers
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 /mol_type="unassigned DNA"
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ORIGIN

Alignment Scores:
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 Best Local Similarity: 99.468 Mismatches: 3
 Query Match: 99.278 Indels: 0
 DB: 6 Gaps: 0

US-10-044-205A-2 (1-553) x AX166511 (1-1662)

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 QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
 Db 121 GGGCTGGAGGGCTGGCGGAGCTCCGCCAGAAAGCTTCCTGAACTTCCACAGCTGTGT 180
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QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
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DB 1021 ATGAGGGTGGCAACCCATCACCCAGAGGCTGGAAACAATGTTACATGGCTCTGAG 1080
QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspThrPheAlaMetGlyCysSer 380
DB 1081 ATCTATGGAAGGTAAGGTATATCTCTATCTGTGACGTGGTTGCCATGGGATGCAGC 1140
QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
DB 1141 ATTATGAAATGGTGTGCTGGAGACACCAATTCAAAGATTACAAAGAAAGGTCACTAA 1200
QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
DB 1201 GAGGATCTGAGAGCAAGAACTGTGCAAGACGAGGTCAATTCGACGATGATACTCACA 1260
QY 421 GlnGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
DB 1261 GAGGAGCAAAAGATATTGGACGGCTCTTCTGGCTAAGAAACAGAGCAACGCTTAAG 1320
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QY 461 ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValValTyrAla 480
DB 1381 CCGCTGGAAGCTGGCTTAATTGAACCCCAATTTGTGCCAGACCTTCAGTGGTTATGCC 1440
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DB 1561 ATTATAGAAACGGGACTGTGTTGAGGAATGAATGACCCCAACAGACTAGGGGTTGTAG 1620
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Search completed: August 13, 2004, 20:25:11
Job time : 4257 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 13, 2004, 16:49:07 ; Search time 449 Seconds
(without alignments)

5232.191 Million cell updates/sec

Title: US-10-044-205A-2
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Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched:

3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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-LOOPTXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blonsum62 -TRANS=human40.cdi
-LIST=45 -DOCAIEN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	2883	99.8	1761	7	ABZ56943
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9	2883	99.8	3186	7	ACC44827
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36	1209.5	41.9	1886	6	AAQ75116
37	1202.5	41.6	2206	2	AAQ75116
38	1189	41.2	1983	2	AAQ87427
39	1013.5	35.1	1420	2	AAQ90222
40	1002.5	34.7	2947	5	AAQ86360
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42	852.5	25.5	1316	7	ABX74511
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ALIGNMENTS

RESULT 1	ABBS7375	ABBS7375 standard; cDNA; 2198 BP.
XX	ABBS7375	
XX	AC	ABBS7375;
XX	DT	04-FEB-2003 (first entry)
XX	DE	cDNA encoding human GPCR kinase (GPCRK) 69087.
XX	KW	Human; G protein coupled receptor kinase; GPCR 69087;
XX	KW	cellular proliferative disorder; differentiative disorder;
XX	KW	haematopoietic neoplastic disorder; leukaemia; carcinoma; sarcoma;
XX	KW	metastatic disorder; cytostatic; gene therapy; gene; ss.
OS	Hom sapiens.	
XX	Key	Location/Qualifiers
FT	CDS	291..1952
FT		/*tag= a
FT		/product= "GPCRK 69087"
FT		/note= "The coding sequence given as SEQ ID No:3 is specifically claimed in Claim 1"
XX	XX	US2002123464-A1.
XX	XX	05-SEP-2002.
XX	XX	22-OCT-2001; 2001US-00044205.
XX	XX	19-OCT-2000; 2000US-0241884P.
XX	XX	20-OCT-2000; 2000US-0241877P.

ACC44827 Human G p
AAC28071 Human kin
AAS06702 Polynucle
ACC44826 Human G p
Aad46351 Human con
ABZ56943 Human RGS
AAH78798 Human G-P
Aad28072 Human kin
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AAV71032 GRK5-gree
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AB161805 Colon ade
AAQ87426 Human GRK
AAH24841 Nucleotid
ADB53307 Primary r
ABK49405 cDNA enco
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AB119581 Drosophila
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Aad58393 Human pol
Aad48363 Novel hum
Aad44622 Novel pro

PR 23-OCT-2000; 2000US-0242428P.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Kessler-Libermann R, Bandaru R;
 PI WPI; 2003-066811/06.
 XX P-PSDB; AB672173.
 DR
 XX Novel isolated G protein coupled receptor kinase, 69087, nuclear
 PT signaling protein, 15821 or mitogen activated protein kinase phosphatase,
 PT 15418, useful for treating cellular proliferative or differentiative
 PT disorders.

XX Claim 1; Fig 1; 989P; English.

XX The present invention relates to the isolation of a novel human G protein
 CC coupled receptor (GPCR) kinase (GPCR) designated 69087, a novel human
 CC nuclear signalling protein designated 15821, and a novel human mitogen-
 CC activated protein kinase (MAPK) phosphatase MAPK designated 15418, and
 CC the polynucleotide sequences encoding them. The sequences of the
 CC invention are useful for treating and diagnosing disorders such as
 CC cellular proliferative and differentiative disorders (e.g. haematopoietic
 CC neoplastic disorders, leukaemia, carcinoma, sarcoma or metastatic
 CC disorders). They are also useful in screening assays, detection assays
 CC (e.g. chromosomal mapping, tissue typing, forensic biology), predictive
 CC medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical
 CC trials and pharmacogenomics), and in methods of treatment (e.g.
 CC therapeutic and prophylactic). The sequences may also be used to screen
 CC public databases to identify other family members or related sequences.
 CC The polypeptide sequences are useful as immunogens to generate antibodies
 CC that bind the polypeptides. The polynucleotide sequences are useful for
 CC mapping their respective genes on a chromosome, identifying gene regions
 CC associated with cellular proliferative or differentiative disorders, and
 CC in gene therapy. The present sequence encodes human GPCR 69087

XX Sequence 2198 BP; 558 A; 557 C; 607 G; 476 T; 0 U; 0 Other:

Alignment Scores:
 Pred. No.: 2,78e-282 Length: 2198
 Score: 2889.00 Matches: 553
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-044-205A-2 (1-553) x ABS57375 (1-2198)

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 DB 351 AACCTCGGACCTCGACACCAAGAGCTGAGGGGGGGGCGTGGCTGGCCGCC 410
 QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
 DB 411 GGGCTGACAGGCTGGGCGAGCTCCCGCAGAAAGCTGCTCTTAACTTCAACAGCTGTGT 470
 QY 61 GlnGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
 DB 471 GAGCAGAGCCCATCGTGGCGCTCTTCCCTGACCTTCCACCAAGTGGCCACGTTTC 530
 QY 81 ArgLysAlaAlaThrPheLeuGlnAspValGlnAsnThrGluLeuAlaGlnGluGlyPro 100
 DB 531 CGAAGCGGCAACCTTCTAGAGAGCTGCGAACTGGAGCTGGCGAGAGGAGGCC 590
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 DB 591 ACCAAGACAGCGCGCTGAGGGCTGTGGCCACTGTGTGGAGTGGCCCTCCCGGG 650
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGln 140

DB 651 AACCGCAACCTTCTCCAGCGGCTGGCCACCACTGCGCAAGCGCACCACTGAG 710
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 DB 711 GAAGAGCGAGTGGCTGAGTGAAGCGTGGCAAGCTGAGGCGCATGGCTTTTGGCAAG 770
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTyrLysLeu 180
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 QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGlnPheArgValLeuGlyLysGly 200
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 DB 951 AACCTGACAAAGAGGCTGAAAGAAAGAGTGGCGAAGATGGCTCTTGGAAAG 1010
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 QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisLe 280
 DB 1071 AAGACCATCTCGCTGCTGATGAGCTGATGATTAAGGAGAGCTTCAAGTTCCACATC 1130
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
 DB 1131 TCAACAGTGGGCAAGCGGTGCTGACATGAGCGGGTGTACTTCTGCGGCCAGATA 1190
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 DB 1431 ATTATGAATGGTGTGTCGACGACCAACATTCAAAGATTTCAGAGAAAGGTGATGATA 1490
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 DB 1491 GAGGATCTGAGAGAAAGAACTCTGCAAGAGAGAGTCAAAATTCAGATGATTAATCTCA 1550
 QY 421 GlnGlnAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGlnGlnArgLeuGly 440
 DB 1551 GAGGAGGAAAGAAATTTTTCAGAGGCTCTTCTTGGCTAAGAAACCAAGGCAACGCTTGA 1610
 QY 441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
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 DB 1671 CGCTGTGAGGCTGCTTAATGACCCCATTTGTGCCAGACCTTCAAGGTTTATGCG 1730
 QY 481 LysAspIleAlaGlnIleAspAspPheSerGlnValArgGlyValGluPheAspAspLys 500

particular medical condition. The proteins of the invention are useful for generating antibodies, as reagents in diagnostic assays for

00-10-044-203A-2 (1-553) X AAH78797 (1-1662

QY	1	MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg	20
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QY	41	GlyLeuGlnGlyCysAlaLeuAlaArgGlnIysLeuSerLeuAsnIleSsrLeuCys	60
Db	121	GGGCTTCAGAGGCTCGCGGAGCTCCGCGAAGAGCTGTCCTCAATTCACACACTGGTGT	180
QY	61	GlnGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe	80
Db	181	GACAGCAGACCCATCGTGGCTGGCCCTTCCTGTAATTCCTAGCCAGGCCACAGTTC	240
QY	81	ArgLysAlaAlaThrPheLeuGlnAspValGlnAsnTrpGluLeuAlaGlnGlnGlyPro	100
Db	241	CGCAGAGGGGAACTCTTCTTAGAGCAGTGCAGAACTGGGAACTGGCCGAGAGGGAAACC	300
QY	101	ThrIysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly	120
Db	301	ACCAAAAGCAGGGCGCTCGAGGGGCTGGTGGCCACTTGGCAGAGGCCCTGGCCCGGGG	360
QY	121	AsnProGlnProPheLeuSerGlnAlaValAlaThrIysCysGlnAlaAlaThrThrGlu	140
Db	361	AAACCGCAACCTTCTTACGCAAGCGCTGGCCACCAAGTCGCAAGCAGCCACCACTAG	420
QY	141	GlnGlnArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu	160
Db	421	GAAGAGGAGTGGCTGCAGTGAAGCGCTGGCCAAAGCTGAAGGCAAGCTTCTTCAAGAG	480
QY	161	GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu	180
Db	481	CAGCCCTTTAAGAGATTGTGACCAAGCGCCCTTCAAGCAAGTTTCTGCAGTGAATCTC	540
QY	181	PheGlnMetGlnProValIserAspLysTyrPheThrGluPheArgValLeuGlyLysGly	200
Db	541	TTGAGATGCACCAAGTGTGAACAAGACTTCACTGAGTTCAGACTGCTGGGAGAAAGGT	600
QY	201	GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys	220
Db	601	GGTTTTGGGAGGTATGTGCCTCAAGTGAATAACACTGGCAAGATGATGACTCTGAAG	660
QY	221	LysLeuAspLysLysArgLeuLysLysGlyGlyGlnLysMetAlaLeuLeuGlnLys	240
Db	661	AAATCGACAAAGAGCGGTGAAATAAAGGTGGCCGAGAGATGGCTCTTGGAAAG	720
QY	241	GlnIleLeuGlnLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGlnSer	260
Db	721	GAATATCTGGAGAAAGGTGACGCCCTTTCATTTCTCTCTGCGCTAATGCTTTGGAGAC	780
QY	261	LysThrThrIleuLysCysLeuValMetSerLeuMetAsnGlyCylAspLeuLysPheAsiLe	280
Db	781	AAATCCCATCTCTGCTTGTATAGCCGATGATGGGAGAGACCTTCAAGTTCCACATC	840
QY	281	TyrZnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle	300

Db 841 TCAACCTGGGACCGCTGGCTGGACATAGACCGGAGTCTTTTACCTGGCCCAATA 900
 Qy 301 ALaCysGluMetLeuHisLeuHisGluLeuGlyIleValIleArgAspMetLysProGlu 320
 Db 901 GCGGTGGGAGTGTGACCTCCATGAACTGGGATCGCTTACGGACATGAAGCTTGG 960
 Qy 321 AsnValLeuLeuAspLysLeuGlyAsnCysArgLeuSerAspLeuLeuAlaGlu 340
 Db 961 AATGCTCTTCGATGATACCTGGCACTGCAAGTTATCTGACCTGGGCGCTGGAG 1020
 Qy 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyIleMetAlaProGlu 360
 Db 1021 ATGAAAGGTGGCAAGCCCATGACCCAGAGGGCTGGAAACCAATGGTCTACAGCTCTGAG 1080
 Qy 361 IleLeuMetGluLysValSerIleSerIleProValAspThrProAlaMetGlyCysSer 380
 Db 1081 ATCTTAATGCAAAAGTAGTATTCCTATCTGAGCTGGCTTTGCCATGGGATGCAAGC 1140
 Qy 381 IleIleGluMetValAlaGlyArgThrProPheLysAspIleLysGlyValSerLys 400
 Db 1141 ATTATGAATGATGTTCTGACGAAACCATTTCAAGATTACAGAAAGGTCAGTAA 1200
 Qy 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnProThr 420
 Db 1201 GAGGATCTGAGCAAGAAAGACTCTGCAAGCAGAGGCTCAATTCACATGATTAATTCACA 1260
 Qy 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
 Db 1261 GAGGAGCAAAAGATTTGAGGCTCTTCTGGCTAAAGAACAGAACAGCTTAAAGCA 1320
 Qy 441 SerArgGluLysSerAspAspProArgLysHisIlePhePheLysThrIleAsnProPro 460
 Db 1321 AGCAGAGAAAGCTGATGATCCAGAAACATCATTTCTTAAACATCACTTCTCT 1380
 Qy 461 ArgPheGluAlaGlyLeuIleGluProProPheValProAspProSerValValIleVal 480
 Db 1381 CGCTGGAGAGCTGGCTGATTAAGAACCCCATTTGGCCAGACCTTCACTGATTTAGCC 1440
 Qy 481 LysAspIleAlaGluIleAspAspPheSerGluValAlaGlyValGluPheAspLys 500
 Db 1441 AAGACATCGCTGAATGATGATTTCTGAGGTTGCGGGGTGGATTTGATGACAA 1500
 Qy 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGlu 520
 Db 1501 GATTAAGCATTTCTTCAAAACCTTGGCAGAGGCTGTTCTTAAGATGCGAGCAAA 1560
 Qy 521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrIleCysGlu 540
 Db 1561 ATTATGAAAGCGGAGCTGTTGAGGAAGTGAATGACCCCAAGACCTACGGGTTGAG 1620
 Qy 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
 Db 1621 GAGGTAATTCATCCAAAGCTGCGTGTGTGTTATG 1659
 RESULT 3
 ABO86178
 ID ABO86178 standard; DNA, 1662 BP.
 AC ABO86178;
 XX 10-SEP-2002 (first entry)
 DE Novel human gene. SEQ ID 49.
 XX
 XX Human: cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian;
 KW neurotropic; neuroprotective; immunosuppressive; haemostatic;
 KW antiinflammatory; cardiant; antitumor; vincristine; antithyroid;
 KW cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
 KW wound healing disorders; atherosclerosis; Parkinson's disease;
 KW Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
 KW inflammation; neoplastic disease; nervous system disorder;
 KW cardiovascular disorders; pancreatitis; respiratory disorder;
 KW

KW hyperproliferation; systemic autoimmune disease; hyper-immunity;
 KW developmental abnormality; gastrointestinal ulceration; neuropathy;
 KW haematological disease; metabolic disease; brain damage; colitis;
 KW thyroid disorder; hypothyroidism; neurological disease; stroke;
 KW cone photo- transduction deficiency; neurological disease; heart;
 KW angiodenesis; ovulation disorder; spinal cord; thyroid gland; heart;
 KW trachea; thymus; lymph node; muscular system; obesity; anorexia;
 KW growth abnormality; precocious puberty; gene; ss.
 OS Homo sapiens.
 XX
 XX MO200250105-A1.
 PN 27-JUN-2002.
 XX
 PD 17-DEC-2001; 2001WO-US049232.
 PF 19-DEC-2000; 2000US-0256710P.
 XX 20-DEC-2000; 2000US-0257048P.
 PR 09-JAN-2001; 2001US-0260482P.
 PR 30-JAN-2001; 2001US-0264922P.
 PR 06-FEB-2001; 2001US-0266797P.
 PR 19-MAR-2001; 2001US-0276988P.
 PR 04-APR-2001; 2001US-0281535P.
 PR 08-MAY-2001; 2001US-0283622P.
 XX
 XX (SMIR) SMITHKLINE BEECHAM CORP.
 PA (SMIR) SMITHKLINE BEECHAM PLC.
 PA (GLAX) GLAXO GROUP LTD.
 PA Agarwal P, Birkeland M, Cogswell JP, Kahnack KF, Lai Y;
 PI Martensen SA, Rizvi SK, Smith RF, Strum JC, Xie Q;
 PI Martensen SA, Rizvi SK, Smith RF, Strum JC, Xie Q;
 DR WPI: 2002-508784/54.
 DR P-PSDB; ABB61013.
 XX
 XX Secreted proteins and polynucleotides useful as vaccines for preventing
 PT or treating various diseases e.g. cancer, wounds, atherosclerosis,
 PT Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.
 PS Claim 2(a); Page 255-256; 335p; English.
 XX
 XX The invention relates to an isolated polypeptide with signal sequences
 CC which allow it to be secreted extracellularly or membrane associated. The
 CC activity of polypeptides of the invention may be described as,
 CC cyostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, neurotropic,
 CC neuroprotective, immunosuppressive, haemostatic, antiinflammatory, anorectic,
 CC cardiant, antitumor, vincristine, antithyroid, cerebroprotective, wound
 CC and metabolic. Polypeptides and polynucleotides of the invention are
 CC useful in the treatment, or as a vaccine in the prevention of, cancer,
 CC wound healing disorders, infection, atherosclerosis, Parkinson's disease
 CC and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,
 CC inflammation, neoplastic diseases, nervous system related disorders and
 CC cardiovascular disorders, pancreatitis, respiratory disorder,
 CC hyperproliferation, systemic autoimmune disease, hyper-immunity,
 CC developmental abnormality, gastrointestinal ulceration, neuropathy,
 CC haematological diseases, metabolic diseases, brain damage, colitis, cone photo-
 CC disorders e.g. hypothyroidism, neurological diseases, stroke, angiodenesis,
 CC transduction deficiency, neurological diseases, Parkinson's disease,
 CC ovulation disorders, diseases in the spinal cord, thyroid gland, heart,
 CC trachea, thymus, lymph node and muscular system, obesity, anorexia,
 CC growth abnormalities, and alleviation of precocious puberty. The
 CC sequences given in records ABO86130-ABO86184 represent novel human cDNA's
 CC of the invention
 XX
 XX Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;
 SO
 XX
 XX Alignment Scores: 1662
 Pred. No.: 7.61e-282
 Score: 2883.00 Matches: 552
 Percent Similarity: 99.82% Conservative: 1
 Best Local Similarity: 99.82% Mismatches: 1
 Query Match: 99.79% Indels: 0

DB: 6 Gaps: 0

US-10-044-205a-2 (1-553) x AB086178 (1-1662)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuLeuAlaAsnThrAlaTyrLeuGlnAlaArg 20

DB 1 ATGCTGACATGGGGGCGCTGACCACTGATGCGCAACACCGCTACCTGCGAGCGCCG 60

QY 21 LysProSerAspCysAspSerLysGluLeuGluArgArgArgSerLeuAlaLeuPro 40

DB 61 AAGCCCTCGACTGCGACAGCAAGAGCTGAGCGCGCGCGCTGACCTGCGCGCCGCC 120

QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGluLysLeuSerLeuAsnProHisSerLeuCys 60

DB 121 GGGCTGCGAGGCTGCGCGGAGCTCGCCAGAACACTCTCCCTGAACTTCCAGACGCTGCT 180

QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80

DB 181 GAGCAGACGCCCATCGCTGCGCGCTCTTCCGACTTCTTACGCAAGTGCCTCCAGCTTC 240

QY 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGlnGlyPro 100

DB 241 CGCAGGCGCGCAACCTTCTTGAAGAGCTGCAAGACTGGAGCTGCGCGAGAGGAGACC 300

QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120

DB 301 ACCAAGACAGCGCGCTGCGAGGCGCTGAGCGCACTTGTGCGAGTGCCTGCGCGGCG 360

QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140

DB 361 AACCCCAACCTTCTCTGACGACGCGCGCGCGCAAGGCGCAAGCGCAAGCGCAAGCTGAG 420

QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGlnAlaMetAlaPheLeuGlnGlu 160

DB 421 GAAGAGCGAGTGGCTGAGTGAAGCTGCGCGCAAGCTGAGCGCATGCTTCTTGGCAAG 480

QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180

DB 481 CGGCCCTTAAAGATTGCTGACACGCGCTTCTGACGACAACTTCTTGGCAAGAACTC 540

QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyGly 200

DB 541 TTGAGATGCAACAGTGCAGACAAAGTACTTCACTGAGTTCAGAGTCTGCGGAAAGCT 600

QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220

DB 601 GGTTTTGGAGAGTATGCTCCTCGAGGTAAACACAGTGGAGAGATGATGCTGCTAG 660

QY 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGlnLys 240

DB 661 AAATGACAAAGAGCGGCTGACAAAGAAAGTGGCGAAGATGGCTCTTGGAAAG 720

QY 241 GluIleLeuGlnLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260

DB 721 GAATCTTGGAGAAAGTGAAGACGCTTCACTTCTCTGCGCTATGCTCTTGGAGAC 780

QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyLysPheLysPheHisIle 280

DB 781 AAGACCATCTGCTGCTGATGAGCTGAAAGTGGGAGAACCTCAAGTTCACATC 840

QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300

DB 841 TCAAGCGTGGACCGCGTGGCTGACATGACCGGGTGAATCTTTTACCGCCCGAGAA 900

QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320

DB 901 GCCTGAGGATCTGCACTTCATGAACTCGCAATCTCTATCGGAGCATGAAGCTGAG 960

QY 321 AsnValLeuLeuAspAspLeuGlyLysCysArgLeuSerAspLeuGlyLysAlaValGlu 340

DB 961 AATGTCTTCTGATGACCTCGGCAACTGCAAGTTATCTGACCTGCGCGCTGAG 1020

QY 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360

DB 1021 ATGAGAGGTGCGAGCGCCATCAACCGAGAGGCTGGACCAATGTTACATGCTCTCGAG 1080

QY 361 IleLeuMetGlnLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380

DB 1081 ATCTTAATGAAAAGAGTAAAGTATTTCTTATCTCTGAGACGTGTTGCCATGGAGATGACGC 1140

QY 381 IleTyrGlnMetValAlaGlyArgThrProPheLysAspTyrLysGlnLysValSerLys 400

DB 1141 ATTATGAATAGTGTGCGACGACACCATTTCAAAATTTCAAGAGAAAGTCAATAA 1200

QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420

DB 1201 GAGGATCTGAAGCAAAACATCTGCAAGACGAGGTCAAAATTCACAGATGATACCTTCA 1260

QY 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgGly 440

DB 1261 GAGCAAGCAAAAGATATTGTCAGGCTCTTCTGCTAAGAAACACAGCAACGCTTAGGA 1320

QY 441 SerArgGluLysSerAspAspProArgLysHisPhePheLysThrIleAsnPro 460

DB 1321 AGCAGAGAAAGTCTGATGATCCAGAAACATCATTTCTTTAAAGCATCAACTTTCCT 1380

QY 461 ArgLeuGlnAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480

DB 1381 CGCTCGAAGCTGCGCTTAATTGAACCCCATTTGTGCGACACCTTCAGTGGTTATGCC 1440

QY 481 LysAspIleAlaGluIleAspAspPheSerGluValAlaArgGlyValGluPheAspLys 500

DB 1441 AAAGCATCGCTGAATTTGATGATTTCTGAGAGTTCGGGGGGTGAATTTGATGACAAA 1500

QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGlu 520

DB 1501 GATTAAGCATGTTCTTCAAAAACCTTGGCAAGGCTGCTTCTTACACAGTGGAGAGAA 1560

QY 521 IleIleGlnThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540

DB 1561 ATTATGAAGCGAGCTGTTGAGAACTGAATGACCCCAACGACCTTACGGGTTGTAG 1620

QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553

DB 1621 GAGGATATTATCCAAAGTCTGCGGTGTGTATG 1659

DB 1659

RESULT 4

ID AAD26466 standard; cDNA; 1662 BP.

XX AAD26466;

AC XX

DT 26-MAR-2002 (first entry)

XX XX

DE Human kinase PKIN-19 cDNA.

XX XX

KW Human; kinase; PKIN-19; cancer; leukaemia; adenocarcinoma; osteoporosis; immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease; allergy; asthma; adult respiratory distress syndrome; multiple sclerosis; autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis; Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis; rheumatoid arthritis; ulcerative colitis; diabetes mellitus; osteoarthritis; hepatitis; hypothyroidism; cerebral palsy; catarract; angina pectoris; cardiovascular disease; hypertension; vasculitis; myocarditis; obesity; congestive heart failure; ischaemic heart disease; lung tumour; gout; fatty liver; Niemann-Pick's disease; gene therapy; ss.

OS Homo sapiens.

XX XX

XX XX

Key Location/Qualifiers

FT CDS 1..1662

FT /tag= a

FT /product= "Human PKIN-19 protein"

PN MO200196547-A2.

XX 20-DEC-2001.
 XX 14-JUN-2001; 2001WO-US019444.
 XX 15-JUN-2000; 2000US-0212073P.
 XX 23-JUN-2000; 2000US-0213467P.
 XX 30-JUN-2000; 2000US-0215651P.
 XX 07-JUL-2000; 2000US-0216052P.
 XX 13-JUL-2000; 2000US-0218372P.
 XX 25-AUG-2000; 2000US-0228056P.
 XX (INCY-) INCTE GENOMICS INC.
 XX Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y,
 XX Gandhi AR, Tribouley CM, Walla NK, Yao MG, Lu DM, Greenwald SR;
 XX Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT;
 XX Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gunraj R;
 XX Lo TP, Khan F, Recipon SA, Azimzal Y, Policky JL, Ding L;
 XX Gether M, Elliott VS, Thangavelu K, Batra S, Ison CH;
 XX WPI; 2002-090207/12.
 XX P-PSDB; AAE16273.
 XX New polypeptides, useful for diagnosing, treating or preventing disorders
 XX of growth and development, cardiovascular and lipid, and diseases such as
 XX cancer, comprise human kinase polypeptides.
 XX
 XX Claim 5; Page 190; 197pp; English.
 XX The invention relates to human kinase PKIN proteins and their
 XX corresponding cDNAs. A composition containing PKIN agonist is useful for
 XX treating a disease or condition associated with decreased expression of
 XX PKIN and a composition comprising PKIN antagonist is useful for treating
 XX a disease or condition associated with overexpression of PKIN. The
 XX disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,
 XX myeloma, sarcoma, teratocarcinoma, Hodgkin's disease), immune disorder,
 XX (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,
 XX atherosclerosis, anaemia, allergies, Crohn's disease, diabetes
 XX mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,
 XX osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
 XX rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,
 XX bacterial, parasitic, fungal, viral, protozoal and helminthic infections)
 XX growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,
 XX Cushing's syndrome, hypothyroidism, cerebral palsy, characters); cardio
 XX vascular disease (arteriovenous fistula, hypertension, vasculitis,
 XX aneurysms, congestive heart failure, angina pectoris, myocarditis,
 XX ischaemic heart disease, chronic bronchitis, lung tumours); lipid
 XX disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,
 XX hypcholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity
 XX of a test compound and in gene therapy. The present sequence is human
 XX PKIN-19 cDNA
 XX
 XX Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;
 XX
 XX Alignment Scores:
 XX Pred. No.: 7.61e-282 Length: 1662
 XX Score: 2883.00 Matches: 552
 XX Percent Similarity: 99.82% Conservative: 0
 XX Best Local Similarity: 99.82% Mismatches: 1
 XX Query Match: 99.79% Indels: 0
 XX Gaps: 0
 XX
 XX US-10-044-205A-2 (1-553) x AAD26466 (1-1662)
 QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
 Db 1 ATGTGTGACATGGGGCCCTGGACCACTGATCGCAACGCCCTACCTCGAGCCCG 60
 QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
 Db 61 AAGCCCTCGGACCTGGACAGCAAGAGCTGGACCGCGCGGCTGAGCTGCGCTCC 120

QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAspPheHisSerLeuCys 60
 Db 121 GGGCTGACAGGGCTGCGCGAGAGCTCGCCAGAACGTGCTCCGAACTTCCACAGCTGTGT 180
 QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
 Db 181 GAGCAGCAGCCCATCGATCGCGCTCTTCCTGATCTTCTTACGACAGCGCCACAGCTTC 240
 QY 81 ArgGlySalAlaThrPheLeuGlnAspValGlnAsnTyrGluLeuAlaGluGluGlyPro 100
 Db 241 CGAAGGCGGCACTTCTTCTTACGAGAGCTGGAAGCTGGAGAGCTGGAGAGAGAGCC 300
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 Db 301 ACCAAGACAGCGCGCTGCGAGGGCTGAGTGCATTTGCGAGTGGCCCTCGCCCGGGG 360
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
 Db 361 AACCCCAACCTTCTCTACGACGAGCCCGTGGCAACAGTGCACAGCAGCAGCAGCTGAG 420
 QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGly 160
 Db 421 GAAAGCGAGTGGCTGAGTGAAGCTGGCCAGAGCTGAGGCTGAGCTTTCTTGCAAGAG 480
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTyrLysLeu 180
 Db 481 CAGCCCTTTAAGATTTGTGACCGAGGCTCTTTCACAGAAAGTTTTCAGAGTGAATC 540
 QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
 Db 541 TTCAGAGTGAACCACTGTCAGAGAGTACTTCACTGAGTTCAGAGTGGGAGAGT 600
 QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
 Db 601 GGTTTTGGGAGGTATGTCGCTCAGGTGAAAACACTGGAAAGATGATGCTGCTGAG 660
 QY 221 LysLeuAspLysLysArgGluLysLysLysGlyGlyGluLysMetAlaLeuGlnGlyLys 240
 Db 661 AAATCGACAGAGAGGGGTGAAGAAAGAGTGGCGAGAAAGATGGCTCTTGAGAAAG 720
 QY 241 GlnLeuGlnGlyLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
 Db 721 GAATCTTGAGAAAGTCAAGACCCCTTATGCTCTCTGCGCTATGCTTTGAGAAC 780
 QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyLysAspLeuLysPheHisIle 280
 Db 781 AAGACCATCTCTGCTGCTGATGAGCTGATGATGGGAGAGCTTCACTTCCACATC 840
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
 Db 841 TACAACTGGGACGCGTGGCTGACATGAGCCGGGTATCTTTTACTCGGCCAGATA 900
 QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
 Db 901 GCGTGGAGATCTGACACTTCATGAACTCGGACATCTGATGAGGAGCATGAACCTGAG 960
 QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
 Db 961 AATGTGCTTCTGATGACCTTGGCACTGAGATTAATCACTGCGGCTGGCGCTGAG 1020
 QY 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
 Db 1021 ATGAAGGATGGCAAGCCATCAACCAAGAGGCTGGAAACATGATGATGATGCTCTGAG 1080
 QY 361 IleLeuMetGluLysValSerTyrSerTyrProValAspTyrPheAlaMetGlyCysSer 380
 Db 1081 ATCTTAATGAAAGAGTAAGTATTCTTAATCTGAGCTGCTGCTGCTGAGAGAGC 1140
 QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
 Db 1141 ATTATGAAATGCTGCTGAGCAACACATTAAGATTAACAGGAAAGAGTCAAGTAA 1200

QY 401 GluAspLeuYsGIATgThrLeuGlnAspGluValIysPheGlnHisAspAsnPheThr 420
 Db 1201 GAGGATCTGAGCAAGAACTCTGCAAGACAGGTCGAATTCGAGCATGATCTTCA 1260
 QY 421 GluGluAlaIysAspIleCysArgPheLeuAlaIysPheGluGlnArgLeuGly 440
 Db 1261 GAGGAGCAAAAGATTTGCGAGCTCTCTGAGTAAAGAACAGACGCAACGCTTAA 1320
 QY 441 SerATGGIuYsSerAspAspProArgIysHisAspPheLeuThrIleAsnPro 460
 Db 1321 ACCAGAGAAAAGTCTGATGATCCAGAAACATCATTTCTTAAACGATCAACTTCT 1380
 QY 461 ArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerValIysAla 480
 Db 1381 GCGCTGGAAGCTGCTTATGAAACCCCATTTGTCAGACCCCTTCACTGTTATGCC 1440
 QY 481 LysAspIleAlaGluIleAspAspSerGluValArgGlyValIlePheAspAsp 500
 Db 1441 AAAGACATCGCTGAATTTGATGATTTCTGAGGTTGCGGAGGAGGAAATTGATG 1500
 QY 501 AspLysGluPhePheLysAsnAspAlaThrGlyAlaValProIleAlaThrGlnGlu 520
 Db 1501 GATAGCAGTTCTTCAAAAACCTTGGCAGAGTCTCTTCTATAGCATGGCAGAA 1560
 QY 521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
 Db 1561 ATTATGAAAGCGAGCTGTTGAGACCTGATGACCCCAACAGACCTACGGGTGTGAG 1620
 QY 541 GluGlyAsnSerIysSerGlyValCysLeuLeuLeu 553
 Db 1621 GAGGTAATTCATCCAGCTGCTGTTGTTGTTATTTG 1659

RESULT 5
 AAD46350
 ID AAD46350 standard; cDNA; 1662 BP.
 AC AAD46350;
 XX 27-JAN-2003 (first entry)
 DE Human cone opsin kinase (GRK7) cDNA.
 XX Human; enzyme; cone opsin kinase; G-protein coupled receptor kinase 7;
 KW GRK7; cone visual signalling; visual sensitivity; visual resolution;
 KW night blindness; colour blindness; Oguchi disease; pineal gland activity;
 KW chromobiological desynchrony; depression; anxiety; memory loss; headache;
 KW mental foginess; fatigue; jet lag; circadian rhythm; ophthalmological;
 KW gene therapy; antidepressant; analgesic; gene; ds.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH 1..1662
 FT /*tag= a
 FT /product= "Human GRK7 protein"
 PN W0200272541-A2.
 PD 19-SEP-2002.
 PF 07-MAR-2002; 2002WO-US007025.
 PR 07-MAR-2001; 2001US-0274006P.
 PA (IMMEX) IMMEX CORP.
 PI Bird TA, Spencer M, Mosley BA;
 DR WPI; 2002-723307/78.
 DR P-PSDB; AAE28952.
 XX Identifying compounds that alter inhibition of cone opsin kinase
 PT polypeptide activity for treating a conditions related to cone visual

PT signaling, comprises mixing a compound with a cone opsin kinase and with
 PT an inhibitory polypeptide.
 XX
 PS Example 4, Page 45-46; 61pp; English.
 CC The present invention relates to novel human cone opsin kinase (G-protein
 CC coupled receptor kinase 7; GRK7) and their corresponding polypeptides.
 CC The invention further relates to a method of identifying compounds that
 CC alter the inhibition of GRK7 polypeptide activity which involves mixing a
 CC test compound with GRK7 protein and an inhibitory polypeptide and
 CC determining if the test compound alters the inhibition of GRK7 protein
 CC activity by the inhibitory polypeptide. GRK7 sequences are useful for
 CC treating conditions related to cone visual signalling (e.g., night
 CC blindness, colour blindness, difficulty with colour vision, visual
 CC sensitivity, visual resolution or in adapting to changes in light
 CC intensity, Oguchi disease or dominant congenital stationary night
 CC depression, anxiety, mental foginess, memory loss, headaches, fatigue,
 CC or jet lag). Agonists of GRK7 polypeptide activity may be used to treat
 CC activity is beneficial, e.g., decreased colour sensitivity or other cone
 CC preparation of a medication for treating a condition or disease related
 CC to cone photoreceptor visual signalling or circadian rhythm, as molecular
 CC probes to screen for inherited defects in colour vision, circadian rhythm
 CC and vision resolution. They are also used as gene therapy tools for
 CC individuals with such disorders. The present sequence is human GRK7 cDNA

Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.:
 Score: 7,616-282 Length: 1662
 Percent Similarity: 2883.00 Matches: 552
 Best Local Similarity: 99.82% Conservative: 0
 Query Match: 99.82% Mismatch: 1
 DB: 99.79% Indels: 0
 Gaps: 0

US-10-044-205A-2 (1-553) x AAD46350 (1-1662)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaIleLeuGlnAlaArg 20
 Db 1 ATGGTGAACATGGGGGCTCTGACAACTGATGCGCAACGCGCTTACCTGACGGCCGG 60
 QY 21 LysProSerAspCysAspSerIysGluLeuGlnArgArgGArgSerLeuAlaLeuPro 40
 Db 61 AAGCCTTCGACCTGCGACAGCAAGAAAGCTGACGCGCGCGCTGACCTGCGCCCTGCC 120
 QY 41 GlyLeuGlnIleGlyAlaGluLeuArgGlnIleLeuSerLeuAsnPheHisSerLeuCys 60
 Db 121 GGGCTGCAAGGCTGCGCGAGCTCCGCAAGAGCTGCTCCGAACTTCCACAGCCCTGTGT 180
 QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
 Db 181 GAGCAGAGCCATGATGCTGCGCTCTTCCGTGACTTCTTACGCCACAGTCCACGTTTC 240
 QY 81 ArgIysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGlnIlePro 100
 Db 241 CGCAAGCGCGCAACTCTTACAGCACTGCAAGATCGGAGCTGCGAGAGAGGACCC 300
 QY 101 ThrIleAspSerAlaLeuGlnIleValAlaThrCysAlaSerAlaProAlaProGly 120
 Db 301 ACCAAGAGAGCGGCGTGCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrIleCysGlnAlaAlaThrThrGlu 140
 Db 361 AACCGCAACCTTCTCCAGCAAGCGCTGCGCAACGCTGCGCAAGCGCAAGCACTGAG 420
 QY 141 GluGluArgValAlaAlaValThrLeuArgIleAlaGluAlaMetAlaPheLeuGlnIle 160
 Db 421 GAAAGCGCAGTGGTCACTGACGCTGCGCAAGCTGAGGCACTGCTTCTTTCGCAAGAG 480
 QY 161 GlnProPheLysAspPheValThrSerAlaPheIleAspLysPheLeuGlnTrpIleLeu 180

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Db 481 CAGCCCTTAAAGATTTCGTGACGAGGCTTCTACGACAAAGTTTCGACGAGGAACTC 540
Qy 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
Db 541 TTCGAGATGCAACCACTGTCACAGAAATCTTCACTGAGATTCAGAGTGTGGGAAAGGT 600
Qy 201 GlyPheGlyGluValCysAlaValGlnValAspThrGlyLysMetCysTyrAlaCysLys 220
Db 601 GGTTCGAGGATGATGTGCTGCTGAGGTAAGAACTGGAGAGATGATGCTGTAAAG 660
Qy 221 LysLeuAspLysLysArgLeuLysLysLysGlyValGlyLysMetAlaLeuLeuGlyLys 240
Db 661 AAACGTGACAAAGCGCTGAAGAAAGAGTGGCGAGAAAGTGGCTCTTGGAAAG 720
Qy 241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
Db 721 GAAATCTTGAGAAAGTCAAGAGCCCTTCACTGCTCTGCTGCTGCTGCTGCTGCTG 780
Qy 261 LysThrHisLeuCyLeuValMetSerLeuMetLeuValGlyValAspLeuLysPheHisLe 280
Db 781 AAGACCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Qy 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
Db 841 TACAACGTGGGCAAGCGTGGCTGACATGAGCGGGGATCTTTTAACTGCGCCAGATA 900
Qy 301 AlaCysGlyMetLeuHisLeuHisGlyLysGlyLysLysLysLysLysLysLysLys 320
Db 901 GCTGTGGGATGCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 960
Qy 321 AsnValLeuLeuAspAspLeuGlyLysCysArgLysSerAspLeuGlyLysAlaValGlu 340
Db 961 AATGGCTTCTGATGATGCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 1020
Qy 341 MetLysGlyLysLysProIleThrGlnArgLysGlyLysLysLysLysLysLysLys 1080
Db 1021 ATGAAGGTGGCAAGCCCATCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 1140
Qy 361 IleLeuMetGluLysValSerTyrSerTyrProValAspThrPheAlaMetGlyCysSer 380
Db 1081 ATCTTAATGAAAGAAAGTAACTATCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Qy 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGlyLysValSerLys 400
Db 1141 ATTATGAAATGTTGCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 1200
Qy 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
Db 1201 GAGGATCTGAAGCAAGAACTCTGCAAGAGCAAGGTCAAAATTCAGCATGATTACTTACA 1260
Qy 421 GluGluAlaLysAspLysCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
Db 1261 GAGGACCAAAATATTTGCAAGGCTCTCTTGGCTAAAGAACCAAGACGCTTGAAGA 1320
Qy 441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPro 460
Db 1321 AGCAGAGAAAGTCTGATGATCCAGAAACATCACTTTCTTAAAGATCAACTTCTTCT 1380
Qy 461 ArgLeuGluIleGlyLeuIleGluProPheValProAspProSerValValTyrAla 480
Db 1381 CCGCTGGAAGCTGCTGCTTAATGAAACCCCATTTGCTCCAGACCTTCAAGGTGTTATGCC 1440
Qy 481 LysAspIleAlaGluIleAspAspPheSerGluValArgLysValGluPheAspAspLys 500
Db 1441 AAGAGCATGCTGAAATTTGATGATTTCTGAGGTTCGGGGGTGGAATTTGATGACAA 1500
Qy 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTyrGlnGluGlu 520
Db 1501 GATTAAGCATGCTTCAAAACTTTGAGACAGGTCTCTTCTATGACATGCGAGAAAGA 1560
Qy 521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540

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Db 1561 ATTATGAAGAGGACTGTTTGAGAGACTGAATGACCCCAAGACCTAGGGTTGTAG 1620
Qy 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
Db 1621 GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTTG 1659
RESULT 6
ABZ56943
ID ABZ56943 standard; DNA; 1761 BP.
AC
XX ABZ56943;
XX
XX 04-APR-2003 (first entry)
XX
XX Human gene sequence relative to the invention # SPQ ID 11.
XX
XX Human: heart disease; cancer; omentopathy; gene; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 26.1687
XX CDS /*tag= a
XX
XX W02002103020-A1.
XX
XX 27-DEC-2002.
XX
XX 14-JUN-2002; 2002W0-JP005942.
XX
XX 15-JUN-2001; 2001JP-0018254.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Koyama N, Tanida S, Yamamoto K;
XX
XX WPI; 2003-157045/15.
XX
XX P-PSDB; ABP60079.
XX
XX Novel disease-associated gene of the RGS gene family and its product,
XX applicable in diagnosis of and screening for drugs for heart diseases,
XX cancers and omentopathy.
XX
XX Example 3, Page 85-86; 96pp: Japanese.
XX
XX The invention relates to a novel disease associated gene and its uses.
XX the gene and its encoded protein are useful for diagnosis of and
XX screening for drugs for heart diseases, cancers and omentopathy. The
XX current sequence represents a human gene sequence relative to the
XX invention
XX
XX Sequence 1761 BP; 441 A; 441 C; 504 G; 375 T; 0 U; 0 Other;
SQ
Alignment Scores: 1761
Pred. No.: 8,256-282
Score: 2883.00 Matches: 552
Percent Similarity: 99.82% Conservative: 0
Best Local Similarity: 99.82% Mismatches: 1
Query Match: 99.79% Indels: 0
Gaps: 0
DB: 7
US-10-044-205A-2 (1-553) x ABZ56943 (1-1761)
Qy 1 MetValAspMetGlyValAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
Db 26 ATGCTGACATGCGGGGCTCTGGAACCTGATCGCAACACCCCTACCTCAGAGCCCG 85
Qy 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
Db 86 AAGCCTTGAGCTGCAACAGAAAGACTGTCAGCGCGCGGTAGCTGCGCTGCGCC 145
Qy 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60

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Db 146 GGGCTGACGGGCTGGGGAGCTCCGCCAAGAGCTGCTCCCTGACCTTCCACAGCGTGTGT 205
 QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgPheLeuAlaThrValProThrPhe 80
 Db 206 GAGCAGCAGCCCATCGGTGCGCGCTCTCCGTGATCTTCTTAGCCACAGGCGCCACGTTCC 265
 QY 81 ArgLysAlaAlaThrPheLeuGlnLysPheValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
 Db 266 CCGAGGGCGGCACTTCTCTAGAGCACTGGCAACTGGAGGCTGGCCGAGAGGAGGCC 325
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 Db 326 ACCAAGACAGCGCGGTGCAAGGGCTGTGTGCTCACTTGGAGTGGCGCTGCGCCGGG 385
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
 Db 386 AACCCGCAACCTTCTCTGAGCAAGCGGTGGCCCAAGATCCCAAGACGACCACTGAG 445
 QY 141 GluGlnArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
 Db 446 GAAAGCGAGTGGCTGAGTACGCTGGCCAAAGCTGAGGCAATGCTTCTTCCGAGAG 505
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrosPheLeuGlnTrpLysLeu 180
 Db 506 CAGCCCTTTAAGGATTTCTGACCCAGCGCTTCTACACAAAGTTTCTGACATGGAGAACTC 565
 QY 181 PheGlnMetGlnProValSerAspLysTyrosPheThrGlnPheArgValLeuGlyGly 200
 Db 566 TTGAGATGCAACCGATGTGACAGCAAGATCTTCACTAGTTCAAGTCTGGGAGAAAGT 625
 QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrosAlaCysLys 220
 Db 626 GGTTTGGGAGGATATGCGCTGCCGTCAAGGAAACACTGGAGAAATGTATGCTTGAAG 685
 QY 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
 Db 686 AAACCTGGACAGAGAGCGGCTGAAGAGAAAGGAGGAGAGAGATGCGCTCTTGGAAAG 745
 QY 241 GlnIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrosAlaPheGlnSer 260
 Db 746 GAAATCTTGGAGAGGTCAGAGCGCTTCTTATGTTCTCTGCGCTTATGCTTGAAGAG 805
 QY 261 LysThrIleLeuLysLeuValMetSerLeuMetAsnGlyLysLeuLysPheIle 280
 Db 806 AAGACCATCTTCTGCTTGTATGATGAGCTGATGAAATGGGGAGAGCTCAAGTTCCACATC 865
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrosAlaGlnIle 300
 Db 866 TACAAGCTGGGACCGCTGGCTGGACATGACCGGGTGAATCTTTACTCGGCCCAATA 925
 QY 301 AlaCysGlyMetLeuIleLeuHISGluLeuGlyIleValTyrTrpAspMetLysProGlu 320
 Db 926 GCGTGGGATCTGCTCACTTCATGAATCTGGCAATCGTATGCGGACATGAACCTGAG 985
 QY 321 AsnValLeuLeuAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
 Db 986 AATGCTCTTCTGAGTACCTGGCAACTGGAGTTATCTGACCTGGGCTGACCGTGGAG 1045
 QY 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyLysArgGlyTyrMetAlaProGlu 360
 Db 1046 ATGAAGGTGGAGCCCATCACCAAGAGGCTGGAGCAACAAATGTTAATGCTCTGAG 1105
 QY 361 IleLeuMetGlyLysValSerTyrosTyrosProValAspTrpPheAlaMetGlyCysSer 380
 Db 1106 ATCTTAATGAGAAAGTAAGTATTCATCTCTGATCTGATGCTTGGCAAGGATGACAGC 1165
 QY 381 IleTyrosMetValAlaGlyArgThrProPheLysAspTyrosGlyLysValSerLys 400
 Db 1166 ATTATGAAATGGTCTCTGAGCAACCACTCAAGATTTCAAGAAAGTCTGATAA 1225
 QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnIleAspAsnMetThr 420
 Db 1226 GAGGATCTGAAGCAAGAACTCTGCAAGAGGTCGTAATTCAGCATATTAATCTTCA 1285

QY 421 GluGlnAlaLysAspLysCysArgLeuPheLeuAlaLysLysProGlnGlnArgLeuGly 440
 Db 1286 GAGGAGCAAAAGATATTGAGGCTCTTCTTGGCTAAGAAACAGAGCAAGCTTGAAGA 1345
 QY 441 SerArgGluLysSerAspProArgLysIleIlePhePheLysThrIleAsnPro 460
 Db 1346 AGCAGAGAAAGTCTGATGATCCAGAGAAACATATTTCTTTAAACGATCACTTCTCT 1405
 QY 461 ArgLeuGlnAlaGlyLeuIleGluProProPheValProAspProSerValIleTyrosAla 480
 Db 1406 CGCTGAGAGCTGGCTTAATTAACCCCATTTGTGCAAGACCTTCAGTGTATTATGCC 1465
 QY 481 LysAspIleAlaGluIleAspAspPheSerGlnValArgGlyValGluPheAspLys 500
 Db 1466 AAAGACATGCTGAATATGATTTCTTGAAGTCTGGGGGGTGGATTTGATGACAA 1525
 QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGlu 520
 Db 1526 GATTAAGCATTTCTTCAAAACCTTGGCAGAGTGTCTTCTATGATGCTGAGAAAGA 1585
 QY 521 IleIleGlnThrArgLysPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
 Db 1586 ATTATGAAGAGGAGCTGTTTGAAGAACTGAATGACCCCAAGACCTAGGGTTGTAG 1645
 QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
 Db 1646 GAGGGTAAATTCATCAAGTCTGCGTGTGTGTTATTG 1684
 RESULT 7
 ID ADC39221 standard; cDNA; 1821 BP.
 XX
 AC ADC39221;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Novel human NOX polypeptide coding sequence SEQ ID NO: 165.
 XX
 KW ds; gene; antidiabetic; cytostatic; immunomodulator; anorectic;
 KW antihypertensive; neurotropic; immunostimulant;
 KW antiparkinsonian; anti-HIV; antiaesthetic; antiinflammatory; hypotensive;
 KW diabetics; osteoclastic; hemostatic; osteopathic; gene therapy; NOX;
 KW dyslipidemia; anorexia; lymphoma; wasting disorder; prostate cancer;
 KW Parkinson's disease; cachexia; cardiomyopathy; Alzheimer's disease;
 KW Crohn's disease; multiple sclerosis; hypertension; atherosclerosis;
 KW hemophilia; graft-versus-host disease;
 KW Albright hereditary osteodystrophy.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 73..1732
 FT /*tag= a
 XX
 PM W02003010327-A2.
 XX
 ED 06-FEB-2003.
 XX
 PF 02-MAY-2002; 2002M0-US014199.
 PR 02-MAY-2001; 2001US-0288063P.
 PR 03-MAY-2001; 2001US-0288395P.
 PR 07-MAY-2001; 2001US-0289087P.
 PR 09-MAY-2001; 2001US-0289817P.
 PR 09-MAY-2001; 2001US-0289818P.
 PR 11-MAY-2001; 2001US-0290194P.
 PR 14-MAY-2001; 2001US-0290753P.
 PR 15-MAY-2001; 2001US-0291181P.
 PR 16-MAY-2001; 2001US-0291243P.
 PR 18-MAY-2001; 2001US-0292001P.
 PR 21-MAY-2001; 2001US-0292374P.

QY	21	lyrProSerAspCyAspSerIysGluLeuGlnArgArgArgSerLeuAlaLeuPro	40
Db	133	AAACCCCTGGAAGCTGCCAGCAAGAAAGACTGCAAGCGCGGCGGAGCTGGCCCTGCC	192
QY	41	GlyLeuGlnGlyCysAlaGluLeuArgGlnIlyLeuSerLeuAspPheHisSerLeuCys	60
Db	193	GAGCTCAAGGCTGCGGAGAGCTCCGCAAGAGCTGTCCTGAACTTCCACAGCTGTGT	252
QY	61	GluGlnGlnProIleGlyArgArgPheArgAspPheLeuAlaThrValProThrPhe	80
Db	253	GAGCAGACCCCATCGGTGCGCCCTCTCTCCGTGACTTCCAGCCACAGTCCACAGCGTTC	312
QY	81	ArgGlyAlaAlaThrPheLeuGlnAspValGlnAsnTrpGluLeuAlaGluGlyPro	100
Db	313	CGAAGGCGGCAACCTTCTTACAGCACTGTCACAACTGGAGCTGGCGAGAGAGAACCC	372
QY	101	ThrIysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly	120
Db	373	ACCAAAAGACGCGCTGCAAGGGGCTGGTGGCCACTTGTGGAGTGCCCTGCCCGGGG	432
QY	121	AsnProGlnProPheLeuSerGlnAlaValAlaThrIysCysGlnAlaAlaThrThrGlu	140
Db	433	AAACCCGAAACCTTCTTCAAGCAAGGCGCTGGCCACCAAGTCCAAAGCAAGCACTGAG	492
QY	141	GluGlnArgValAlaAlaValaThrLeuArgIysAlaGluAlaMetAlaPheLeuGlnIle	160
Db	493	GAAGAGCAATGGCTGCGAGTGCAGTGCAGAGGCTGAGGCGCATGGCTTTCTTGGAAAG	552
QY	161	GlnProPheIysAspPheValaThrSerAlaPheIysAspIysPheLeuGlnTrpIysLeu	180
Db	553	CAGCCCTTAAGATTTGTGTGACACAGGCTTCTTACGACAACTTTCTGCAGTGAAACTC	612
QY	181	PheGluMetGlnProValSerAspIysIysPheThrGluPheArgValLeuGlyIysGly	200
Db	613	TTGCAAGGCAACCAAGTGCAGACAACTACTTCACTAGTTCAGAGTCTCGGGAAAGGT	672
QY	201	GlyPheGlyLeuValCysAlaValaGlnValIysAsnThrGlyIysMetTrpAlaCysIys	220
Db	673	GGTTTGGGAGGATGTGCGCTGCAGGTGAAACAACTGGAAAGATGATGCTGTAAAG	732
QY	221	IysLeuAspIysIysArgLeuIysIysGlyIysGlnIysMetAlaLeuLeuGlnIys	240
Db	733	AAACTGGAACAAGACCGGCTGAAAGAAAGAGGCGCAAGAAAGTGGCTCTTCTGAAAG	792
QY	241	GluIleLeuGlnIysValSerSerProPheIleValaSerLeuAlaTrpAlaPheGlnSer	260
Db	793	GAATCTTGGAGAAAGGTGACAGCCCTTCAATGTCTCTGCGCTATGCTCTTGAAGAGC	852
QY	261	IysThrHisIeLeuCysLeuValaMetSerLeuMetAsnGlyIysAspIysPheHisIle	280
Db	853	AAAGCCCATCTGCTGCTTGCATGAGCTGTATGATAGGGGAGAGCTCAAGTTCCACATC	912
QY	281	TrpAsnValGlyThrArgGlyLeuAspMetSerArgValaIlePheIysSerAlaGlnIle	300
Db	913	TKCAACGTGGGCAACGCGTGGCTGGCAAGAGAGCGGGTATCTTTTACTCGGCGCAAGTA	972
QY	301	AlaCysGlyMetLeuHisIleuHisIleGlyLeuGlyIleValaTrpArgAspMetIysProGlu	320
Db	973	GGCTGTGGATGTGCAGCTCATGAACCTCGGATCGCTATTCGGGACATGAAGAGCTTAG	1032
QY	321	AsnValaIleuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValaGlu	340
Db	1033	AAATGGCTTCTGATGACTCGGCACTGCAAGGTATTTCACTCGAGGCTGGCGCGTGGAG	1092
QY	341	MetIysGlyGlyIysProIleThrGlnArgAlaGlyIysAsnGlyTrpMetAlaProGlu	360
Db	1093	ATGAAGAGTGGCAAGCCCATACCCAAAGAGGCTGGAACCAATGTTTCAATGGCTCTGAG	1152
QY	361	IleLeuMetGlnIysValaSerTrpSerTrpProValaSerTrpPheAlaMetGlyCysSer	380
Db	1153	ATCCTAATGAAAAGGTAAAGTTATTCCTATCCTGTGGACTGTTGCTCAATGGAGTGGAGC	1212

QY 381 ILeTyrGluMeValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
 Db 1213 ATTATGAATGTTGGCTGACGAAACCATTAAGATTACAGAGAAAGGTCACTAA 1272
 QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
 Db 1273 GAGAGCTGAAAGCAAAAGACTCTGCAGAACAGAGGTCAATTCCAGCATGATTACTTCA 1332
 QY 421 GluGluAlaLysAspLysCysArgPheLeuAlaLysLysProGluGlnArgLeuGly 440
 Db 1333 GAGGAAGCAAAAGATTGTCAGGCTCTTCTGCTTAAGAACAGAGCAACGCTTAGGA 1392
 QY 441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrLysAsnPro 460
 Db 1393 AGCAGAGAAAGTCTGATGATCCAGGAAACATCATTTCTTAAAGATCAACTTCTCT 1452
 QY 461 ArgLeuGlnAlaGlyLeuLeuGluProProPheValProAspProSerValValTyrAla 480
 Db 1453 CCGCTCGAGAGCTGAGCTTAATGAACCCCATTTGGCCAGACCTTCAGTGGTTTATGCC 1512
 QY 481 LysAspLysLeuAlaGluLysAspPheSerGluValArgGlyValGluPheAspLys 500
 Db 1513 AAAGACATCGCTGAATGATGATTTCTCTGAGGTTGCGGGGTGGAAATTGATGACAA 1572
 QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProLysLeuGlnGlu 520
 Db 1573 GATAGAGAGTCTTCAAAACCTTGGCAGAGGTGCTTCTTACATGCGAGAGAA 1632
 QY 521 IleLeuGlnThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
 Db 1633 ATTTAGAAACGGACCTGTTGAGAACCTGATGACCCCAAGACCTTACGGGTGTGAG 1692
 QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeu 553
 Db 1693 GAGGTAAATTATCCAGTCTGCGCTGTGTTTATG 1731

RESULT 8
 AAH78799

ID AAH78799 standard; cDNA; 2249 BP.
 AC AAH78799;
 XX
 DT 08-MAR-2002 (first entry)
 XX
 DE Human G-protein coupled receptor kinase 3 cDNA sequence.
 XX
 KW G-protein coupled receptor kinase; GRK; human; ss; gene therapy;
 KW novel human protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200168869-A2.
 XX
 PD 20-SEP-2001.
 XX
 PE 08-MAR-2001; 2001WO-US007500.
 XX
 PR 10-MAR-2000; 2000US-0188449P.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Walke DW, Wilganowski NL, Turner CA;
 DR WPI, 2001-570872/64.
 XX
 PT New polynucleotides encoding human proteins that share sequence
 PT similarity with animal kinases e.g. G-protein coupled receptor kinases,
 PT useful for drug screening, diagnosis and in gene therapy of biological
 XX disorders.
 XX
 PS Disclosure; Page 33-34; 34pp, English.
 XX

CC The present cDNA sequence encodes a human G-protein coupled receptor
 CC kinase (GRK), also designated NRP (novel human protein) in the
 CC specification, which is shown in the sequence listing. The invention
 CC comprises novel human nucleotide and protein sequences which have
 CC similarity to G-protein coupled receptor kinases. Oligonucleotides
 CC derived from the nucleotides of the invention are useful as hybridisation
 CC probes for screening libraries and assessing gene expression patterns.
 CC The nucleotides of the invention are also useful in drug screening and
 CC gene therapy for the modulation of GRK expression. The nucleotides of the
 CC invention can be used to genetically engineer host cells to express GRK
 CC products in vivo. The nucleotide sequences of the invention are also
 CC useful in addressable arrays for identifying and characterising the
 CC temporal and tissue specific expression of the invention are also
 CC screen collections of genetic material from patients and in microarrays to
 CC particular medical condition. The proteins of the invention are useful
 CC for generating antibodies, as reagents in diagnostic assays, for
 CC identifying other cellular gene products related to GRK, and as reagents
 CC in assays for screening for compounds that are useful in the treatment of
 CC mental, biological or medical disorders/diseases
 XX

Sequence 2249 BP; 582 A; 577 C; 608 G; 482 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	Length:
Score: 2883.00	2249
Percent Similarity: 99.82%	Matches: 552
Best Local Similarity: 99.82%	Conservative: 0
Query Match: 99.79%	Mismatches: 1
DB: 4	Indels: 0
	Gaps: 0

US-10-044-205A-2 (1-553) x AAH78799 (1-2249)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaSerThrAlaTyrLeuGlnAlaArg 20
 Db 354 ATGTGTGACATGAGGGGCGCTGGAACCTGATCGCAACCGCTTACCTGACGGCCCG 413
 QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
 Db 414 AAGCCCTCGAGCTGCGACAGCAAGAGCTGACGGCGGGGTAGCTGCGCTGCC 473
 QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
 Db 474 GGGCTGACGGCTGCGCGAGCTCGCCAGAGCTGCTTGAACCTTCAACAGCTGTGT 533
 QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
 Db 534 GAGAGCAACCCATCGGTGCGCGCTCTTCCGTGACTTCTTACCAAGTCCCAAGTTC 593
 QY 81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluPro 100
 Db 594 CGCAAGCGGCAACCTTCTTCAAGAGAGCTGCGAGAACTGGAGACTGCGAGAGAGACC 653
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 Db 654 ACCAAAGACAGCGGCTGCGAGGGCTGAGTGCACCTTGGCAAGTCTTCCGCGGAG 713
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrTrpGlu 140
 Db 714 AACCGCAACCTTCTTCAAGAGAGCTGCGAGAGCTGCGAGAGCTGCGAGAGAGAG 773
 QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGln 160
 Db 774 GAAAGCGAGTGGCTCACTGACGCTGCGCAAGCTGAGGCAATGCTTCTTGGCAAG 833
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
 Db 834 CAGCCCTTAAAGATTCTGTACAGCGCTTCTTCAAGAGTCTTCCGAGTGGAACTC 893
 QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
 Db 894 TTCAGATGCAACCAAGTGTGACAAAGTACTTCACTGAGTTCAAGATGCTGGGAGAAAGT 953
 QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220

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Db      954 GGTITGGGAGGTAATGCGCTCCAGGTGAAAAACACTGGAGATGATGCTGTAAAG 1013
QY      221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGlyGlyMetAlaLeuLeuGlyLys 240
Db      1014 AAATGGACAGAGAGCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1073
QY      241 GluLeuLeuGlyLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGlnSer 260
Db      1074 GAAATCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1133
QY      261 LysThrHisLeuCysLeuValMetSerLeuMetValGlyLysLeuLysPheHisIle 280
Db      1134 AAGACCACTCTGCTTGTATGATGAGCTGATGAATGGGAGAGAGAGAGAGAGAGAG 1193
QY      281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
Db      1194 TCAACGTGGGACAGCGGCTGAGACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1253
QY      301 AlaCysGlyMetLeuHisLeuHisGlyLeuGlyIleValTyrArgAspMetLysProGlu 320
Db      1254 GCGTGTGGAGATGCTGACCTCCATGACCTGGCATGCTATCGGAGCATGAGAGCTGAG 1313
QY      321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
Db      1314 AATGTCCTTCTGATGATGCTGCGCACTGCGAGATGATGATGATGATGATGATGATG 1373
QY      341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
Db      1374 ATGAGGGGTGGCAAGCCCATCACAGAGGGCTGAGAGAGAGAGAGAGAGAGAGAGAG 1433
QY      361 IleLeuMetGlnLysValSerTyrSerTyrProValAspTyrPheAlaMetGlyCysSer 380
Db      1434 ATCCATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1493
QY      381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGlyLysValSerLys 400
Db      1494 ATTTATGAAATGTTGTCGAGACAGACACATTCAAAGATTAACAGAGAGAGAGAGAG 1553
QY      401 GluAspLeuLysGlnArgThrLeuGlnAspGlyValLysPheGlnHisAspAsnPheThr 420
Db      1554 GAGATCTGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1613
QY      421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGlnArgLeuGly 440
Db      1614 GAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1673
QY      441 SerArgGluLysSerAspAspProArgLysHisIlePhePheLysThrIleAsnPhePro 460
Db      1674 AGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1733
QY      461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
Db      1734 CGCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1793
QY      481 LysAspIleLeuGlnLeuAspAspPheSerGlnValArgGlyValGluPheAspAspLys 500
Db      1794 AAGAGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1853
QY      501 AspLysGlnPhePheLysAsnPheAlaThrGlyValValProIleAlaTyrGlnGlu 520
Db      1854 GATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1913
QY      521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
Db      1914 ATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1973
QY      541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
Db      1974 GAGGTAATTAATCAAGCTGCGGTGTTGTTATG 2012

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RESULT 9
ACCA4827

```

ID      ID      ACC44827 standard; cDNA; 3186 BP.
XX      XX
AC      AC      ACC44827;
XX      XX
DT      DT      04-JUN-2003 (first entry)
XX      XX
DE      DE      Human G protein-coupled receptor kinase encoding cDNA SEQ ID NO:4.
XX      XX
KW      KW      Human; G protein coupled receptor kinase; GRK; cytosolic; antidiabetic;
KW      KW      neuroprotective; nootropic; cardiovascular; anti-Parkinsonian; cardiant;
KW      KW      vasotrophic; antisthmatic; gene therapy; cancer; diabetes; CNS disorder;
KW      KW      central nervous system disorder; cardiovascular disorder; asthma; COPD;
KW      KW      chronic obstructive pulmonary disorder; anxiety; mood disorder; enzyme;
KW      KW      Alzheimer's disease; Parkinson's disease; congestive heart failure;
KW      KW      myocardial infarction; ischemic disease; hypertensive vascular disease;
KW      KW      gene; ss.
XX      XX
OS      OS      Homo sapiens.
XX      XX
FH      FH      Key
XX      XX      Location/Qualifiers
FT      FT      CDS
XX      XX      85..1746
XX      XX      /tag= a
XX      XX      /product= "G protein-coupled receptor kinase (GRK)"
XX      XX
PD      PD      MO2003018815-A2.
XX      XX
XX      XX      06-MAR-2003.
XX      XX
XX      XX      19-AUG-2002; 2002MO-EP009235.
XX      XX
XX      XX      21-AUG-2001; 2001US-0313464P.
XX      XX
XX      XX      (FARB ) BAYER AG.
XX      XX
XX      XX      Xiao Y;
XX      XX
XX      XX      WPI; 2003-278669/27.
XX      XX
XX      XX      P-PSDB; ABP96709.
XX      XX
XX      XX      New G-protein coupled receptor kinase polypeptides and polynucleotides,
XX      XX      useful in identifying modulators of the enzyme for treating cancer.
XX      XX      PT      diabetes, a central nervous system disorder, a cardiovascular disorder or
XX      XX      asthma.
XX      XX
XX      XX      Claim 1; Fig 11; 129pp; English.
XX      XX
XX      XX      The present sequence encodes a human G protein-coupled receptor kinase
XX      XX      (GRK) protein (I). (I) has cytosolic, antidiabetic, neuroprotective,
XX      XX      nootropic, cardiovascular, anti-Parkinsonian, cardiant, vasotrophic and
XX      XX      antisthmatic activities, and can be used in gene therapy. (II) can be
XX      XX      regulated to treat cancer, diabetes, a central nervous system (CNS)
XX      XX      disorder (e.g. anxiety or mood disorders, Alzheimer's disease and
XX      XX      Parkinson's disease), cardiovascular disorders (e.g. congestive heart
XX      XX      failure, myocardial infarction, ischemic diseases of the heart or
XX      XX      hypertensive vascular disease), asthma and chronic obstructive pulmonary
XX      XX      disorder (COPD). GRK molecules are useful in screening for agents that
XX      XX      regulate or decrease the activity of a GRK. GRK sequences may also be used
XX      XX      for detecting diseases and abnormalities or susceptibility to diseases
XX      XX      and abnormalities related to the presence of mutations in the nucleic
XX      XX      acid sequences that encode the GRK enzyme
XX      XX
XX      XX      Sequence 3186 BP; 857 A; 737 C; 784 G; 808 T; 0 U; 0 Other;
XX      XX
XX      XX      Alignment Scores:
XX      XX      Pred. No.: 1,896-281 Length: 3186
XX      XX      Score: 2883.00 Matches: 552
XX      XX      Percent Similarity: 99.82% Conservative: 0
XX      XX      Best Local Similarity: 99.82% Mismatches: 1
XX      XX      Query Match: 99.79% Gaps: 0
XX      XX      DB: 7
XX      XX
XX      XX      US-10-044-205A-2 (1-553) x ACC44827 (1-3186)

```

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
 Db 85 ATGTGGACATGGGGGCCCCCTGGACCACTGATCGCCACACCGCTTACTGGAGGCCGG 144
 QY 21 LysProSerAspCysAspSerLysGlnLeuGlnAlaArgAlaArgSerLeuAlaLeuPro 40
 Db 145 AAGCCCTCGACTCCGACAGCAAGAGCTGACGGCGCGGCTGACCTGGCCCTGGCC 204
 QY 41 GlyLeuGlnGlyCysAlaGlnLeuArgGlnLysLeuSerLeuAsnProIleSerLeuCys 60
 Db 205 GGGCTGGAGGGCTGGCGGAGCTCGCCCAACACTGCTCCCTGAATCTTCCACAGCCTGTGT 264
 QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
 Db 265 GAGCAGCAGCCCATCGCTGCGGCTCTTCCGATCTTCCAGCAGAGTGGCCACCTTC 324
 QY 81 ArgLysAlaAlaThrPheLeuGlnAspValGlnAsnTyrGlnLeuAlaGlnGlyPro 100
 Db 325 CGCAAGCGGCACCTTCTCTAGAGAGAGTGGAGACTGGAGCTGGCCGAGAGAGGCC 384
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 Db 385 ACCAAAGACAGCGCGCTGCGAGGGCTGTGGCCACTGTGTGCGAGTGGCCCGGG 444
 QY 121 AspProGlnProPheLeuSerGlnAlaAlaThrLysCysGlnAlaAlaThrThrGlu 140
 Db 445 AACCCGCAACCTTCTCTACGCGAGCGCTGGCCACCAAGTCCAGAGCCACACCTGAG 504
 QY 141 GluGlnArgValAlaAlaValThrLeuArgLysAlaGlnAlaPheLeuGlnGlu 160
 Db 505 GAAGAGCGAGTGGCTGCGAGTGGCGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 564
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTyrLysLeu 180
 Db 565 CAACCCCTTAAAGATTTGCGACCGCCCTTCTGACAACTTCTGCGAGTGGAACTC 624
 QY 181 PheGlnMetGlnProValSerAspLysTyrPheThrGlnPheArgValLeuGlnGlySer 200
 Db 625 TTGAGATGCAACCAAGTGCAGACAACTTCACTGAGATTCAGAGTGGGAGAAAGT 684
 QY 201 GlyPheGlyGlnValCysAlaValGlnValAsnThrGlyLysMetTyrAlaCysLys 220
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 QY 241 GluIleLeuGlnLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGlnSer 260
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 QY 261 LysThrHisLeuCysLeuValMetSerLeuMetSerGlnGlyAspLeuLysPheHisIle 280
 Db 865 AAGGCCCATCTGCTGCTGTGATGAGCTGATGATGGGGAGACCTCAAGTTCACATC 924
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
 Db 925 TACACGTGGGACGGCGCTGACATGAGCCGGGTGATCTTTTACTCGGCCAGATA 984
 QY 301 AlaCysGlyMetLeuHisIleuHisGlnLeuGlyIleValTyrArgAspMetLysProGlu 320
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 QY 321 AsnValLeuLeuAspPheLeuGlyAsnArgLeuSerAspLeuGlyLeuAlaGln 340
 Db 1045 AATGTGCTTCTGATGACTCGGCACTGCGAGTATGCTGACCTGGGCTGGCGCGAG 1104
 QY 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
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 QY 361 IleLeuMetGlnLysValSerTyrSerTyrProValAspTyrPheAlaMetGlyCysSer 380

Db 1165 ATCTTATGAGAAAGATTAATTCCTATCCTGAGACGTGTTCCATGGAGATGAGC 1224
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 QY 441 SerArgGlnLysSerAspAspProArgLysHisPhePheLysThrIleAsnPro 460
 Db 1405 AGCAGAGAAAGTCTATGATATCCAGAAACATCATTTCTTAAACGATCACTTCT 1464
 QY 461 ArgLeuGlnAlaGlyLeuIleGlnProProPheValProAspProSerValTyrAla 480
 Db 1465 CGCTGGAGCTGGCTTATGAAACCCCATTTGTGCGAGACCTTCAAGTGTATGCC 1524
 QY 481 LysAspIleAlaGlnIleAspAspPheSerGlnValArgGlyValGlnPheAspLys 500
 Db 1525 AAAGACATCGCTGAATGATGATTTCTGAGAGTTCGGGGGTGAAATTTATGACAA 1584
 QY 501 AspLysGlnPhePheLysAspPheAlaThrGlyAlaValProIleAlaTyrGlnGln 520
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 QY 521 IleIleGlnThrGlyLeuPheGlnGlnLeuAsnProAsnArgProThrGlyCysGlu 540
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 Db 1705 GAGGTAATTCATCCAGTGTGCGGTGTGTATTG 1743

RESULT 10
 AAD28071
 ID AAD28071 standard; cDNA; 1662 bp.
 AC XX
 DT 22-APR-2002 (first entry)
 XX XX
 DE Human Kinase cDNA.
 KW Human; kinase; G-protein coupled receptor kinase; tissue differentiation;
 XX chromosome 3; therapeutic; immune response; drug screening; enzyme; ss.
 OS Homo sapiens.
 XX XX
 FT Key Location/Qualifiers
 FT CDS 1..1662
 FT /*tag= a
 FT /product= "Human kinase protein"
 XX XX
 W0200192496-A2.
 XX XX
 PD 06-DEC-2001.
 XX XX
 PF 31-MAY-2001; 2001WO-US017510.
 XX XX
 ER 01-JUN-2000; 2000US-0208331P.
 XX XX
 PR 18-DEC-2000; 2000US-00738894.
 XX XX
 PA (APPL-) APPLERA CORP.
 XX XX
 PI Guegler K, Di Francesco V, Beasley EM;
 XX XX
 DR WPI, 2002-130533/17.

DR P-PSDB; AAE17136.

XX New isolated human kinase proteins and nucleic acids, useful as a major
PT target for drug action and development, particularly for screening
modulators of the kinase peptides.

XX Claim 4; Fig 1; 87bp; English.

XX The invention relates to human kinase proteins that are related to G-
XX protein coupled receptor kinase subfamily. Human kinase gene is located
XX on chromosome 3. The kinase peptide and nucleic acid are useful in the
XX development of human therapeutic and diagnostic compositions. The peptide
XX is useful as a major target for drug action and development, and is
XX valuable to the field of pharmaceutical development to identify and
XX characterize modulators of the kinase. The proteins may also be used to
XX raise antibodies or to elicit an immune response, as a reagent in assays
XX designed to quantitatively determine levels of the protein in biological
XX fluids and as markers for tissues in which the corresponding protein is
XX preferentially expressed (either constitutively or at a particular stage
XX of tissue differentiation or development in a disease state). The
XX kinase proteins are also useful for providing a target for diagnosing a
XX disease or predisposition to disease mediated by the peptide. The nucleic
XX acid molecules are useful for probes, primers, chemical intermediates and
XX in biological assays. The nucleic acids are also useful in making vectors
XX containing the gene regulatory regions of the nucleic acid molecules and
XX for drug screening to identify compounds that modulate kinase nucleic
XX acid expression. The present sequence is human kinase cDNA expressed in
XX skins, germinal center B cells, colon, kidney and lung

XX Sequence 1662 BP; 419 A; 411 C; 480 G; 352 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.9e-281 Length: 1662
Score: 2876.00 Matches: 551
Percent Similarity: 99.64% Conservative: 0
Best Local Similarity: 99.64% Mismatches: 2
Query Match: 99.55% Indels: 0
DB: Gaps: 0

US-10-044-205a-2 (1-553) x AAD28071 (1-1662)

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DB 1 ATGTGTGACATGGGGGCGCTGACAACTGATGCGCAACGCCCTTACCTGAGGCCCG 60
QY 21 LysProSerAspCysAspSerLysGlnLeuGlnAArgArgArgSerLeuAlaLeuPro 40
DB 61 AAGCCCTCGGACTGGGACAGCAAGAGCTGAGCGCGCGGCTGAGCTGCGCCCTGCC 120
QY 41 GLeuGlnGlyCysAlaGlnLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
DB 121 GGGCTGACAGGAGCTGCGGAGCTCGCCAGACCTGCTCCCTGAACTTCCACGCTGTGT 180
QY 61 GlnGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
DB 181 GAGCGACGACCCATGCGGTGCGCGCTCTCCGACTTCTTCAGCCACAGTCCCACTTC 240
QY 81 ArgLysAlaAlaThrPheLeuGlnAspValGlnAsnTrpGlnLeuAlaGlnGlnGlyPro 100
DB 241 CCGAAGCGCGCACTCTTCTAGAGGAGCTGCAACTGGAGAGCTGGCGAGAGGAGGCC 300
QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
DB 301 ACCAAGAGAGGCGCTGCGAGGCGTGGTGGCCACTTGTGCAAGTGCCTCGCGGCG 360
QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrTrpGln 140
DB 361 AACCCGCAACCTTCTTCACCGCAGCGCGTGGCCACCAAGGCGACGACCACTGAG 420
QY 141 GlnGlnArgValAlaAlaValThrLeuArgLysAlaGlnAlaMetAlaPheLeuGlnGly 160
DB 421 GAAAGAGCGAGTGGCTGAGTACGCTGGCCAAAGGCTGAGGCACTGCTTCTTCAAGAG 480

QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
DB 481 CAGCCCTTTAAGGATTTGTGACAGCGGCTTCTACGCAAGTTCTGCGAGTGAACATC 540
QY 181 PheGlnMetGlnProValSerAspLysTyrPheThrGlnPheArgValLeuGlyLysGly 200
DB 541 TTCGATGTCACACAGTGTGACAGCAAGTACTTCACTGAGTTCAGAGTGTGGGAGAAAGT 600
QY 201 GlyPheGlyGlnValCysAlaValGlnValLysAsnTrpGlyLysMetTyrAlaCysLys 220
DB 601 GGTTTGGGAGGTATGTGCGCTCCAGGTAAACACTGGAGAAAGTGTATGCTCTGTAG 660
QY 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGlyLysMetAlaLeuLeuGlnLys 240
DB 661 AAACGCAAGAGAGGCGCTGAAAGAAAGAGTGGCAGAAAGTGGCTCTCTTGGAAAG 720
QY 241 GlnLeuLeuGlnLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGlnSer 260
DB 721 GAATCTTGGAGAGGTGCGAGCGCTTCAATGTCTCTGCGCTATGCTTTGAGAGC 780
QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyValAspLeuLysPheHisIle 280
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QY 301 AlaCysGlyMetLeuHisLeuHisGlyLeuGlnGlyLysValTyrThrAspMetLysProGln 320
DB 901 GCTGTGGAGTCTGACCTTCATGAACTCGCACTGCTATGCGGACATGAACTCGAG 960
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DB 961 AATGTCTTGTGATGACCTTGCACTGCACTGATTAATGACCTGGGCGTGGCGCTGAG 1020
QY 341 MetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGln 360
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QY 361 IleLeuMetGlnLysValSerTyrSerTyrProValAspTrpPheIleMetGlyCysSer 380
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QY 381 IleTyrGlnMetValAlaGlyArgThrProPheLysAspTyrLysGlnLysValSerLys 400
DB 1141 ATTATGAATGTGTCTGACAGCAACCATTTCAAGAAATTCAGAAAGTCAAGTAA 1200
QY 401 GlnAspLeuLysGlnArgThrLeuGlnAspGlnValLysPheGlnHisAspAsnPheThr 420
DB 1201 GAGGATCTGAAGCAAGACTCTGCAAGAGAGGTCAAAATTCAGCAATGATCACTTACA 1260
QY 421 GlnGlnAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGlnGlnArgLeuGly 440
DB 1261 GAGGAAGCAAAATATTTGACGCTCTTCTTGGCTAAGAAACAGAGCAAGCTTAGGA 1320
QY 441 SerArgLysLysSerAspAspProArgLysHisAspPheLysThrIleAsnPhePro 460
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DB 1381 CGCTGGAGACTGCGCTAATTAAGACCCCATTTGGCCAGACCTTCAAGTGTATAGCC 1440
QY 481 LysAspIleAlaGlnLysAspPheSerGlnValArgGlyValGlnPheAspAspLys 500
DB 1441 AAAGACATCGCTGAATGATGATTTCTGAGGTTGCGGGGCTGGAATTTGATGACAA 1500
QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGln 520
DB 1501 GATAGGAGTCTTCAAACTTTGACAGAGGTGCTTCTATAGATGCGAGGAGAA 1560
QY 521 IleIleGlnThrGlyLeuPheGlnGlnLeuAsnAspProAsnArgProThrGlyCysGln 540

DB 1561 ATTATGAAACGGACCTGTTGAGAACTGATGACCCCAAGACCTACGGGTGTAG 1620
 QY 541 GUGUyAaNsSerSerlySerglyValCysLeuLeuLeu 553
 DB 1621 GAGGGTAATTCATCCAAAGCTGCGGTGTGTTTATTTG 1659
 RESULT 11
 ID AAS06702 standard; cDNA; 1662 BP.
 AC AAS06702;
 XX 12-SEP-2001 (first entry)
 DE Polynucleotide sequence encoding human protein kinase #2.
 XX
 KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
 KW metabolic disorder; immune related disease; neurological disorder;
 KW neurodegenerative disorder; inflammatory disorder; infectious disease;
 KW reproductive disorder; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO20038503-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 22-NOV-2000; 2000WO-US032085.
 XX
 PR 24-NOV-1999; 99US-0167482P.
 XX
 PA (SUGE-) SUGEN INC.
 XX
 PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
 PI Flanagan P, Clary D;
 DR WPI; 2001-343950/36.
 DR P-PSDB; AAT03502.
 XX
 PT Nucleic acids encoding human kinase polypeptides, useful for preventing
 PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
 PT neuronal-associated diseases, and microbial infections.
 XX
 XX Example 1; Fig 1; 433bp; English.
 CC AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel
 CC serine/threonine kinase have been identified as members of the tyrosine or
 CC encoding protein kinases (PTK and STK) families. The polynucleotides
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate kinase expression. For example, they may be used to treat
 CC cancers (especially cancers of haematopoietic origin), cardiovascular
 CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
 CC immune related diseases (e.g. rheumatoid arthritis), neurological
 CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
 CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
 CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
 CC Additionally, polynucleotides encoding protein kinases may be used for
 CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
 CC against the protein kinases and in assays to identify modulators of
 CC protein kinase expression and activity
 XX
 SQ Sequence 1662 BP; 421 A; 411 C; 479 G; 351 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2.52e-280
 Score: 2868.00 Length: 1662
 Percent Similarity: 99.46% Matches: 50
 Best Local Similarity: 99.46% Conservative: 50
 Query Match: 99.27% Mismatches: 3
 DB: Indels: 0
 Gaps: 0

US-10-044-205A-2 (1-553) x AAS06702 (1-1662)
 QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
 DB 1 ATGGTGCACATGGGGGCGCTCGACCAACCTGATGCGCCAAACCGCTACCTGACAGCCCGG 60
 QY 21 LysProSerAspCysAspSerIysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
 DB 61 AAGCCCTCGAGCTCGACAGCAAGAGCTGAGGGGCGGCGGAGCTGGGCGCTGGCCC 120
 QY 41 GlyLeuGlnIlyCysAlaGlnLeuArgGlnIlyLeuSerLeuAsnProHisSerLeuCys 60
 DB 121 GGGCTCGAGGCGCTGCGGAGGCTCGGACAGAGCTGCTCCGAGACTTCCCGAACCTTCCAGCTTC 180
 QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
 DB 181 GAGCAGACAGCCCATCGGTGCGCTCTTCCGAGACTTCCAGCAGAGGCCACAGCTTC 240
 QY 81 ArgIysAlaAlaThrPheLeuGluAspValGlnAsnTyrGlnLeuAlaGlnIlyPro 100
 DB 241 GGCAGAGCGGCAACCTTCTTACAGAGAGCTGGAACCTGGAGCTGGCGAGAGGAGCC 300
 QY 101 ThrIysAspSerAlaLeuGlnIlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 DB 301 ACCAAACACAGCGCGCTCGAGGAGCTGGGCACTTGTGGAGTCCCTGCGCCCGG 360
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrIlyCysGlnAlaAlaThrThrGlu 140
 DB 361 AAGCCGCAACCTTCTTACAGAGCGCGGCGGCAACAGGCGCAAGGCGCAAGCGCACCTGAG 420
 QY 141 GluGluArgValAlaAlaValAlaThrLeuArgIysAlaGlnAlaMetAlaPheLeuGln 160
 DB 421 GAAGACCGAGTGGCTGCGAGAGCGTGGCAAGCTGAGGCCATGGCTTCTTCCAAAG 480
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspIlyPheLeuGlnIlyPhe 180
 DB 481 CAGCCCTTAAAGATTTGTCGACAGCGCCCTTCTTACAGCAAGTTCTTCCAGTGGAACTC 540
 QY 181 PheGluMetGlnProValSerAspIlySerPheThrGluPheArgValLeuGlyIly 200
 DB 541 TTCGAGATGCACACAGTGCACACAGACTTCACTGAGCTTCAAGTGGGGAAGGT 600
 QY 201 GlyPheGlyGluValCysAlaValGlnValIysAsnThrGlyIlyMetCysTyrAlaCys 220
 DB 601 GGTTTGGGAGATGATGTCCTGCAAGTAAACCTGGAGAGATGATGCTGTAG 660
 QY 221 LysLeuAspIlyLysArgLeuIlyLysGlyGlyIlyIlyMetAlaLeuLeuGlnIly 240
 DB 661 AACTGACAAAGAGCGCTGAAGAAAGAGGCGGAGAGATGCTCTTGGAAAAG 720
 QY 241 GluIleLeuGlnIlyValSerSerProPheIleValSerLeuAlaTyrAlaPheGlnSer 260
 DB 721 GAATCTTGGAGAGGTAGAGAGCTTTCATTTGCTTCCGCTATGCTTGAAGGC 780
 QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyIlyAspLeuPheHisIle 280
 DB 781 AAGACCATCTGCTGCTGATGACCTGATGATGGGGAACCTCAAGTTCCACATC 840
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
 DB 841 TACACCTGGGACCGGCTGCTGACATGAGCGGGGTATCTTTAACTCGGCCCAATA 900
 QY 301 AlaCysGlyMetLeuHisLeuHisGlnLeuGlyIlyLeuValTyrArgAspMetLysProGln 320
 DB 901 GCGTGGGATGCTGACCTCCATTAATCTCGCATCTTATCGGACATACCAAGCTGAG 960
 QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
 DB 961 AATGGCTTTCGATGACCTCGGCAAGCTGAGGTATCTGACCTTGGGCTGGCGGTGGAG 1020
 QY 341 MetLysGlyIlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGln 360

Db 1021 ATGAAGGCTGGCAAGCCATCAACCAAGGCTGAAACCAATGTTATCATGCTCTGAG 1080
 QY 361 TLeuMetGluValSerTyrSerTyrProValAspTyrPheAlaMetGlyCysSer 380
 Db 1081 ATCTTAATGAAAGAGTATGATTCCTATCTGATGCTGATGCTGTTGGCAATGGATGACG 1140
 QY 381 TLeuTyrGluMetValAlaGluValThrProPheLeuAspTyrTyrGluValSerTyr 400
 Db 1141 ATTTAAGAAATGTTGCTGACGACACCATTTCAAAATTAACAAGAAAGGCTAGTAA 1200
 QY 401 GluAspLeuTyrGluValThrLeuGluValGluValGluValGluValGluValGluVal 420
 Db 1201 GAGGATCTGAAACCAAGACTCTGCAAGCAAGGCTCAAAATTCAGATGATTAATTCACA 1260
 QY 421 GluGluAlaValAspTyrLeuValGluPheLeuAlaValSerProGluValGluValGluVal 440
 Db 1261 GAGGAGCAAAAGATATTTGAGGCTCTTCTTGCTTAAAGAAACCAAGCAAGGCTTAAAG 1320
 QY 441 SerArgGluValSerAspAspProArgTyrSerHisPhePheLeuThrTyrLeuPhePro 460
 Db 1321 AGCAGAGAAAGTCTGATGATCCAGGAAACATCTTTCTTAAACGATCAACTTCTCT 1380
 QY 461 ArgLeuGluAlaGluValLeuValGluValProPheValProAspProSerValValTyrAla 480
 Db 1381 CCCTGGAAGCTGGCTTATGAAACCCCAATTTGCGCAAGCCCTTCAAGTGTATTATGCC 1440
 QY 481 LysAspTyrLeuAlaGluValLeuAspPheSerGluValAlaGluValGluValGluVal 500
 Db 1441 AANAGCATCTCGTAAATGATGATTTCTTGAAGGTTCCGGGGGCGGAAATTTGATGACAAA 1500
 QY 501 AspLysGluPhePheLeuAspPheAlaThrGluValAlaValProLeuAlaTyrGluGlu 520
 Db 1501 GATAAGCACTGTTCAAAAACCTTCCAGACAGTGTCTTCTATAGATGAGCGCAAGAA 1560
 QY 521 TLeuGluThrGluValLeuPheGluGluValLeuAspProAsnArgProThrGluCysGlu 540
 Db 1561 ATTATGAAACGGGACGTTTGAGGACAGTGAATGACCCCAACGACTTACGGGTTGTAG 1620
 QY 541 GluGluAsnSerSerLysSerGluValCysLeuLeuLeu 553
 Db 1621 GAGGTAATTCATCCAAAGTCTGCGGTGTTGTTATTG 1659
 Db
 RESULT 12
 ACC44826
 ID ACC44826 standard; cDNA, 1662 BP.
 XX
 AC ACC44826;
 DT 04-JUN-2003 (first entry)
 XX
 DE Human G protein-coupled receptor kinase encoding cDNA SEQ ID NO:1.
 XX
 KW Human; G protein coupled receptor kinase; GRK; cytosolic; antidiabetic;
 KW neuroprotective; neurotrophic; cardiovascular; anti-Parkinsonian; cardiant;
 KW vasotrophic; antiaesthetic; gene therapy; cancer; diabetes; CNS disorder;
 KW central nervous system disorder; cardiovascular disorder; asthma; COPD;
 KW chronic obstructive pulmonary disorder; anxiety; mood disorder; enzyme;
 KW Alzheimer's disease; Parkinson's disease; congestive heart failure;
 KW myocardial infarction; ischemic disease; hypertensive vascular disease;
 KW gene; ss.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT CDS 1..1662
 FT /*tag= a
 FT /product= "G protein-coupled receptor kinase (GRK)"
 XX
 PN W02003018815-A2.
 XX
 PD 06-MAR-2003.
 XX
 PF 19-AUG-2002; 2002MO-EP009235.

XX
 PR 21-AUG-2001; 2001US-0313464P.
 XX
 PA (FARB) BAYER AG.
 XX
 PI xiao Y;
 XX
 DR WPI: 2003-278669/27.
 DR P-PSDB; ABP96707.
 XX
 PS Claim 1; Fig 1; 129pp; English.
 XX
 CC The present sequence encodes a human G protein-coupled receptor kinase
 CC (GRK) protein (1). (1) has cytosolic, antidiabetic, neuroprotective,
 CC neurotrophic, cardiovascular, anti-Parkinsonian, cardiant, vasotrophic and
 CC antiaesthetic activities, and can be used in gene therapy. (1) can be
 CC regulated to treat cancer, diabetes, a central nervous system (CNS)
 CC disorder (e.g. anxiety or mood disorders, Alzheimer's disease and
 CC Parkinson's disease), cardiovascular disorders (e.g. congestive heart
 CC failure, myocardial infarction, ischemic diseases of the heart or
 CC hypertensive vascular diseases), asthma and chronic obstructive pulmonary
 CC disorder (COPD). GRK molecules are useful in screening for agents that
 CC regulate or decrease the activity of a GRK. GRK sequences may also be used
 CC for detecting diseases and abnormalities or susceptibility to diseases
 CC and abnormalities related to the presence of mutations in the nucleic
 CC acid sequences that encode the GRK enzyme
 XX
 SQ Sequence 1662 BP; 421 A; 411 C; 479 G; 351 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2,52e-280 Length: 1662
 Score: 2868.00 Matches: 550
 Percent Similarity: 99.46% Conservative: 0
 Best Local Similarity: 99.46% Mismatches: 3
 Query Match: 99.27% Indels: 0
 DB: Gaps: 0
 US-10-044-205A-2 (1-553) x ACC44826 (1-1662)
 QY 1 MetValAspMetGluValAlaLeuAspAsnLeuLeuAlaSerThrAlaTyrLeuGluAlaArg 20
 Db 1 ATGTGTGACATGGGGGCTGCTGACACCTGATGCTGACACCTGACCTGACCTGACCTG 60
 QY 21 LysProSerAspCysAspSerLysGluLeuGluValArgTyrArgTyrSerLeuAlaLeuPro 40
 Db 61 AAGCCCTGAGCTGCGACAGCAAGCAAGCTGACAGCGGCGCGCTGACCTGCGCTGCGCC 120
 QY 41 GLeuGluGluGluCysAlaGluValGluValGluValSerLeuAsnPheHisSerLeuCys 60
 Db 121 GGGCTGCAAGGCTGCGGAGCTCGCGCAAGCTTCTTCAACTTCCACACCTGCTGT 180
 QY 61 GluGluGluProLeuGluValArgTyrArgTyrPheArgAspPheLeuAlaThrValProThrPhe 80
 Db 181 GACACACAGCCCATCGTGTGCGCTCTTCCGTGACTTCTGACCAAGTGCACAGTCCAGCTTC 240
 QY 81 ArgLysAlaAlaThrPheLeuGluValGluValGluValGluValGluValGluValGluVal 100
 Db 241 CGCAAGCGGCAACTTCTTCAAGCAAGCTGCAAGCTGCAAGCTGCAAGCTGCAAGCTG 300
 QY 101 ThrLysAspSerAlaLeuGluGluValAlaThrCysAlaSerAlaProAlaProGly 120
 Db 301 ACCAAGACAGCGCGCTGCAAGGCTGCGCACTTGTGCAATGCTGCTGCTGCTGCTGCTG 360
 QY 121 AsnProGluProPheLeuSerGluAlaValAlaThrTyrCysGluAlaAlaThrThrGlu 140
 Db 361 AACCCGCAACCTTCTTCAAGCAAGCTGCGCAAGCTGCGCAAGCTGCGCAAGCTGCGCA 420
 QY 141 GluGluValValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGluGlu 160

Db 421 GAAGACCAAGTGGCTGAGTGAAGCTGAGCCCAAGGCTTCTTGGTCAAGAG 480
 Qy 161 GlnProPheLysAspPheValThsSerAlaPheTyrAspLysPheLeuGlnTyrLysLeu 180
 Db 481 CAGCCCTTMAAGATTCTGTCAGACGAGCCCTTCTACGACAGATTCTGCGAGTGGAACTC 540
 Qy 181 PheGlnMetGlnProValSerAspLysTyrPheThsGlnPheAspValLeuGlnLysGly 200
 Db 541 TTCGAGATGCAACCAAGTGCAGACAGACTTCACTGAGCTTCAAGAGTGGGAGAAAGT 600
 Qy 201 GlyPheGlnValValValGlnValLysAsnThrGlnLysMetTyrAlaCysLys 220
 Db 601 GCTTTGGGAGGTATGTCCTGACGTCGAGTGAAGAAACCTGGGAAGATGATCTCTGTAAG 660
 Qy 221 LysLeuAspLysLysThrGlnLysLysGlyGlyGlnLysMetAlaLeuGlnLys 240
 Db 661 AAACCTGCAAGAGAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 Qy 241 GlnLysLeuGlnLysValSerSerProPheLysValSerLeuAlaTyrAlaPheGlnSer 260
 Db 721 GAAATCTTGGAGAGAGTCAAGAGCTTTCATGCTCTCTGCTGCTTATGCTTGGAGAGC 780
 Qy 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisLe 280
 Db 781 AAGACCCATCTCTGCTTGTGCATGACCTGATGAGATGGGAGAGAGAGAGAGAGAGAGAG 840
 Qy 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgAlaLePheTyrSerAlaGlnLe 300
 Db 841 TACACAGTGGGAGAGCTGAGCTGAGACATGAGCCGAGTGAATCTTTTATCTGCGCCAGATA 900
 Qy 301 AlaCysGlyMetLeuHisLeuHisGlnLysGlyLysValTyrAspAspMetLysProGln 320
 Db 901 GCCGTGGGAGTGTGACCTCCCATGAACTCGGAGCTGCTATGCGAGACATGAGAGCCTGAG 960
 Qy 321 AsnValLeuLeuAspAspLeuGlnLysCysArgLeuSerAspLeuGlyLeuAlaValGln 340
 Db 961 AATGGCTTCTGGAGATGACCTCGGCACTGAGGTATCTGACCTGGGAGCTGGCCTGAGAG 1020
 Qy 341 MetLysGlyLysProLysProLysThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGln 360
 Db 1021 ATGAGAGGTGGCAAGCCCATCACTCCAGAGGAGCTGAGAACCAATGTTATCATGGCTCTGAG 1080
 Qy 361 IleLeuMetGlnLysValSerTyrSerTyrProValAspTyrPheAlaMetCysSer 380
 Db 1081 ATCCCTAATGAGAAAGGTAGTTATCTTATCTGCTGAGCTGCTGCTGCTGCTGCTGCTG 1140
 Qy 381 IleTyrGlnMetValAlaGlyArgThrProPheLysAspTyrLysGlnLysValSerLys 400
 Db 1141 ATTTATGAAATGCTGTGAGAGAACCACTTCAAAAGTTACAAAGAAAGGTCACTAA 1200
 Qy 401 GlnAspLeuLysGlnArgThrLeuGlnAspGlnValLysPheGlnHisAspAsnPheThr 420
 Db 1201 GAGGATCTGAGAGAAAGAACTTGGCAAGAGAGAGTCAAAATTCAGAGATATATCACTCA 1260
 Qy 421 GlnGlnLysAlaLysAspTyrCysArgLeuPheLeuAlaLysLysProGlnArgLeuGly 440
 Db 1261 GAGGAGCAAAAGATATTGAGAGCTCTTCTGGCTAAGAACAGAGCAACGCTTAAAGA 1320
 Qy 441 SerArgGlnLysSerAspAspProAlaGlyHisHisPhePheLysThrLysAsnPhePro 460
 Db 1321 AGCAGAGAAAGAGTGTGATGCCAGAGAAACATCATTTCTTTAAACATTAACCTTCTT 1380
 Qy 461 ArgLeuGlnAlaGlyLeuLysGlnProPheValProAspProSerValValTyrAla 480
 Db 1381 CGCTTGGAGAGCTGGCTTAATTAACCCCATTTGTGACAGACCTTCAAGTGTATATGCG 1440
 Qy 481 LysAspTyrLeuAlaGlnLysAspPheSerGlyValArgGlyValGlnPheAspAspLys 500
 Db 1441 AAGAGCATGCTGAAATTTGATGTTCTCTGAGGTTGCGGAGGAGGAGATTGATGACAA 1500
 Qy 501 AspLysGlnPhePheLysAsnPheAlaThrGlyValAlaProLeuAlaTyrGlnGlnGln 520

Db 1501 GATAGAGCTTCTTCAAAAATTGCGACAGGTCTGTTCTATAGCATGAGAGAGAA 1560
 Qy 521 IleLeuGlnThrGlyLeuPheGlnGlnLysAspProAsnArgProThrGlyCysGln 540
 Db 1561 ATTATAGAAAGGAGCTGTTTGAAGACTGAAATACCCCAAGAGACTTACGGTGTGAG 1620
 Qy 541 GlnGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
 Db 1621 GAGGATATATCATCAAGTCTGCGCTGTGTGTTGTTATG 1659
 RESULT 13
 ID AAD46351
 ID AAD46351 standard; cDNA; 1486 BP.
 AC AAD46351;
 XX
 DT 27-JUN-2003 (first entry)
 XX
 DE Human cone opsin kinase (GRK7) OK6 splice variant cDNA.
 XX
 KW Human; enzyme; cone opsin kinase; G-protein coupled receptor kinase 7;
 KW GRK7; cone visual signalling; visual sensitivity; visual resolution;
 KW night blindness; colour blindness; Oguchi disease; pineal gland activity;
 KW chromobiological desynchrony; depression; anxiety; memory loss; headache;
 KW mental foginess; fatigue; jet lag; circadian rhythm; ophthalmological;
 KW gene therapy; antidepressant; analgesic; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1062
 FT /tag= a
 FT /product= "Human GRK7 OK6 splice variant protein"
 XX
 PN WC02022541-A2.
 XX
 PD 19-SEP-2002.
 XX
 PF 07-MAR-2002; 2002WC-US007025.
 XX
 PR 07-MAR-2001; 2001US-0274006P.
 XX
 PA (IMMUNEX CORP.
 XX
 PI Bird TA, Spencer M, Mosley BA;
 XX
 DR WPI; 2002-723307/78.
 DR P-PSDB; AAB28953.
 XX
 PT Identifying compounds that alter inhibition of cone opsin kinase
 PT polypeptide activity for treating a conditions related to cone visual
 PT signaling, comprises mixing a compound with a cone opsin kinase and with
 XX an inhibitory polypeptide.
 XX
 PS Example 4; Page 48-49; 61pp; English.
 XX
 CC The present invention relates to novel human cone opsin kinase (G-protein
 CC coupled receptor kinase 7; GRK7) and their corresponding polynucleotides.
 CC The invention further relates to a method of identifying compounds that
 CC alter the inhibition of GRK7 polypeptide activity which involves mixing a
 CC test compound with GRK7 protein and an inhibitory polypeptide and
 CC determining if the test compound alters the inhibition of GRK7 protein
 CC activity by the inhibitory polypeptide. GRK7 sequences are useful for
 CC treating conditions related to cone visual signalling (e.g., night
 CC blindness, colour blindness, difficulty with colour vision, visual
 CC sensitivity, visual resolution or in adapting to changes in light
 CC intensity, Oguchi disease or dominant congenital stationary night
 CC blindness), pineal gland activity (e.g., chromobiological desynchrony,
 CC depression, anxiety, mental foginess, memory loss, headaches, fatigue,
 CC or jet lag). Agonists of GRK7 polypeptide activity may be used to treat
 CC or ameliorate symptoms of a disease for which increased GRK7 polypeptide
 CC activity is beneficial, e.g., decreased colour sensitivity or other cone
 CC photoreceptor-mediated diseases. The GRK7 proteins are also useful in the

CC preparation of a medication for treating a condition or disease related
 CC to cone photoreceptor visual signaling or circadian rhythm, as molecular
 CC probes to screen for inherited defects in colour vision, circadian rhythm
 CC and vision resolution. They are also used as gene therapy tools for
 CC individuals with such disorders. The present sequence is human GRK7 OK6
 CC splice variant cDNA

XX Sequence 1486 BP; 353 A; 387 C; 434 G; 312 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.74e-225 Length: 1486
 Score: 2326.00 Matches: 460
 Percent Similarity: 83.03% Conservative: 0
 Best Local Similarity: 83.03% Mismatches: 1
 Query Match: 80.51% Indels: 93
 Gaps: 1

US-10-044-205a-2 (1-553) x AAD46351 (1-1486)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuLeuAlaAsnThrAlaTyrLeuGlnAlaArg 20
 Db 1 ATGGTGGACATGGGGGCTCTGGACACCTGATGGCAACCGCTTACCTGCAGGCCCGG 60
 QY 21 LysProSerAspCysAspSerIysGluLeuGlnArgAlaGlyArgSerLeuAlaLeuPro 40
 Db 61 AAGCCCTCGACCTGGACAGCAAGAGCTGCAGCGCGCGCTGAGCTTGGCCCTGGCC 120
 QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLeuSerLeuAsnProIleAsnLeuGly 60
 Db 121 GGGCTGCAGGGCTGCGGAGCTCCGCCAAGCTGTCTCTGACCTTCCACACCTGGT 180
 QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgPheLeuAlaThrValProThrPhe 80
 Db 181 GAGCAGACGCCCATGGTCCCGCTCTTCCGTGACCTCTTCCACAGGCCACAGCTTC 240
 QY 81 ArgLeuAlaAlaThrPheLeuGlnAspValGlnAsnTrpGluLeuAlaGluGlnGlyPro 100
 Db 241 CGGAGGCGGACCTTCTTACAGAGACGTGCAGAACTGGGAGCTGGCGAGAGAGAGCC 300
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 Db 301 ACCAAGACAGCGCTCCAGGGGCTGGTGGCACTTGTGCGAGTCCCTGCCCGGGG 360
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGln 140
 Db 361 AACCCGCAACCTCTCTACGCCAGCGCTGGCAACAGGCCAACAGCCACCACTGAG 420
 QY 141 GluGlnArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
 Db 421 GAGAGCGAGTGGCTGCAGTACGCTGCCAAGGCTGAGGCGCATGGCTTTCGAGAG 480
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
 Db 481 CAGCCCTTTAGGATTTGCTAGCCAGGCTTCTTACGACAAAGTTTCGAGAGGAACTC 540
 QY 181 PheGlnMetGlnProValSerAspLysTyrPheThrGlnPheArgValLeuGlyLysGly 200
 Db 541 TTCGAGATGCAACCATGTCAGACACATGACTTCACTGAGTTCAGAGTCTGGGAAAGGT 600
 QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
 Db 601 GGTTTTGGGAGGATATGCTCCAGGTGAAAAACATGGGAGAGATGATGCTGTAG 660
 QY 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGlyLysMetAlaLeuLeuGlnLys 240
 Db 661 AAACCTGCAAGAGCGCTGAGAGAAAGAGGCTGGAGAAATAGCTCTTGGAAAG 720
 QY 241 GluIleLeuGlnLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGlnSer 260
 Db 721 GAATCTTGGAGAAAGCTCAGCAGCCCTTCACTGTCTCTGCTTGGCTTGGAGAC 780
 QY 261 LysThrIleLeuCysLeuValMetSerLeuMetAsnGlyLysAspLeuLysPheIle 280

Db 781 AAGACCATCTCTGCTTGTGATGAGCTGATGATGGGGAGACCTCAAGTTCACATC 840
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
 Db 841 TACACCTGGGACCGGCTGACATGACCGGAGATCTTACTGCGCCAGATA 900
 QY 301 AlaCysGlyMetLeuIleLeuIleGlyLeuValTyrArgAspMetLysProGlu 320
 Db 901 GCGTGTGGAGTGTGACCTCATGAACTGGCATGTCTATGGGACATGAAAGCTTAG 960
 QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaGln 340
 Db 961 AATGTCTTCTGATGACCTGCGCAACGTGAGGTATCTGACCTGGGGCTGGCGAG 1020
 QY 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
 Db 1021 ATGAAGGGTGGCAAGCCCATCCACCGG----- 1047
 QY 361 IleLeuMetGlnLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
 Db 1047 ----- 1047
 QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGlnLysValSerLys 400
 Db 1047 ----- 1047
 QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnIleAspAsnPheThr 420
 Db 1047 ----- 1047
 QY 421 GluGlnAlaLysAspLysCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
 Db 1047 ----- 1047
 QY 441 SerArg-GluLysSerAspAspProArgLysHisIlePhePheLysThrIleAsnPhePr 460
 Db 1048 ---AGAGAAAGACTGATGATCCAGAGAAACATCATTTCTTAAACATCACTTCC 1104
 QY 460 ArgLeuGlnAlaGlyLeuIleGluProProPheValProAspProSerValTyrAl 480
 Db 1105 TCGCTGGAGCTGGCTTATTTGAACCCCATTTGTCCAGACCTTCTGAGTGTATGC 1164
 QY 480 AlaAspLysAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
 Db 1165 CAAGAACATGCGGAATTGATTTCTCTGAGGTTGGGGGGTGGAAATTGATGACAA 1224
 QY 500 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGly 520
 Db 1225 AGATAGCAGTTCTTCAAACTTGGCAGACGTGCTGTTCTTATGACATGGCAGGAGA 1284
 QY 520 uilelleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysG 540
 Db 1285 AATTATGAAACGGGACTGTTGAGAACTGATGACCCCAACACACTACGGGTTGTGA 1344
 QY 540 uGluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
 Db 1345 GAGGGTATTTCAATCCAGCTGGCTGTGTTGTATTG 1384

RESULT 14

ABZ56934 standard; DNA; 1191 BP.

ABZ56934;

04-APR-2003 (first entry)

Human RGSN9 encoding DNA # SEQ ID 2.

Human; RGSN9; heart disease; cancer; omentopathy; gene; ds.

Homo sapiens.

Key Location/Qualifiers

FT CDS 1. 1191
 FT /*tag= a
 FT /product= "RGSNo9"
 PD WO2002103020-A1.
 PD 27-DEC-2002.
 PF 14-JUN-2002; 2002WO-JP005942.
 PR 15-JUN-2001; 2001JP-00182654.
 PA (TAKE) TAKEKA CHEM IND LTD.
 PI Koyama N, Tanida S, Yamamoto K;
 DR WPI; 2003-157045/15.
 DR P-PSDB; ABB60078.
 XX
 PT Novel disease-associated gene of the RGS gene family and its product,
 PT applicable in diagnosis of and screening for drugs for heart diseases,
 PT cancers and omentopathy.
 PS Claim 6; Page 81-82; 96pp; Japanese.
 CC The invention relates to a novel disease associated gene and its uses.
 CC The gene and its encoded protein are useful for diagnosis of and
 CC screening for drugs for heart diseases, cancers and omentopathy. The
 CC current sequence represents the human RGSNo9 encoding DNA sequence
 XX
 SQ Sequence 1191 BP; 274 A; 320 C; 363 G; 234 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.8e-198 Length: 1191
 Score: 2058.00 Matches: 396
 Percent Similarity: 99.75% Conservative: 0
 Best Local Similarity: 99.75% Mismatches: 1
 Query Match: 71.24% Indels: 0
 DB: Gaps: 0
 US-10-044-205a-2 (1-553) x ABZ56934 (1-1191)
 QY 1 MetValaspMetGlyAlaLeuaspAsnLeuIleAlaasnThrAlaTyrLeuGlnAlaArg 20
 DB 1 ATGTGTGACATGAGGGGCGCTGAGCAACTGATGCGCCACACCGGCTTCTGAGGCGCG 60
 QY 21 LysProSeraspCysaspSerIysGlnLeuGlnArgArgArgSerLeuAlaLeuPro 40
 DB 61 AGCCCTGAGACTGCGACAGCAAGAGCTGACGCGCGGCGCTTACCTGCGCTTGC 120
 QY 41 GlyLeuGlnGlyCysAlaGlnLeuArgGlnLeuSerLeuAsnPheHisSerLeuGly 60
 DB 121 GGGCTGCGAGGCTGCGCGAGCTCGCCCAAGCTGTCCCGAAGCTTCCACAGCCTGT 180
 QY 61 GlnGlnGlnProIleGlyArgArgLeuPheArgaspPheLeuAlaThrValProThrPhe 80
 DB 181 GAGCAGCAGCCATCGGTGCGCGCTTCCGAGCTTCCAGCCACAGTGGCCACGCTTC 240
 QY 81 ArgYsaAlaIaThrPheLeuGlnAspValGlnAsnTrpGlnLeuAlaGlnGlyPro 100
 DB 241 CGCAAGCGGCAACCTTCTTGAAGAGCGTGCAGACTGGAGGCTGGCGAGAGGAGACC 300
 QY 101 ThrLysaspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 DB 301 ACCAAGACAGCGCGCTGCGAGGCGTGTGCGCACTTGTCCAGTCCCTGCGCCCGGG 360
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaIaThrThrGln 140
 DB 361 AACCCGCAACCTTCTTCAAGCAGCGCGTGGCCACCAAGTCCACAGCCACCTGAG 420
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 QY 181 PheGlnMetGlnProValSerAspLysTyrPheThrGlnPheArgValLeuGlyLysGly 200
 DB 541 TTGAGATGCAACCAAGTGTGACAGCAAGTCACTTCACTGAGTTCAGAGTCTCGGAGAAAG 600
 QY 201 GlyPheGlyGlnValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
 DB 601 GCTTTGGGAGGATGTGCGCTGCGAGTAAACACCTGGAGAGATGATGCTTCTGAGAG 660
 QY 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGlyLysMetAlaLeuLeuGlnLys 240
 DB 661 AAACCTGACAGAAAGCGGCTGAAAGAAAGGTGGAGAAATGCTCTTCTTGGAGAAAG 720
 QY 241 GlnLeuLeuGlnLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGlnSer 260
 DB 721 GAAATCTTGGAGAGGTCAGAGCGCTTTCATTTGATGCTCTTCTGCGCTTTCAGAGC 780
 QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyLysAspLeuLysPheHisIle 280
 DB 781 AAGACCATCTCTGCTGCTTGTATGAGCTGATGATGAGGAGAGCTCAAGTTCCACATC 840
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
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 QY 301 AlaCysGlyMetLeuHisLeuHisGlnLeuGlyIleValTyrArgaspMetLysProGln 320
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 DB 1021 ATGAAAGGTGGACCCCATCACCCAGAGCGCTGAAACCAATGTTACATGGCTCTTGA 1080
 QY 361 IleLeuMetGlnLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
 DB 1081 ATCTTAATGAAAGAGTAAAGTAAATCTTCACTGTGAGCTGTTGCCATGAGATGAG 1140
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 DB 1141 ATTATGAATATGCTTGTGAGAGCAACCATTTCAAAATTTACAGAGAAAG 1191
 RESULT 15
 ID AAH78798 standard; cDNA; 1062 BP.
 XX AAH78798;
 DT 08-MAR-2002 (first entry)
 XX
 DE Human G-protein coupled receptor kinase 2 cDNA sequence.
 KW G-protein coupled receptor kinase; GRK; human; ss; gene therapy;
 KW drug screening; gene expression characterization; NHP;
 KW novel human protein.
 OS Homo sapiens.
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 FH Key Location/Qualifiers
 FT CDS 1..1062
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 PD WO200168869-A2.
 XX 20-SEP-2001.

XX 08-MAR-2001; 2001MO-US007500.
 XX 10-MAR-2000; 2000US-0188449P.
 XX (LEXI-) LEXICON GENETICS INC.
 PA Walke DW, Wilganowski NL, Turner CA;

XX WPI; 2001-570872/64.
 DR P-SDB; AAG77816.

XX New polynucleotides encoding human proteins that share sequence
 PT similarity with animal kinases e.g. G-protein coupled receptor kinases,
 PT useful for drug screening, diagnosis and in gene therapy of biological
 PT disorders.

XX Claim 4; Page 32; 34pp; English.

XX The present cDNA sequence encodes a human G-protein coupled receptor
 CC kinase (GRK), also designated NRP (novel human protein) in the
 CC specification, which is claimed in the invention. The invention comprises
 CC novel human nucleotide and protein sequences which have similarity to G-
 CC protein coupled receptor kinases. Oligonucleotides derived from the
 CC nucleotides of the invention are useful as hybridisation probes for
 CC screening libraries and assessing gene expression patterns. The
 CC nucleotides of the invention are also useful in drug screening and gene
 CC therapy for the modulation of GRK expression. The nucleotides of the
 CC invention can be used to genetically engineer host cells to express GRK
 CC products in vivo. The nucleotide sequences of the invention are also
 CC useful in addressable arrays for identifying and characterising the
 CC temporal and tissue specific expression of a gene and in microarrays to
 CC screen collections of genetic material from patients who have a
 CC particular medical condition. The proteins of the invention are useful
 CC for generating antibodies, as reagents in diagnostic assays, for
 CC identifying other cellular gene products related to GRK, and as reagents
 CC in assays for screening for compounds that are useful in the treatment of
 CC mental, biological or medical disorders/diseases

XX SQ Sequence 1062 BP; 237 A; 296 C; 330 G; 199 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,676-172 Length: 1062
 Score: 1801.00 Matches: 349
 Percent Similarity: 99.71% Conservative: 0
 Best Local Similarity: 99.71% Mismatches: 1
 Query Match: 62.34% Gaps: 0
 DB: 4

US-10-044-205a-2 (1-553) x AAH78798 (1-1062)

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 QY 41 GlyLeuGlnGlyCysAlaGlnLeuArgGlnIysLeuSerLeuAsnPheHisSerLeuCys 60
 Db 121 GGGCTGCGAGGCGCTCGCGGAGCTCGCCAGAGCTGTCTCGAATCTTCCACAGCTGTGT 180
 QY 61 GlnGlnGlnProIleGlyArgArgPheArgAspPheLeuAlaThrValProThrPhe 80
 Db 181 GAGCAGCAGCCCATGGTGGCGCTCTTCCGTGACTCTTACGCCAGAGTGCACAGTTC 240
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 Db 361 AACCCGCAACCTTCTCTTCCAGCGCGGTGGCCACCAAGTGCAGAGCACCACTGAG 420
 QY 141 GlnGlnArgValAlaAlaValThrLeuArgIysAlaGlnAlaMetAlaPheLeuGlnIu 160
 Db 421 GAAGAGCAGAGTGGCTGGAGTGAAGCTGGCCAGAGCTGAGGCCATGGCTTCTTGCAGAG 480
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTyrLysLeu 180
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 QY 181 PheGlnLeuGlnProValSerAspLysTyrPheThrGlnPheArgValAlaLeuGlnGly 200
 Db 541 TTGAGATGCAACCAAGTGCAGCAAGATCTTCACTGAGTCAAGTCTGGGAAAAGGT 600
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 Db 1021 ATGAAGGTTGGCAAGCCCATCAACCAAGAG 1050

Search completed: August 13, 2004, 19:14:24
 Job time : 481 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 13, 2004, 18:42:11 ; Search time 2705 Seconds

(without alignments)
6104.912 Million cell updates/sec

Title: US-10-044-205A-2

Perfect score: 2889

Sequence: 1 MWMGALDNLANTAYLQAR.....NRPIGCEGNSKSVCLL 553

Scoring table:

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2/1/USPTO.spool/US10044205/runat_06082004_104322_23369/app.query.fasta_1.711
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-OUTPM=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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Database:

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27: em_estdb: *
28: gb_estc: *

29: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1262	43.7	2329	11	BC027597 Homo sapi
2	1219.5	42.2	2998	11	BC057206 Mus muscu
3	1218.5	42.2	2978	11	AK051405 Mus muscu
4	955.5	33.1	1721	29	AY406080 Homo sapi
5	940.5	32.6	1721	29	AY406082 Mus muscu
6	883.5	30.6	1201	13	EX404586 BX404586
7	826.5	28.5	998	13	BQ066445 AGNCOURT
8	822.5	28.5	998	13	BQ057613 AGNCOURT
9	813.5	28.2	1017	13	BQ061150 AGNCOURT
10	803.5	27.8	1019	13	BQ061148 AGNCOURT
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27	737	25.5	937	12	BQ477593 AGNCOURT
28	731.5	25.3	660	13	BQ052019 AGNCOURT
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33	720.5	24.9	765	9	AJ442768 AGNCOURT
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37	700.5	24.2	696	10	BE677821 AGNCOURT
38	700	24.2	906	14	CH195708 AGNCOURT
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41	686.5	24.1	1067	12	BM927442 AGNCOURT
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43	680.5	23.9	726	14	CF520008 AGNCOURT
44	685	23.7	1095	13	BQ058855 AGNCOURT
45	681	23.6	1032	12	BM472080 AGNCOURT

ALIGNMENTS

RESULT 1
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DEFINITION
BC027597
ACCESSION
BC027597
KEYWORDS
BC027597.1 GI:20379554
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2329)

AUTHORS
Straussberg R.
TITLE
Direct Submission
Submitted (08-Apr-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-9250,
USA

REMARK
COMMENT
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: gcgaps-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NIGMS) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadan@systemsbio.org
Anup Madan, Jessica Faney, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LIML at: <http://image.liml.gov>
Series: IRK Plate: 34 Row: 1 Column: 14
This clone was selected for full length sequencing because it
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This clone has the following problem: frame shifted.

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ORIGIN

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Query Match: 43.68% Indels: 25
DB: 11 Gaps: 9

US-10-044-205a-2 (1-553) x BC027597 (1-2329)

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QY 104 ----SerAlaLeuGlnGlnIysLeuValAlaThrCysAlaSerAlaProAlaProGluAsnPro 122
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DB 1807 GACATCACTTCAAGAGGCTGAGGCAACCATGCTGAGGCCCTTCTGCTCATCT 1866
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FEATURES

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 putative"

ORIGIN

Alignment Scores:

Pred. No.: 2,886-112 Length: 2978
 Score: 1218.50 Matches: 236
 Percent Similarity: 67.20% Conservative: 102
 Best Local Similarity: 46.92% Mismatches: 153
 Query Match: 42.18% Indels: 12
 DB: 11 Gaps: 6

US-10-044-205A-2 (1-553) x AK051405 (1-2978)

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 D b 310 C G T G A C T A C C A G C C T A T G T G A G C C C A G C C A T T G G G G C C T G T A T T T T C G T G A G T T C 369
 QY 74 L e u a l a t h r v a l p r o t h r p h e a r g l y s a l a l a t h r p h e l e u g l u a s p v a l g l n a n t p r 93
 D b 370 T G T G C T A G C A G A C C T G A G C T G A C C C G G T G T A C T C C T T C T G A T G G G G T G T C T G A A T A T 429
 QY 94 G l u l e u a l a g l u g l i n g l y p r o t h r l y s a s p s e r a l a ----- l e u g l i n g l y l e u a l 110
 D b 430 G A G G T G A C C C C T G A T G A A G G A A G C A T G T G G G C C C G A C T A T A T C A G A A C T T T C T G 489
 QY 111 A l a t h r c y s a l a s e r a l a p r o l a p r o g l y a s n p r o g l i n p r o p h e l e u s e r g l n a l a v a l 130
 D b 490 A G C A C A C G G G T C C T G A C C T C A T C C C T G A A G T T C A G G C A G C T G T G A G T A A C T G T --- 546
 QY 131 A l a t h r l y s c y s g l n a l a l a t h r t h r g l u g l u g l u a r g v a l a l a l a - v a l t h r l e u a r 150
 D b 547 G C C A G C G G C T A G A G G A G G A C C C T G C A A A G A C T T C T T C C A G A G C T G A C C C G G C T G - 604
 QY 150 g l y s a l a g l u a l a w e r a l a p h e l e u g l i n g l i n p r o p h e l y s a s p h e v a l t h r s e r a l 170
 D b 605 ----- A C C A G A G A T A C T T A G C A G C G C C C T T T T G C A C T A C T T C A C A G A C A T 654
 QY 170 a p h e t y z a s p l y s p h e l e u g l i n t r p l y s l e u p h e g l u m e t g l n p r o v a l s e r a s p l y s t y 190
 D b 655 C T A C T T C A A C C G T T T C T C A G T G G A A G T G G T G A A A G C A C A C A T G A C A A A A A C 714
 QY 190 r p h e t r g l u p h e a r g v a l l e u g l y l y s g l y g l y p h e g l y g l u a l a l y s a l a v a l g l n a 210
 D b 715 C T T C A G C A G A C C G A G C T C T T G G C A A A G G T G G C T T T G G G A G G T A T G T G C C T G C A G G T 774
 QY 210 l l y s a s n t h r g l y l y s m e t t y r a l a c y l s l y s l e u a s p l y s t y s t y r g l e u l y s t y l y 230
 D b 775 G C G G C A A C A G C A A G T A C G A T C A A G A A A C T G A A A A A A G A G C A T T A A A A C G 834
 QY 230 s g l y g l y l y s m e t a l a l e u g l u l y s g l u l l e u g l u l y s v a l s e r s e r p r o p h 250
 D b 835 A A A G G G A G G C C A T G C T C T C A C G A A A A C A G A C T T T G A G A A A G T A A C A G A C A G A G T T 894

QY 250 e l l e v a l s e r l e u a l a t y r a l a p h e g l u s e r l y t h r i s l e u c y s l e u a l a w e t s e r i e 270
 D b 895 T G A G A G A C C T T A G C C T A C C C T A T G A G A C A A G A T G A C A T G T C C T G G T G C T G A C A T T 954
 QY 270 u m e t a s n g l y g l y a s p l e u l y s p h e i s l e t y a s n v a l g l y t h r a r g l y l e u a s p h e 290
 D b 955 G A T G A T G G A G G T A C C T T A A G T T C A C A T T C A C A T G G C C A G G C T T T C C T T A 1014
 QY 290 t s e r a g v a l l e p h e t y s e r a l g l n l e a l a c y s g l y m e t l e u i s l e u i s g l u e 310
 D b 1015 A G A C C T G C T C T T A T G C T G A G A T C T G T G G C C T G A A A C C T G A C C G G A 1074
 QY 310 u g l y l e v a l t y z a s p m e t l y s p r o g l u a s n v a l l e u a s p a s p l e u g l y a n c y 330
 D b 1075 A C C A T T G T G A C G G A T C T A A G C C A G A A T A C C T T C G A T A C A C A T G C C A C A T 1134
 QY 330 s a r g l e u s e r a s p l e u g l y l e u a l a l a g l u m e t l y s g l y g l y s p r o i l e t h r g l n r 350
 D b 1135 T C G A T C T C G A C C T G G A C T G G C C G T G C A T G T C C T G A G G C C A G C A T C A A A G C C G 1194
 QY 350 g a l a g l y t h r a s n g l y t y r m e t a l a p r o g l u l l e u m e t g l u s v a l s e r t y s e r t y 370
 D b 1195 T G T G G C A C T G T G G C C T A C A T G C T C C A G A G T G T G A G A A T A G --- C C T A C A C G T T 1251
 QY 370 r p r o v a l a s p t r p h e a l a m e r g l y c s e r i l e t y r g l m e t v a l a l a g l y a r g t h r p r 390
 D b 1252 C A G T C C T A C T G T G G C C C T A G G T G C C T C C T G A G A T G A T G C C A G C A G C A G T C G C C 1311
 QY 390 o p h e l y s a s p t r l y s g l u l y s v a l s e r l y s g l u s p l e u l y s g l n r t h r g l e u a s 410
 D b 1312 C T T C C A G A G A G A G A A G A A G A T A A G C C C A A G A G T G --- G A G G C T G T G A A A G A 1368
 QY 410 p g l u v a l y s p h e g l n i s a s p a s n p h e t h r g l u g l u a l a l y s a s p l l e c y a r g l e u p h 430
 D b 1369 A C T G C C A G A G A C A C A G A C C C C T T T C T C A C A G C G C G T C A C T C T G T T C A G C T 1428
 QY 430 e l e u a l a l y s l y s p r o g l u g l n a r g l e u g l y s e r g --- g l u l y s e r a s p a s p r o a r 449
 D b 1429 T C T T A G C A A G A C C T T C T G A G C C C T G G G T G T G T G A G A G T G G C C C G G A G T A A 1488
 QY 449 g l y s h i s h i s p h e p h e l y t h r l l e a s n p h e p r o a r g l e u g l u a l a g l y l e u l l e g l u p r 469
 D b 1489 G A A C A C C C C T T T C A A G A A C A G A A T T C A A G C G C T G G A A C T G G A C T T G A G C C 1548
 QY 469 o p r o p h e a l p r o a p p r o s e r v a l v a l t y r a l a l y s a s p l l e a l a g l u l l e a s p h e 489
 D b 1549 A C C T T T A A G C C T G A T C C C A G G C T A T T A T T A G A A G A T G C C T G A C A T T A A C A G T T 1608
 QY 489 e s e r g l u a l a r g l y v a l g l u p h e a s p l y s p l y s g l n p h e p h e l y s a s n p h e a l 509
 D b 1609 C T T A C A G T T A A G G T G A T C T G A G C C C A G A C C A A G A C T T C T A C A A A G T T T G C 1668
 QY 509 a t t h r g l y a l a l a p r o i l e a t r p g l n g l u g l u l l e i l e g l u t h r g l y l e u p h e g l u g l 529
 D b 1669 C A C A G G A C T G T G C A T C C C C T G G A G A T G A T G T G A A C C G A G T C T T C A G A 1728
 QY 529 u l e u a s n 531
 D b 1729 A C T C A A T 1735

RESULT 4
 AY406080 1721 bp DNA linear GSS 15-DEC-2003
 LOCUS Homo sapiens GPRK5 gene, VIRUTAL TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AY406080
 VERSION AY406080.1 GI:39762054
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1721)

AUTHORS
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarimal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Snihsy, J.J.,
Adams, M.D. and Cargill, M.

TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios

JOURNAL
Science 302 (5652), 1960-1963 (2003)

REFERENCE
PUBMED
14671302

AUTHORS
2 (bases 1 to 1721)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarimal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Snihsy, J.J.,
Adams, M.D. and Cargill, M.

TITLE
Direct Submission

JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment

FEATURES
Location/Qualifiers
source
1..1721
/organism="Homo sapiens"
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ORIGIN
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Score: 955.50 Matches: 198
Percent Similarity: 61.95% Conservative: 82
Best Local Similarity: 43.81% Mismatches: 141
Query Match: 33.07% Indels: 31
DB: 29 Gaps: 8

US-10-044-205a-2 (1-553) x AY406080 (1-1721)

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543 NNNNGTCGTGCTGCGCAGGTTCCGGCCAGCGG9TAAATGATATCCCTCGCAACGCTTGGAAG 602
224 LysLysArgLeuLysGlyLysGlyGlyLysMetAlaLeuGlnLysGlyLysLeu 243
603 AAGAAAGGATCAAAAAGAGAGAGGAGGTCATGGCTCCCTCAATGAGAGCAATCTTC 662
244 GlnLysValSerSerProPheLeuValSerLeuAlaThrAlaPheGlnSerLysThrHis 263
663 GAGAGGTCACAGAGTCAGTTCGTCGTCACCTCGGCTCATCTCCAGAGCAAGATGCA 722
723 CTGTCGTGCTGCTGTCATCATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 782
284 GlyThrArgGlyLeuAspMetSerArgValIlePheThrSerAlaGlnIleAlaCysGly 303
783 GGCACCCCTGCTTCGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 842
304 MetLeuHisLeuHisGlnLeuGlyLysValLysArgAspMetLysProGlnValLeu 323
843 TTAGAAGACCTCCACCGTCGAGAGACACCGTCCTACGAGATCTGAACCTGAAACATCTG 902
324 LeuAspAspLeuGlyLysCysArgLeuSerAspLeuGlyLysLeuAlaValGlnMetLysGly 343
903 TTAGATGATATATGACCATATGACATATGACATATGACATATGACATATGACATATGAC 962
344 GlyLysProLysThrGlnArgAlaGlyThrAsnGlyLysMetAlaProGlnLeuMet 363
963 GGAAGACCTGATCCG 1022
364 GlnLysValSerLysSerLysProValAspThrPheAlaMetGlyCysSerLysLeuGly 383
1023 AACGAG---AGTAAAGGCTGAGCCGACCTACTGCGGCTTGGCTGCTCCATATGAG 1079
384 MetValAlaGlyLysThrProPheLysAspThrLysGlnLysValSerLysGlnAspLeu 403
1080 ATGATCGAGGCG 1139
404 LysGlnArgThrLeuGlnLysGlnValLysPheGlnHisAspAsnThrGlnLysAla 423
1140 GACCCGCGGCTCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1196
424 LysAspLysCysArgLeuPheLeuAlaLysLysProGlnLysArgLeuGlySerArgLys 443
1197 AAGTCATCTCAAGATGCTGCTACGAAAGATGCGAAGACAGAGGCTGCGCGAGGAG 1256
444 Lys---SerAspAspProArgLysHisHisPhePheLysThrIleAsnPheProArgLeu 462
1257 GAGGAGGCTGAGAGGTCAG 1316
463 GlnAlaGlyLeuIleGlnLysProPheValProAsp 474
1317 GAAAGCGGAGATGAGACCTCCCTTCCTCCAGAC 1352

RESULT 5
AY406082 1721 bp DNA linear GSS 15-DEC-2003
LOCUS
DEFINITION
Mus musculus GPRK5 gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY406082
VERSION
AY406082.1 GI:39762056
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Scuriognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1721)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarimal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Snihsy, J.J.,

TITLE Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1721)
AUTHORS Todd, M.A., Tanenbaum, D.M., Clevello, D.R., Lu, F., Murphy, B.,
Perriera, S., Wang, G., Zheng, X.H., White, T.J., Smitsky, J.J.,
Adams, M.D. and Cargill, M.
DIRECT SUBMISSION
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"
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ORIGIN

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Percent Similarity: 61.88% Conservative: 83
Best Local Similarity: 43.27% Mismatches: 151
Query Match: 32.55% Indels: 19
Gaps: 7

US-10-044-205a-2 (1-553) x AY406082 (1-1721)

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QY 57 HisSerLeuGlyGlnGlnProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 176
DB 108 TACAGTCTATGTGACAGAGACCAATTTGGAGAGCTGCTTTTGCACAGTTCTGTGAACC 167
QY 77 ValProThrPheArgGlyAlaAlaThrPheLeuGlnAspValGlnAsnTrpGlnLeuAla 96
DB 168 AGGCTGCTGGCTGAGAGTCTACATTCAGTTCTGAGCTTACAGCAATATGAATTACT 227
QY 97 GlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 116
DB 228 -----CCAGATGAACCTTTGGGCGAAGGGG--AAGGAATATATGACCAAGTAC 275
QY 117 ProAlaProGlyAsnPro-----GlnProPheLeuSerGlnAla 129
DB 276 CTCACCTCCAAAGTCCCACTTCATTGCGCCCAAGTTGAGACAGACCTGCTCCAGACA 335
QY 130 ValAlaThrGlyCysGlnAlaAlaThrThrGlnGlnGlnGlnGlnGlnGlnGlnGln 149
DB 336 GAGAGAGAGCTCTGCGAGAGCCCTGCAAAAGAACTCTCTGCTGCTGCTGCTGCTGCT 395
QY 150 ArgGlyAlaGlnAlaMetAlaPheLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 169
DB 396 CATGAC-----TACTGGAAGGAGAGACCCCTTCCAGAGTACCTGAGTAC 440
QY 170 AlaPheTyrAspLeuPheLeuGlnTrpLeuPheGlnMetGlnProValSerAspGly 189
DB 441 ATGTATTTTACGCTTTTCTGCAAGGAAATGTTAGAAAGNNNNNNNNNNNNNNNNNNNN 500
QY 190 TyrPheThrGlnPheArgValLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 209
DB 501 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 560
QY 210 ValLysAsnThrGlyLysMetTyrAlaCysGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 229
DB 229 -----

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QY 230 LysGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 249
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QY 250 PheLeuValSerLeuAlaTyrAlaPheGlnSerLeuThrHisLeuGlyValMetSer 269
DB 681 TTTTGCTCAACCTGGCTTATCCCTATGAACCAAGATGACATATGCTGCTGCTGAC 740
QY 270 LeuMetAsnGlyGlyAspLeuPhePheHisLeuAsnValGlyThrArgGlyLeuAsp 289
DB 741 ATTATGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 800
QY 290 MetSerArgValIlePheTyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuGln 309
DB 801 GAAGAGGAGCCTTATTTTATGACAGTCAATCTCTGCTGCTGCTGCTGCTGCTGCT 860
QY 310 LeuGlyIleValTyrArgAspMetLeuProGlnAsnValLeuLeuAspAspLeuGln 860
DB 861 GAGAACCTCTCTTATGAGATCTTAAACCGAAGAACATCTTGTGATATATATGAGCC 920
QY 330 CysArgLeuSerAspLeuGlyLeuAlaValGlnMetGlyGlyGlyGlyGlyGlyGly 949
DB 921 ATTAAGATCTCAAGCTCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG 980
QY 350 ArgAlaGlyThrAsnGlyTyrMetAlaProGlnIleLeuMetGlnLysValSerTyr 369
DB 981 CGGATAGGACATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1037
QY 370 TyrProValAspTrpPheAlaMetGlyCysSerIleTyrGlnMetValAlaGlyThr 389
DB 1038 CTGAGCCCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1097
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QY 410 AspGlnValLysPheGlnHisAspAsnPheThrGlnGlnAlaLysAspIleCysArg 429
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DB 1215 CTGCTACCAAGAGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1274
QY 449 ArgLysHisHisPhePheThrLeuAsnPheProArgLeuGlnAlaGlyLeuGln 468
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QY 469 ProProPheValProAsp 474
DB 1335 CCTCCCTTCTGCTGAGAT 1352

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RESULT 6
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LOCUS
DEFINITION BX404586 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
ACCESSION BX404586
VERSION BX404586.1 GI:30648023
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1201) mRNA EST 13-MAY-2003
AUTHORS Li, W.B., Gruber, C., Tessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France

Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3090.f for
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0A004AG03NP1&cluster=3090.f. Contact:
Feng-Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CS0A004AG03NP1.

FEATURES

source

Location/Qualifiers
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/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
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double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Alignment Scores:
Pred. No.: 8,966-79 Length: 1201
Score: 883.50 Matches: 166
Percent Similarity: 74.59% Conservative: 63
Best Local Similarity: 54.07% Mismatches: 75
Query Match: 30.58% Indels: 3
DB: Gaps: 13

US-10-044-205a-2 (1-553) x BX404586 (1-1201)

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195 ArgValLeuGlnGlyGlyGlyPheGlnGlyValGlyAlaValGlnValLysAsnThrGly 214
943 CGAGTCTCTGGGCAAGGAGTCTTGGGAGAGTGTGGCGCTGCGAGTGGGCGCACAGGT 884
215 LysMetTyrAlaCysLysLysLeuAspLysLysLysLysLysLysLysLysLysLys 234
883 AAGATGTAAGCTGCAAGAGAGTGAAGAAAAGCGATCAAGACCGAAGCGAGCGCC 824
235 MetAlaLeuLeuGlnGlyGlnGlyGlnGlyGlnGlyGlnGlyGlnGlyGlnGlyGln 254
823 ATGGCGCTGAAGAGAGAGATCCGAGAAAGTGAACAGTGTGATGATGATGATG 764
255 AlaTyrAlaPheGlnSerLysThrLysLeuCysLeuValMetSerLeuMetAsnGlyGly 274
763 GCCTACGCTCATGAGACCAAGAGAGCGCTGTCTCCGTGGTGTGACACTGATGAAGCGG 704
275 AspLeuLysPheHisLysLysValGlnValGlnValGlnValGlnValGlnValGln 294
703 GACCTCAAGTCCACATCTACCATGAGCGAGCTGTCTCCCGAAGCGGCGCGCTC 644
295 PheTyrSerAlaGlnLysLysLysLysLysLysLysLysLysLysLysLysLysLys 314
643 TTCACGCGCCCGAGATCTGCTGTGGCTGAGAGACTTGCACCGGAGCGCATCTGTAC 584
315 ArgAspMetLysProGlnValLeuLeuAspLeuGlnValGlnValGlnValGlnValGln 334
583 AAGAGACCTGAAGCCCAAGAACTCTGTGTGATGACACAGCGCACATCCCATCTCTAC 524
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415 GlnHisAspAsnPheThrGlnGlnAlaLysAspLysLysLysLysLysLysLysLys 434
289 TATTCGAGCGCTTCCCGCAGCGCCGCTCATCTTGTCTCAAGCTCTCTGCAAGGAC 220
435 ProGlnLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 453
229 CTGCGCAAGCGCTGT 170
454 PheLysThrLysAsnPheProArgLeuGlnAlaGlyLeuLysLysLysLysLysLys 473
169 TTTAAGAGCTGAAGCTTCAAGCGCTGTGAGAGTGTGAGAGTGTGAGAGTGTGAGAGCT 110
474 AspProSerValValTyrAla 480
109 GACGTGATGAGCGCCACTCC 89

RESULT 7

B0066445 968 bp mRNA linear EST 02-APR-2002
LOCUS B0066445
DEFINITION AGENCOURT 6861074 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5931090
5', mRNA sequence.
ACCESSION B0066445
VERSION B0066445.1 GI:19895491
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Ion Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: Lick2111 row: n column: 19
High quality sequence stop: 636.
Location/Qualifiers
1..968
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5931090"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH MGC 99"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

FEATURES

source

Location/Qualifiers
1..968
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5931090"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH MGC 99"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN

Alignment Scores:

Pred. No.: 4.12e-73
 Score: 826.50
 Percent Similarity: 70.97%
 Best Local Similarity: 50.97%
 Query Match: 28.61%
 Gaps: 13
 Matches: 158
 Conservative: 62
 Mismatches: 79
 Indels: 11
 Gaps: 5

US-10-044-205A-2 (1-553) x B0066445 (1-968)

QY 236 AlaLeuLeuGluGluSerValSerSerProPheIleValSerLeuAla 255
 Db 3 GCCCTCAATGAGAGAGATCTCTGAGAGAGTCAACATCTGCTTGGTGTCAACCTGGCC 62
 QY 256 TyrAlaPheGluSerLysThrHisLeuGlyLeuValMetSerLeuMetSerGlyAsp 275
 Db 63 TATGCTTACGAGACCAAGATGACCTGTGCTTGGTGTGCTTACGACCTCAATGAGAGAGTGCAC 122
 QY 276 LeuLysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePhe 295
 Db 123 CTGAAGTTCACATCTTACACATGAGGCAACCTGCTTGGAGAGAGAGGCGCTTGT 182
 QY 296 TyrSerAlaGlnIleAlaCysGlyMetLeuHisIleGluLeuGlyIleValTyrArg 315
 Db 183 TATGCGGAGAGATCTCTGCTGCTTACGACCTTCAACCGTGAACACCGCTTACCA 242
 QY 316 AspMetLysProGluAsnValLeuLeuAspAspLeuGlyAsnGlyArgLeuSerAspLeu 335
 Db 243 GATCTGAAACCTGAAACATCTGTATGATATTAAGGCAATTAAGATCTCAACCTG 302
 QY 336 GlyLeuAlaValGluMetLysGlyLysProIleThrGlnArgAlaGlyThrAsnGly 355
 Db 303 GGCTTGGCTGGAAGATCCCGAGGAGACCTGATCCGCGCGGGGCGCACTGTGGC 362
 QY 356 TyrMetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTyrPhe 375
 Db 363 TACATGCTCCAGAGGCTCTGAACAACAG--AGGTACGGCTGACCCCGCACTACCTGG 419
 QY 376 AlaMetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLys 395
 Db 420 GCGCTGCTGCTCATCTATGATGATGAGAGGCGCATGCTGCGCGCGCGCAAG 479
 QY 396 GlnLysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGlnValLysPheGln 415
 Db 480 GAGAAAGTGAAGCGGAGAGTGAACCGCGCTCTGAGACGAGAGAGGTGATCC 539
 QY 416 HisAspAsnPheThrGluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysPro 435
 Db 540 CAC--AAGTTCCTCCAGAGAGCGCAAGTCCATCTGCAAGTCTGCTCAAGAAAGATGCG 596
 QY 436 GlnGlnArgLeuGlySerArgGluLys--SerAspAspProArgLysHisPhePhe 454
 Db 597 AAGCAAGGCTGGCTGCGCAGAGAGAGGCGCTGCAAGGTCAAGAGACCCCTTCTTC 656
 QY 455 LysThrIleAsnPheProArgLeuGlnAlaGlyLeuIleGluProProPheValProAsp 474
 Db 657 AGGAATCATCACTTCAAGCGCTTGAAGCGCGGATGTGGACCTCCCTTGTTCACAGAC 716
 QY 475 ProSerValValTyrAlaLysAspIleAlaGlnIleAspAspPheSerGlnValArgGly 494
 Db 717 CCGCGCGCTGTGTACTGTAGACGCTGCGACGCTGCAAGATTTCTTCCACTGTGAAGGAC 776
 QY 495 ValGlnPheAspAspLysAspLysGlnPhePheLysAsnPheAlaThrGlyAlaValPro 514
 Db 777 GTCAATCTGACCAACAGACGACGACCTTACCTTACCAAGTTTCTCAAGGCTCTGTGTC 836
 QY 515 IleAlaTyrGlnGlnGlnIleIleGlnThrGlyLeuPheGlu-----528
 Db 837 ATCCATGCGCAAAACAGATGATAGAAACGAAATGCTTAAAGACCTGAACCTGTTTG 896
 QY 529 GlnLeuAsnAspProAsnArgProThrGly 538
 Db 897 GAACCTTAAT-----GTTACCCCTTCCGCG 920

RESULT 8
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 LOCUS
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 AGENCOURT 7047352 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5813275
 5', mRNA sequence.
 ACCESSION B0057613
 VERSION B0057613.1 GI:19816953
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC <http://mgi.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapds-remail.nih.gov
 Tissue Procurement: Lou Staudt
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLNI at:
<http://image.llnl.gov>
 Plate: LICM2065 row: a column: 20
 High quality sequence stop: 753.
 Location/Qualifiers
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 /clone="IMAGE:5813275"
 /tissue_type="lymphoma, cell line"
 /lab_host="MD10B (phage-resistant)"
 /clone_id="NIH_MGC_99"
 /note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAAGAG(G). Size-selected >500bp for average insert size
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."

ORIGIN

Alignment Scores:

Pred. No.: 1.09e-72
 Score: 822.50
 Percent Similarity: 70.87%
 Best Local Similarity: 51.46%
 Query Match: 28.47%
 Gaps: 4

US-10-044-205A-2 (1-553) x B0057613 (1-998)

QY 236 AlaLeuLeuGluGluSerValSerSerProPheIleValSerLeuAla 255
 Db 3 GCCCTCAATGAGAGAGATCTCTGAGAGAGTCAACATCTGCTTGGTGTCAACCTGGCC 62
 QY 256 TyrAlaPheGluSerLysThrHisLeuGlyLeuValMetSerLeuMetSerGlyAsp 275
 Db 63 TATGCTTACGAGACCAAGATGACCTGTGCTTGGTGTGCTTACGACCTCAATGAGAGAGTGCAC 122
 QY 276 LeuLysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePhe 295
 Db 123 CTGAAGTTCACATCTTACACATGAGGCAACCTGCTTCAAGAGAGAGCGCGCTTGT 182
 QY 296 TyrSerAlaGlnIleAlaCysGlyMetLeuHisIleGluLeuGlyIleValTyrArg 315
 Db 183 TATGCGGAGAGATCTCTGCTGCTTACGACCTTCAACCGTGAACACCGTTCACCA 242

QY 316 AspMetLysProGluValLeuLeuAspAspLeuGlyAsnCySargLeuSerAspLeu 335
 Db 243 GATCTGAACCTGAAACATCTCTGTATGATATTAATGAGCATTAAGATCTCAGACCTG 302
 QY 336 G1yLeuAlaValGluMetLysGlyGlyLysProL1eThGlnAgaAlaGlyThrAsnGly 355
 Db 303 GCGTGGCTGTGAAGATCCCGAGGAGACCTGATCCGGCGCGGGGAGGACATGTTGGC 362
 QY 356 TyrMetAlaProGluLeuMetGluLysValSerTyrSerTyrProValAspTyrPhe 375
 Db 363 TACATGCTCCAGAGGCTCTGAACAACAG---AGTACGCGCTGAGCCCGCACTACTCG 419
 QY 376 AlaMetGlyCysSerLeuTyrGluMetValAlaGlyArgThrProPheLysAspTyrLys 395
 Db 420 GCGCTGGCTGCTCATCTATGAGATGATGAGGAGGCGGCGCTGCGCGGCGCGCAG 479
 QY 396 GluLysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGln 415
 Db 480 GAGAAGGTGAAGCGGAGAGAGTGTGACCCGCGCTGCTGAGACGAGAGAGTGTACTCC 539
 QY 416 HisAspAsnPheThGluGluAlaLysAspL1eCysArgLeuPheLeuAlaLysLysPro 435
 Db 540 CAC---AAGTTCCTCCAGAGAGCCAGAGTCTCATCTGCAAGATGCTGCTCAGAAAGATGCG 596
 QY 436 GluGlnArgLeuGlySerArgGluLys---SerAspAspProArgLysHisAspPhe 454
 Db 597 AAGCAGAGGCTGGGCTGCGAGAGAGGCGGCTGCGAGGTCAGAGACACACCCCTTCTTC 656
 QY 455 LysThrL1eAsnPheProArgLeuGluGlnAlaGlyLeuL1eGluProPheValProAsp 474
 Db 657 AGGAACATGAACCTCAAGCGCTTAGAGCCGGAGTTGAGACCTTCTCTGCTTCACAGC 716
 QY 475 ProSerValValTyrAlaLysAspL1eAlaGluL1eAspAspPheSerGluValArgLys 494
 Db 717 CCCCAGCTGTGACTGTAAAGACGTGCTGACATGCAAGATTCTCACGTGAAGGAGC 776
 QY 495 ValGluPheAspAspLysAspLysGlnPheLysAsnPheAlaThrGlyAlaValPro 514
 Db 777 GTCATCTGAGCACACACACACACACACTTCTACTCAAGTCTCCACGCGGCTGTGTCC 836
 QY 515 L1eAlaTyrGlnGluGluL1eL1eGluThr-GlyLeuPheGluGluLysLeuAsn----- 531
 Db 837 ATCCCATGGCAAAACGATGATGAGAAACAGATGCTTTTAAAGAGTGAACGCTTTGG 896
 QY 532 -----AspProAsnArgPro 536
 Db 897 AACCTATGATACCTCCCGCCCA 921
 RESULT 9 1017 bp mRNA linear EST 02-APR-2002
 B0061150 LOCUS AGENCCOURT_6662973 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5920182
 DEFINITION 5', mRNA sequence.
 ACCESSION B0061150 GI:19884936
 VERSION B0061150
 KEYWORDS EST Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1017)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 AUTHORS Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgsab-remail.nih.gov
 Tissue Procurement: Lou Staudt
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 http://image.lnl.gov

Plate: LICM2083 row: h column: 07
 High quality sequence stop: 697.
 Location/Qualifiers
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 /db_xref="taxon:9606"
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 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 99"
 /note="Organ: lymph. Vector: pOT7; Site 1: XhoI; Site 2:
 EcoRI. cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACAGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH-MGC
 library."

ORIGIN

Alignment Scores: 9,22e-72 Length: 1017
 Pred. No.: 813.50 Matches: 154
 Score: 71.72% Conservative: 59
 Percent Similarity: 51.85% Mismatches: 81
 Best Local Similarity: 28.16% Indels: 3
 Query Match: 13 Gaps: 3

US-10-044-205A-2 (1-553) x B0061150 (1-1017)

QY 236 AlaLeuLeuGluLysGluL1eLeuGluLysValSerSerProPheL1eValSerLeuAla 255
 Db 3 GCCCTCAATGAGAGACACATCTCTGAGAGAGTCAACAGTGTGCTGCTCAACTGAGC 62
 QY 256 TyrAlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsnGlyLysAsp 275
 Db 63 TATGCTTACGAGACCAAGATGACATGCTGTGCTGCTGACCATCATGATGAGGAGTAC 122
 QY 276 LeuLysPheHisLeuTyrAsnValGlyThrArgLysLeuAspMetSerLysValLysPhe 295
 Db 123 CTGAGATTCACATCTACACATGAGGACCCCTGCTTGAAGAGAGAGCGGCGCTTGT 182
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 Db 183 TATGGGAGAGATCTCTGCGGCTTAGAAGACTTCCACCTGAGAAACCCGTACCGGA 242
 QY 316 AspMetLysProGluValLeuLeuAspAspLeuGlyAsnCySargLeuSerAspLeu 335
 Db 243 GATCTGAACCTGAAACATCTCTGTATGATATTAATGAGCATTAAGATCTCAGACCTG 302
 QY 336 G1yLeuAlaValGluMetLysGlyGlyLysProL1eThGlnAgaAlaGlyThrAsnGly 355
 Db 303 GCGTGGCTGTGAAGATCCCGAGGAGACCTGATCCGGCGCGGGGAGGACATGTTGGC 362
 QY 356 TyrMetAlaProGluLeuMetGluLysValSerTyrSerTyrProValAspTyrPhe 375
 Db 363 TACATGCTCCAGAGGCTCTGAACAACAG---AGTACGCGCTGAGCCCGCACTACTCG 419
 QY 376 AlaMetGlyCysSerLeuTyrGluMetValAlaGlyArgThrProPheLysAspTyrLys 395
 Db 420 GCGCTGGCTGCTCATCTATGAGATGATGAGGAGGCGGCGCTGCGCGGCGCGCAG 479
 QY 396 GluLysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGln 415
 Db 480 GAGAAGGTGAAGCGGAGAGAGTGTGACCCGCGCTGCTGAGACGAGAGAGTGTACTCC 539
 QY 416 HisAspAsnPheThGluGluAlaLysAspL1eCysArgLeuPheLeuAlaLysLysPro 435
 Db 540 CAC---AAGTTCCTCCAGAGAGCCAGAGTCTCATCTGCAAGATGCTGCTCAGAAAGATGCG 596
 QY 436 GluGlnArgLeuGlySerArgGluLys---SerAspAspProArgLysHisAspPhe 454

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Oy	455	LysThrIleAsnPheProArgLeuGlnAlaGlyLeuIleGluProProPheValProAsp	474
Db	657	AGGAACATGAACTTAAAGCGCTTAAAGCCCGGAGATGTGAGACCTCCCTTCGTTCACAAAC	716
Oy	475	ProSerValValTyrAlaIleAspIleAlaGlnIleAspAspPheSerGlnValArgIle	494
Db	717	CCCCGGCGGTGTACTGTAAAGACGTGGTCGACATCGAACAACTTCTCACTGGTAAAGC	776
Oy	495	ValGlnPheAspAspIleAspIleGlnPhePheIleAsnPheAlaThrGlnValAlaValPro	514
Db	777	GTCATCTGGACCAACAAGACGACCACTTCTTACTCCAAATTCTCCAGCGGCTCTGTGCC	836
Oy	515	IleAlaTrpGlnGluGlnIleIleGlnThrGlyLeuPheGlnGlnIleAsn	531
Db	837	ATCCCATGCGCAACAGAGATGATAGAAACGAATGCTTTAAAGAGCTGAAC	887

RESULT 10				
B0061148				
LOCUS	B0061148	1019 bp	mRNA	linear
DEFINITION	AGNCOUNT 6862941 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5920180			
	5', mRNA sequence.			
ACCESSION	B0061148			
VERSION	B0061148.1	GI:19884933		
KEYWORDS	EST.			
SOURCE	Homo sapiens	(human)		
ORGANISM	Homo sapiens			

REFERENCE	(pages 1 to 1019)
AUTHORS	NiH-MGC http://mgc.ncbi.nlm.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, ph.D

Email: cgabbs-remail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution by: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
<http://image.llnl.gov>
Plate: LINC2083 row: h column: 05
High quality sequence stop: 704.

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location/Qualifiers
1. 1019
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5920180"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1b="NH1 MCC_99"
/note="Organ: lymph; Vector: pOTR1; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
G3CACGACGG). Size-selected >500bp for average insert size
1.8kb. library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NH1 MCC
library."

```

Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:

9.58e-71	Length:	101
803.50	Matches:	151
72.54%	Conservative:	55
53.17%	Mismatches:	77
27.81%	Indels:	1
13	Gaps:	1

US-10-044-205A-2 (1-553) x BQ061148 (1-1019)

[illegible]

RESULT 11	
BQ063841	
LOCUS	
DEFINITION	BQ063841
AGENCY	6832078 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5925495
VERSION	5, mRNA sequence.
KEYWORDS	BQ063841
SOURCE	BQ063841.1 GI:19891943
ORGANISM	EST.
	Homo sapiens (human)
	Homo sapiens

QY 197 LeuGlyLysGlyGlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMet 216
 DB 135 CTGGGCAAGAGTGGCTTTGGGAGAGTGTGCGCTCCAGGTGGGCGCACAGTAAATG 194
 QY 217 TTTAACTGlyLysLeuAspLysLysPheGlyLysGlyGlyGlyGlyMetAla 236
 DB 195 TATGCTGCAAGAGTGGTGAAGAAAGGAGTCAAGAGGAGGAGGAGGAGGAGGAGG 254
 QY 237 LeuGluGluGlyGluLeuGluValLysSerProPheLeuValSerLeuAlaTyr 256
 DB 255 CTGAACAGAGAGAGTCTGGAAGAGTGAAGAGTGTGAGAGTGTGAGTGTGAGTGT 314
 QY 257 AlaPheGlyLysThrThrIleuGlyLeuValMetSerLeuMetLeuGlyGlyAspLeu 276
 DB 315 GCGTATGAGACCAAGAGAGCGCTGCTGCTGCTGCACTGATGAACGAGGAGGAGCTTC 374
 QY 277 LysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyr 296
 DB 375 AAGTTCACATCTACCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 434
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 DB 791 AGCGCTTTTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 850
 QY 436 uGlnArgLeuGlySerArgGluLysSerAspAspProArgLys----- 450
 DB 851 CGAAGCGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 910
 QY 451 -HisIlePhePheLysThrIleAsn 458
 DB 911 CCTCTCTTTTAAAGGTAAAC 935
 RESULT 14
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 DEFINITION Homo sapiens cDNA clone CS0D1010YD11 3-PRIME, mRNA sequence.
 ACCESSION EX392018
 VERSION EX392018.1 GI:30607809
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 917)
 AUTHORS Li W.B., Gruber C., Jessee J. and Polayes D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 3090.f for
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0BA1046ZH12_CS04416_1&cluster=3090.f
 Contact : Feng Liang Email : fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0BA1046ZH12_CS04416_1.
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 /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
 /clone_id="Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Alignment Scores:
 Pred. No.: 1,37e-69 Length: 917
 Score: 791.50 Matches: 149
 Percent Similarity: 72.82% Conservative: 60
 Best Local Similarity: 51.92% Mismatches: 71
 Query Match: 27,40% Indels: 7
 DB: 13 Gaps: 3

US-10-044-205A-2 (1-553) x EX392018 (1-917)
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 DB 891 CCTGATCCCTAAGTCCCGCCGAGCTGTGTGAGACCTGACCCAGCGGCTGAGAGAGGT 832
 QY 141 -----GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeu 158
 DB 831 CCTGCAAAAGACTTTTTCAGAACTACCCGCGTACCCAGAGG-----TACTG 781
 QY 159 GlnGluGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnThr 178
 DB 780 ACGTGGGCCCTTTTCCGACATCTGACAGCATCTTCAACCGTTTCTGCAAGTGG 721
 QY 179 LysLeuPheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGly 198
 DB 720 AAGTGTGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 661
 QY 199 LysGlyGlyPheGlyGlyValAlaCysAlaValGlnValLysAsnThrGlyLysMetTyrAla 218
 DB 660 AAGAGTGTCTTTGGGAGGAGTGTGCGCTGCGAGGTCCGGGCGCAAGAGTAAAGATGTGCG 601
 QY 219 CysLysLysLeuAspLysLysArgLeuLysLysGlyGlyGlyLysMetAlaLeuLeu 238
 DB 600 TCGAAGAGCTAGAGAAAGGAGGATCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 541
 QY 239 GlnLysGluIleLeuGluLysValSerProPheIleValSerLeuAlaTyrAlaPhe 258
 DB 540 GAGAGACAGATCTCGAGAAAGTGAAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 481
 QY 259 GluSerLysThrHisIleuGlyLeuValMetSerLeuMetAsnGlyLysAspLeuLysPhe 278
 DB 480 GAGACCAAGAGAGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421
 QY 279 HisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAla 298
 DB 420 CACATCTACATAGAGGCGAGGCTGGCTTCCCGAAGCGGAGCGCTGCTTCTAGCGCGCC 361

QY 299 GlnlIleAlaCysGlyMetIleuHisLeuHISgluIleuGlyIleValTyrArgAspMetLys 318
 Db 360 GAGATCTGCTGGCTGGAGGACCTGCACCGGAGGCGCATCTGTACAGGAGCTGAG 301
 QY 319 ProGluAlaValLeuLeuAspAspLeuGlyAsnGlySerLeuSerAspLeuGlyLeuAla 338
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 Db 240 GTGATGTCGCCGAGAGGCCAGACCATCAAGGCGCTGGGCGACGCTGATCATGCT 181
 QY 359 ProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTyrPheAlaMetGly 378
 Db 180 CCGAGAGTGCTGAATAATGAA---CGTACAGCTTCAGCCCTGATCTGGTGGCGCTGCG 124
 QY 379 CysSerTyrGluMetValAlaGlyArgThrPheLeuAspTyrLysGluLysVal 398
 Db 123 TGCTCTCTGATGAGATGATCGAGCGCATGCTCTTCCAGAGAGAGAAAGAAAGATC 64
 QY 399 SerLysGluAspLeuLysGln 405
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RESULT 15
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 VERSION EX849055
 KEYWORDS EX849055.1 GI:39744402
 SOURCE EST.
 ORGANISM Xenopus laevis (African clawed frog)
 Xenopus laevis
 Buxarjota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 Xenopodinae; Xenopus.
 1 (bases 1 to 838)
 Heil, O., Neubert, P., Peters, M., Radelof, U., Schneider, D.,
 Schrot, A., Korn, S. and Landgrebe, J.
 Xenopus laevis UniGene Set 1 (RZPDLIB No.988)
 Unpublished (2003)
 Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
 RZPD: IMAGE998G249027.
 RZPDLIB, I.M.A.G.E. cDNA Clone Collection (amp- resistant) (RZPDLIB
 No.998) http://www.rzpd.de/cgi-
 bin/products/showlib.pl.cgi/response?libNo=998 RZPDLIB; Xenopus
 laevis UniGene Set 1 (RZPDLIB No.988) http://www.rzpd.de/cgi-
 bin/products/showlib.pl.cgi/response?libNo=988 Contact: Ina Rolfs
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
 Heidenweg 6, D-14059 Berlin, Germany
 Tel.: +49 30 32639 101
 Fax: +49 30 32639 111
 www.rzpd.de

FEATURES
 source This clone is available royalty-free from RZPD;
 contract RZPD (clone=rzpd.de) for further information. Seq primer:
 m31r, 5' TTTCACAGAGAAACGCTATGAC 3'.
 Location/Qualifiers
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 /clone="IMAGE998G249027 ; IMAGE:3746735"
 /tissue_type="oocyte (stages 5 and 6)"
 /lab_host="Top-10 F."
 /clone_lib="Xenopus laevis oocyte"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI; cDNA was prepared from 2ug of poly A+ RNA.
 EcoRI-XhoI cut cDNA was then ligated into unizap-XR
 (Stratagene) with EcoRI at the 5' end and XhoI at the 3'
 end. SS-library phagmids were prepared by mass excision

from the original library and normalized by hybridization
 to biotinylated driver (prepared from the same library by
 PCR) to Cot-omega of 11. After removal of hybrids and
 excess driver by streptavidin sepharose chromatography,
 the ss-phagemids were made double stranded and
 electroporated into Top-10 F. Original library
 construction by Bruce Blumberg (Blumberg et al., 1991
 Science 253, 194-196; Hawlet et al., 1995, Genes Dev. 9,
 2923-2935). Normalized by Uihwan Song (Song, Cho and
 Blumberg, unpublished). Note: This is a Xenopus Gene
 Collection (Xgc) library."

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Best Similarity:	787.00	838	152	53	60	23	4
Best Local Similarity:	71.18						
Query Match:	52.78						
DB:	27.24						

US-10-044-205a-2 (1-553) x EX849055 (1-838)

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 Db 23 AATCCC-----AGCAAGAAATATCTCACTAGCTC----- 52
 QY 141 GluGluAlaValAlaAlaValAlaThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnlu 160
 Db 53 -----ATTAGCAATCCATGATCTTACGGG 82
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTyrLysLeu 180
 Db 83 TCCCGCTTCGAGATACCCAGAAAGATATGATCTTCATGCTTTCAGTGAAGAAAGC 142
 QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGlnPheArgValLeuGlyLysGly 200
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 QY 201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
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 QY 221 LysLeuAspLysArgLeuLysLysLysGlyGlyLysMetAlaLeuLeuGlnLys 240
 Db 263 AAATCTGAGAAAGAGATCAAGAAAGAAAGGAATCAATGATGCTGAATGAGAG 322
 QY 241 GlnIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGlnSer 260
 Db 323 CAGATCTGGAGAAAGTGAACAGCCGTTTGTGTTAGTCTGCTTACTCTTATGAAAGC 382
 QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyLysAspLeuLysPheHisile 280
 Db 383 AAAGAGCGCCGTGTCTGTGCTGACATGACGAGTGGTGGTCACTCAAGTCCATATC 442
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
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 Db 623 ATACCAAGAGGAGACGTTCCGGGAAAGATGAGACAGTGGGTTATATGCCCCCAAGAA 682
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 Db 682

Db 683 GTGATTAAGATGAA---CGCTACACTTTTACCCCGACTGTGGGTTTGAGTTC 739
 QY 381 ILLETCGLWETVal-ALAGIYArgThrProPheLysAspTyrLysGluYValSerIy 400
 Db 740 ATTATGAGATGATCGAAGGGCCATCTTCCTTTGGCAGCGGAAAGAACGATAAAAA 799
 QY 400 s---GluAspLeuLysGlnArg 406
 Db 800 GCGAAGAGGTTGAAAAAAGG 821

Search completed: August 13, 2004, 21:10:27
 Job time : 2727 secs

GenCore version 5.1.6
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Run on: August 13, 2004, 18:45:41 ; Search time 92 Seconds

(without alignments)
3335.737 Million cell updates/secTitle: US-10-044-205A-2
2889

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Ygapop 10.0, Ygapext 0.5	
Rgapop 6.0, Rgapext 7.0	
Delop 6.0, Delext 7.0	

Searched: 682709 segs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2883	99.8	2249	4	US-09-802-117-5
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4	2876	99.6	1662	4	US-09-964-469-1
5	1801	62.3	1062	4	US-09-802-117-3
6	1528	52.9	36651	4	US-09-738-894A-3
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9	1252.5	43.4	2511	4	US-09-417-197-60
10	1252.5	43.4	2529	4	US-09-417-197-42
11	1252.5	43.4	2557	4	US-09-016-434-1298
12	1250.5	43.3	1975	4	US-09-614-748A-9

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14	1240	42.9	2848	3	US-08-464-954A-2	Sequence 2, Appl1
15	1238	42.9	2204	1	US-08-221-817-12	Sequence 12, Appl1
16	1238	42.9	2204	1	US-08-454-439-12	Sequence 12, Appl1
17	1238	42.9	2204	5	PCT-US94-10487-12	Sequence 12, Appl1
18	1236.5	42.8	2257	3	US-08-464-954A-1	Sequence 10, Appl1
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21	1209.5	41.9	2206	1	US-08-221-817-10	Sequence 10, Appl1
22	1209.5	41.9	2206	1	US-08-454-439-10	Sequence 10, Appl1
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24	1189	41.2	1983	1	US-08-221-817-21	Sequence 21, Appl1
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27	1023.5	35.4	1420	4	US-09-614-748A-11	Sequence 11, Appl1
28	981.5	34.3	1305	4	US-09-614-748A-12	Sequence 12, Appl1
29	725.5	25.1	2362	4	US-09-620-312D-273	Sequence 273, App
30	721.5	25.0	2067	4	US-09-016-434-1306	Sequence 1306, Ap
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32	493	17.1	2754	3	US-09-429-322-3	Sequence 3, Appl1
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35	469	16.2	2104	3	US-09-023-655-1191	Sequence 1191, Ap
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37	469	16.2	2549	4	US-09-394-455-5	Sequence 5, Appl1
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41	465	16.1	1788	4	US-09-417-197-68	Sequence 68, Appl1
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45	458.5	15.9	2610	3	US-09-091-058-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-802-117-1
; Sequence 1, Application US/09802117
; Patent No. 6444456
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Made
; APPLICANT: Wiganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. 6444456 Human G-Coupled Protein Receptor Kinases and Polymu
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/09/802,117
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/188,449
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-802-117-1
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Length: 1662
Matches: 552
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Conservative: 0
Best Local Similarity: 99.82%
Mismatch: 1
Query Match: 99.79%
Indels: 0
Gaps: 0
US-10-044-205A-2 (1-553) x US-09-802-117-1 (1-1662)

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 QY 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
 DB 661 AATGTGACAAAGACCGCTGAAGAAAGAGGTGCGAGAAAGTGGCTCTCTTGGAAAG 720
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 DB 781 AAGGCCATCTGCTGCTGTGATGAGCTGATGAATGGGGAGAGCTCAAGTTCACATC 840
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
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 QY 441 SerArgLysLysSerAspAspProArgLysHisPhePheLeuThrIleAsnPhePro 460
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 DB 1441 AAGACATCGCTGAATGATGATTTCTGAGGTTCGGGGGTGGAATTTGATGACAAA 1500
 QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaThrGlnGluGlu 520
 DB 1501 GATAGCAGTTCTCAAAAACCTTGGACAGAGTGTGTTCTTATACATAGCGAGAGAA 1560
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 DB 1561 ATTTAGAAACGGGACTGTTGAGAACTGAATGACCCCAACAGACTTACGGTTGTAG 1620
 QY 541 GluLysAsnSerSerLysSerGlyValCysLeuLeuLeu 553
 DB 1621 GAGGTATTCATCCCAAGCTGGGTGTGTTATTATG 1659

RESULT 2
 US-09-802-117-5
 ; Sequence 5, Application US/09802117
 ; Patent No. 6444456
 ; GENERAL INFORMATION:
 ; APPLICANT: Walke, D. Wade
 ; APPLICANT: Wilganowski, Nathaniel L.
 ; APPLICANT: Turner, C. Alexander Jr.
 ; TITLE OF INVENTION: No. 6444456 Human G-Coupled Protein Receptor Kinases and Polymuk
 ; TITLE OF INVENTION: Encoding the Same
 ; FILE REFERENCE: Lex-0147-USA
 ; CURRENT APPLICATION NUMBER: US/09/802,117
 ; PRIOR FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: US 60/188,449
 ; PRIOR FILING DATE: 2000-03-10
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 2249
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-09-802-117-5

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 Score: 2883.00 Matches: 552
 Percent Similarity: 99.82% Conservative: 0
 Best Local Similarity: 99.82% Mismatches: 1
 Query Match: 99.79% Indels: 0
 Gaps: 0

US-10-044-205a-2 (1-553) x US-09-802-117-5 (1-2249)
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 DB 354 ATGTGTGACATGGGGGCTGTGGCAACCTGATCGCAACCGCTTACTGCAAGGCCCGG 413

QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuGly 60
 DB 121 GGGCTGACAGGGCTGCGCGAGCTCGCCAGAACCTGTCCCGAACTTCCACAGCTGTGT 180
 QY 61 GluGlnGlnProIleValArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
 DB 181 GAGCAGCAGCCCATCGGTGCGCGCTCTCCGATGCTTCTTACCCAGCAGGCCACAGCTTC 240
 QY 81 ArgLysAlaAlaThrPheLeuGlnAspValGlnAsnTrpGluLeuAlaGluGlnGlyPro 100
 DB 241 CCGAAGCGCGCACTTCTTACAGGACCTGCAAGCTGGCGAGCTGGCCGAGGAGGAGCC 300
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 DB 301 ACCAAAGACAGCGCGCTGACAGGGGCTGTGTGCGCACTTGTGCGAGGCGCCCTGCGCG 360
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
 DB 361 AACCGCAACCTTCTTCCAGCCAGCGCTGGCCAGCAGCAGCAGCAGCAGCAGCAGCAG 420
 QY 141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
 DB 421 GAAGGCGAGGTGGCTGACAGGACCTGGCCAGAGCTGAGGCGCATGGCTTCTTGGCAAG 480
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTrpAspLysPheLeuGlnTrpLysLeu 180
 DB 481 CAGCCCTTTAGAGATTCTGTGACAGCGCTTCTTACAGCAAGTTCTGCGAGTGAACCTC 540
 QY 181 PheGluMetGlnProValSerAspLysTrpPheThrGluPheArgValLeuGlnLysGly 200
 DB 541 TTGAGATGACACAGTGTCAAGCAAGTCTTCTTCACTGAGTCAAGTCTGGGGAAGGT 600
 QY 201 GlyPheGlnGluValCysAlaValGlnValLysAsnThrGlyLysMetTrpAlaCysLys 220
 DB 601 GCTTTGGGAGAGTATGTGCGCTCCAGGTGAACAACTGGGAGAGTATGCTGTGAAG 660
 QY 221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGlnLysMetAlaLeuLeuGlnLys 240
 DB 661 AAACGTGACAAAGCGCTGAAAGAAAGGTGGCGCAAGATGGCTCTCTTGGAAAAG 720
 QY 241 GlnIleLeuGlnLysValSerSerProPheIleValSerLeuAlaTrpAlaPheGluSer 260
 DB 721 GAATCTCTGAGAAAGTACAGAGCTTCTTCACTGTCTCTGCGCCATGCTTGGAAAG 780
 QY 261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyLysAspLysPheHisIle 280
 DB 781 AAGGCCATCTGTGCTTGTATGATGACCTGATGATGGGAGAGCTCAAGTCCACATC 840
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTrpSerAlaGlnIle 300
 DB 841 TACAACTGTGGACCGCGTGGCTGACATGACGCGGTGATCTTTTACTCGGCCAGATA 900
 QY 301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
 DB 901 GCGTGTGAGATGTGCTCACTTCACTGAACTCGGACCTCGTATGGGACATGAAGCTGAG 960
 QY 321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
 DB 961 AATGTGCTTGTGATGATGACCTCGCACTGCAAGTATGTGACCTGGGCGCTGGCGT 1020
 QY 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTrpMetAlaProGlu 360
 DB 1021 ATGAAGGCTGGCAAGCCCATCCAGAGGCGCTGAAACCAATGGTATCATGCTCTCGAG 1080
 QY 361 IleLeuMetGlnLysValSerTrpSerTrpProValAspTrpPheAlaMetGlyCysSer 380
 DB 1081 ATCTTAATGGAAAGGTAAAGTATTTCTATCTGTGAGCTGTGTGCAATGGAGTCAAGC 1140
 QY 381 IleTrpGluMetValAlaGlyArgThrProPheLysAspTrpLysGlyLysValSerLys 400
 DB 1141 ATTATAGAAATGGTCTCTGAGCAACCATTAAGAGATTAACAAGAAAGGTACGTGAAA 1200
 QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnThr 420

DB 1201 GAGGATCTGAAGCAAGAACTCTGACAGACGAGGTCAATTCACATGATTAATTCA 1260
 QY 421 GluGlnAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
 DB 1261 GAGAGCAAGAAAGATTTGCAAGGCTCTTGTGGCTTAAGAAACAGAGCAACGCTTAGA 1320
 QY 441 SerArgGluLysSerAspAspProArgLysHisIlePhePheLysThrIleAsnPro 460
 DB 1321 AGCAGAGAAATCTGATGATGATCCAGAAACATCATTTCTTAAACGATCACTTCTCT 1380
 QY 461 ArgLeuGlnAlaGlyLeuIleGluProPheValProAspProSerValValTyrAla 480
 DB 1381 CGCTGGAACTGGCGCTTAATTGAACCCCATTTGTGCAACCTTCACTGATGATGATGCC 1440
 QY 481 LysAspIleAlaGluIleAspAspPheSerGlnValArgGlyValGluPheAspAspLys 500
 DB 1441 AAAGACATGCTGAAATTTGATGATTTCTTCAAGTTCGGGGGTGAATTTGACAGAA 1500
 QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGlnGlu 520
 DB 1501 GATAGCAGTCTTCAAAAACCTTTCGACAGGTCGTCTTCTTACATGAGGAGAGAA 1560
 QY 521 IleIleGlnThrGlyLeuPheGlnGluLeuAsnAspProAsnAspProThrGlyCysGlu 540
 DB 1561 ATTATAGAAACGGGACTTTTGAAGAACTGAATGACCCCAACACTTACGGGTTGTGAG 1620
 QY 541 GluLysAsnSerSerLysSerGlyValCysLeuLeuLeu 553
 DB 1621 GAGGATATCATCAAGTCTGGGTGTGTGTATTG 1659

RESULT 4
 US-09-964-469-1
 ; Sequence 1, Application US/09964469
 ; Patent No. 6579709
 ; GENERAL INFORMATION:
 ; APPLICANT: GUEGLER, Karl et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: C0000636DIY
 ; CURRENT APPLICATION NUMBER: US/09/964,469
 ; CURRENT FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: 60/208,331
 ; PRIOR FILING DATE: 2000-06-01
 ; PRIOR FILING DATE: 2000-12-18
 ; PRIOR APPLICATION NUMBER: 09/738,894
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1662
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-964-469-1

Alignment Scores:
 Pred. No.: 0 Length: 1662
 Score: 2876.00 Matches: 551
 Percent Similarity: 99.64% Conservative: 0
 Best Local Similarity: 99.64% Mismatches: 2
 Query Match: 99.55% Indels: 0
 DB: 4 Gaps: 0

US-10-044-205A-2 (1-553) x US-09-964-469-1 (1-1662)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
 DB 1 ATGTGTGACATGGGAGGCTCTTGAACAACCTGATGCGCAACCGCTTACTGACGGCGGG 60
 QY 21 LysProSerAspCysAspSerLysGlnLeuGlnArgArgArgSerLeuAlaLeuPro 40
 DB 61 AAGCCTTGGACTGCGACAGCAAGAGAGCTGACGGGGGGGAGTACCTGGCCCTGCGCC 120

QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnIleuSerLeuSerLeuPheHisSerLeuCys 60
 DB 121 GGGCTGCAAGGGCTGCGCGAGAGCTCCGCGAAGAGCTCTCCGAGACTTCCAGAGCTCTGGT 180
 QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
 DB 181 GAGGAGAGAGCCCATCGTGGCGGCTCTTCCGAGCTTCCAGGACAGATGGCCACGTTTC 240
 QY 81 ArgValAlaIleThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGlnGluPro 100
 DB 241 CGCAAGCGGCAACCTCTTAGAGAGAGTGCAGAACTGCGAGCTGCGCGAGAGAGAGCC 300
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 DB 301 ACCAAGACAGCGCCCTCGAGGAGCTGCGGCACTTGTGAGTGGCCCTGCGCCCGGG 360
 QY 121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
 DB 361 AACCCGCAACCTTCTCAGCGAGCGCGTGGCGAACAGTCCAGCCAGCCAGCCAGCATCTGAG 420
 QY 141 GluGluArgValAlaAlaValThrLeuArgGlyAlaGluAlaMetAlaPheLeuGlnGlu 160
 DB 421 GAAGAGCGAGTGGCTGCGAGTGCAGTGGCGAGGCTGAGGCGCATGGCTTCTTTCAGAG 480
 QY 161 GlnProPheLysAspPheValThrSerAlaPheThrAspLysPheLeuGlnTrpLysLeu 180
 DB 481 CAGCCCTTAAAGATTTCGAGACAGCGCTCTTCAGACAGATTTCTGCGAGTGAACCTC 540
 QY 181 PheGluMetGlnProValSerAspLysTrpPheThrGluPheArgValLeuGlyLysGly 200
 DB 541 TTCAGATGCAACAGTGTGACAGCAAGTACTTCAGAGTTCAGAGTCTCGGGGAAGGT 600
 QY 201 GlyPheGlnGluValCysAlaValGlnValIleAsnThrGlyLysMetTrpAlaCysLys 220
 DB 601 GGTTTGGGAGGATATGTGCTGCGAGGTGAAAACATCGGGAAGATGATGCTGTAG 660
 QY 221 LysLeuAspLysLysArgLeuLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
 DB 661 AAACCTGGACAGAGGCGCTGAGAGAGAGAGGCGCGAGAGATGGCTCTTTCGAGAAAG 720
 QY 241 GluIleLeuGlnLysValSerSerProPheIleValSerLeuAlaTrpAlaPheGluSer 260
 DB 721 GAATCTTGGAGAGGTCAGAGCCCTTTCATGCTCTCTGCGCTATGCTTTCAGAGC 780
 QY 261 LysTrpHisLeuCysLeuValMetSerLeuMetAsnGlyLysAspLeuLysPheHisIle 280
 DB 781 AAGACCCATCTGCTGCTGTCAATGAGCTGATGATGAGGAGGAGCACTCAAGTTCCAGCAT 840
 QY 281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTrpSerAlaGlnIle 300
 DB 841 TACAACTGGGCAAGCGTGGCTGAGATAGCGCGGAGTCTTTTACCTGGCCCAAGATA 900
 QY 301 AlaCysGlyMetLeuHisLeuHisGlnLeuGlyIleValTyrArgAspMetLysProGlu 320
 DB 901 GCGTGTGGAGTGTGCACTCCATGAACTCGGATGTCATGCGGACATGAAGCTTGAG 960
 QY 321 AsnValIleuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaGlu 340
 DB 961 AATGTGCTTCTGATGATGCTGCGCACTGAGAGTATCTGACCTGGGCGCTGGCGAG 1020
 QY 341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTrpMetAlaProGlu 360
 DB 1021 ATGAAGGGTGGCAAGCCATCAACCAAGGCGCTGAGAACATGATGATGATGCTTCAGAG 1080
 QY 361 IleuMetGlnLysValSerTrpSerTrpProValAspTrpPheAlaMetGlyCysSer 380
 DB 1081 ATCTTAATGGGAAAGTAAATTAATCTCTGAGCTGAGTCTGCTCCATGGAGTGAAGC 1140
 QY 381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTrpLysGlnLysValSerLys 400
 DB 1141 ATTATGAAATGTTGCTGAGCAACCAATTCAGAAAGATTAACAAGGAAAGGTCAGTAA 1200
 QY 401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420

DB 1201 GAGAGATCTGAAAGCAAGAAACTCTGCAAGAGAGCTTAATTCAGACATGATTAATTCACA 1260
 QY 421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysProGluGlnArgLeuGly 440
 DB 1261 GAGGAGGAAAGATATTTGAGCGCTCTTCTGCTMAAACAAGAGCAAGCCTTAGGA 1320
 QY 441 SerArgGlyLysSerAspAspProArgLysHisPhePheLysTrpIleAsnPhePro 460
 DB 1321 AGCAGAGAAAGTCTATGATATCCAGAAACATCATTTCTTAAAGATCAACTTCTCT 1380
 QY 461 ArgLeuGlnAlaGlyLeuIleGluProProPheValProAspProSerValIleTyrAla 480
 DB 1381 CGCTCGAAGACTGGCTTAATTAAGACCCCATTTGTGGCAAGACCTTCAGGTGTTATGCC 1440
 QY 481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
 DB 1441 AAGACATCCCTGAATTAATGATTTCTGAGGTTCCGGGGGTGAGATTTATGACAAA 1500
 QY 501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGlu 520
 DB 1501 GATTAAGCATGTTCTCAAAAACCTTTCAGACAGGTGCTGCTTATAGCATGGAGAAATA 1560
 QY 521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProLeuArgProThrGlyCysGlu 540
 DB 1561 ATTATAGAAAGGAGACTGTTGAGAACTGAAATGACCCCAACAGACCTACGGGTTGTGAG 1620
 QY 541 GluGlyAsnSerSerLysSerGlyValCysLeuLeu 553
 DB 1621 GAGGATTAATTCACAAAGTGGCGTGTGTTGTTATTG 1659

RESULT 5

US-09-802-117-3
 : Sequence 3, Application US/09802117
 : Patent No. 6444456
 : GENERAL INFORMATION:
 : APPLICANT: Walke, D. Made
 : APPLICANT: Milgowski, Nathaniel L.
 : APPLICANT: Turner, C. Alexander Jr.
 : TITLE OF INVENTION: No. 6444456 Human G-Coupled Protein Receptor Kinases and Polymic
 : FILE REFERENCE: LEX-0147-USA
 : CURRENT APPLICATION NUMBER: US/09/802,117
 : PRIOR FILING DATE: 2001-03-08
 : PRIOR APPLICATION NUMBER: US 60/188,449
 : NUMBER OF SEQ ID NOS: 5
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 3
 : LENGTH: 1062
 : TYPE: DNA
 : ORGANISM: homo sapiens
 : US-09-802-117-3

Alignment Scores:

Pred. No.: 3,77e-202 Length: 1062
 Score: 1801.00 Matches: 349
 Percent Similarity: 99.71% Conservative: 0
 Best Local Similarity: 99.71% Mismatches: 1
 Query Match: 62.34% Indels: 0
 DB: 4 Gaps: 0

US-10-044-205A-2 (1-553) x US-09-802-117-3 (1-1062)

QY 1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
 DB 1 ATGTGTGACATGGGGGCTCTGAGACATGATGCGCAACCGCTTACTGCAAGGCTCCG 60
 QY 22 LysProSerAspCysAspSerLysGlnLeuGlnArgGatGatGatGatGatGatGatGat 40
 DB 61 AAGCCCTGGACATGCGACAGCAAGAGAGCTTCAGCGGCGGCGGTGAGCTGGCCCTGGCC 120
 QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuPheHisSerLeuCys 60

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Db      121 GGGCTGCAAGGCGGAGCTCCGCAAGAGCTGCTCGAATCTCCAGCCTGTGT 180
Qy      61 GlnGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
Db      181 GAGGACGAGCGCCATCGGTCGCGCTCTTCCTCGATCTTCAGACAGAGCGCCACGCTTC 240
Qy      81 ArgValAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
Db      241 CGCAAGGCGGCAACCTTCCTAGAGGAGCGTGCAGAACCTGGGAGCTGGCGGAGAGGAGCC 300
Qy      101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
Db      301 ACCAAGACAGCGCGCTGCAGGGGCGTGTGTGCACTTGAGAGTGGCCCTGCGCCGCGGG 360
Qy      121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
Db      361 AACCGGCAACCTCTCTCAGCCAGCGCTGGCCAGAGTGCCAGAGCGCACCACTGAG 420
Qy      141 GlnGluArgValAlaAlaValThrLeuArgValAlaGluAlaMetAlaPheLeuGlnGlu 160
Db      421 GAAGGCGAGTGGCTGAGTGCAGCTGGCCAGAGCTGAGGCCATGCGCTTCCTTGCAAGAG 480
Qy      161 GlnProPheLysAspPheValThrSerAlaPheThrAspLysPheLeuGlnTrpLysLeu 180
Db      481 CAGCCCTTTAAGATTCGTCGACGAGCGCTTCACAGACAGTTTCTGCGAGTGGAAACTC 540
Qy      181 PheGlnMetGlnProValSerAspLysTrpPheThrGluPheArgValLeuGlyLysGly 200
Db      541 TTGAGATGCAACAGTGTGCAGACAGTACTTCACTGAGTGCAGAGTCTGGGAGAAAGGT 600
Qy      201 GlyPheGlnGlyValCysAlaValGlnValLysAsnThrGlyLysMetTrpAlaCysLys 220
Db      601 GTTTTGGGAGGATGATGCGCTCCAGGTGAAACACTGGGAGAGTATGCTGTGTAAG 660
Qy      221 LysLeuAspLysLysArgLeuLysLysLysGlyValGluLysMetAlaLeuLeuGluLys 240
Db      661 AAACCTGACAGAGAGCGCTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Qy      241 GlnIleLeuGlnLysValSerSerProPheIleValSerLeuAlaThrAlaPheGlnSer 260
Db      721 GAAATCTGAGAGAGTGCAGACGCTTCCTTCATGTCCTCTGCGCATAGCTTGTAGAGAC 780
Qy      261 LysThrIleLeuCysLeuValMetSerLeuMetAsnGlyValAspLeuLysPheHisIle 280
Db      781 AAGACCATCTGCTGCTGTGATGACCTGATGATGATGATGATGATGATGATGATGATG 840
Qy      281 TyrAsnValGlyThrArgLysLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
Db      841 TACAACTGGGACCGCGTGCAGATGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Qy      301 AlaCysGlyMetLeuHisIleLeuHisGlnLeuGlyIleValTyrArgAspMetLysProGlu 320
Db      901 GCGTGGAGATGCTGCACTTCATGAACTGGGCATGCTGCTATGCGGACATGAACTGAG 960
Qy      321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuLysLeuAlaValGlu 340
Db      961 AATGTCTTGTGATGACCTGCGCACTGAGAGTTATCTGACCTGGGAGCTGCGCTGAG 1020
Qy      341 MetLysGlyLysPheProIleThrGlnArg 350
Db      1021 ATGAAGGAGTGGCAAGCCCATCAACCAAGAG 1050

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RESULT 6

US-09-738-894A-3
 ; Sequence 3, Application US/09738894A

; Patent No. 6331423

; GENERAL INFORMATION:

; APPLICANT: GUEGLER, Karl et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; FILE REFERENCE: CLO00636

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; CURRENT APPLICATION NUMBER: US/09/738,894A
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 36651
; TYPE: DNA
; ORGANISM: Human
; FEATURES:
; NAME/KEY: misc feature
; LOCATION: (1) (36651)
; OTHER INFORMATION: n = A,T,C or G
; US-09-738-894A-3

Alignment Scores:
Pred. No.: 1,77e-167 Length: 36651
Score: 1528.00 Matches: 349
Percent Similarity: 41.40% Conservative: 0
Best Local Similarity: 41.40% Mismatches: 1
Query Match: 52.89% Indels: 493
DB: Gaps: 1

US-10-044-205A-2 (1-553) x US-09-738-894A-3 (1-36651)

Qy      1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaThrLeuGlnAlaArg 20
Db      2076 ATGGTGAACATGGGGGCGCTGCAGCAACCTGATCGCAACCGCTTACTCTGAGGCCCCG 2135

Qy      21 LysProSerAspCysAspSerLysGlnLeuGlnArgArgArgSerLeuAlaLeuPro 40
Db      2136 AAGCCTCGACTGCGACAGAGAGAGCTGCAGCGGGGGGGGTAGCTGCTGCTGCC 2195

Qy      41 GlyLeuGlnGlyCysAlaGlnLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
Db      2196 GGGCTGAGGGGCTGGCGGAGCTCCGCAAGAGCTGTCCCTGAACTTCCACAGCCTGTGT 2255

Qy      61 GlnGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
Db      2256 GAGCAGACAGCCCATGCTGCTGCGCGCTCTCTCGTGCCTTACGACAGTGCACGCTTC 2315

Qy      81 ArgValAlaAlaThrPheLeuGlnAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
Db      2316 CGCAAGGCGGCAACCTTCCTAGAGAGAGTGCAGAACTGGAGCTGGCCAGAGGAGACC 2375

Qy      101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
Db      2376 ACCAAGACAGCGCGCTGCAGAGGAGTGTGTCGACCTGCGAGTGCCTGCCCGGAG 2435

Qy      121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
Db      2436 AACCCGCAACCTTCCTCAGCGAGCGGTGAGCCACCAAGTGCAGAGCGACGACCTAG 2495

Qy      141 GlnGluArgValAlaAlaValThrLeuArgValAlaGluAlaMetAlaPheLeuGlnGlu 160
Db      2496 GAAGAGCGAGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2555

Qy      161 GlnProPheLysAspPheValThrSerAlaPheThrAspLysPheLeuGlnTrpLysLeu 180
Db      2556 CAGCCTTTAAGATTCGTCGACGAGCGCTTCACAGAACCTTTCGACGTGAAACTC 2615

Qy      181 PheGlnMetGlnProValSerAspLysTrpPheThrGluPheArgValLeuGlyLysGly 200
Db      2616 TTGAGATGCAACAGTGTGCAGACAGTACTTCACTGATTCAGAGTGTGGGAGAAAGGT 2675

Qy      201 GlyPheGlyGlu----- 204
Db      2676 GGTTTTGGGAGGTAAGTGTCTCCAGTAGCCAGGCTAGAGAGTAGAGTAGAGCANTGA 2735

Qy      204 ----- 204
Db      2736 AAGGGGTAATGTTGCTTCTTTTAAATCAAGTTACTTAAGACTAATTTCAGACAC 2795

Qy      204 ----- 204

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NAME/KEY: misc feature
 LOCATION: (1)... (36651)
 OTHER INFORMATION: n = A,T,C or G
 US-09-964-469-3

Alignment Scores:
 Pred. No.: 1,77e-167 Length: 36651
 Score: 1528.00 Matches: 349
 Percent Similarity: 41.40% Conservative: 0
 Best Local Similarity: 41.40% Mismatches: 1
 Query Match: 52.89% Indels: 493
 DB: 4 Gaps: 1

US-10-044-205a-2 (1-553) x US-09-964-469-3 (1-36651)

QY 1 MetValaAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
 Db 2076 ATGTGTGACATGGGGGCTTGGACCACTATATGCCAACACCGCTTACTGGACGGCCGG 2135
 QY 21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgSerLeuAlaLeuPro 40
 Db 2136 AAGCCCTCGACTCGACAGCAAGAGCTGCGAGCGGCGGCGCTGAGCTTGGCCCTGCCC 2195
 QY 41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAspPheHisSerLeuCys 60
 Db 2196 GGGCTGCGAGGGCTGCGGAGCTCGCGAAGACTTGTCCCTAACTTCCACAGCTGTGT 2255
 QY 61 GluGlnGlnProIleGlyArgArgLeuPheArgPheLeuAlaThrValProThrPhe 80
 Db 2256 GAGCAGACCCCATCGTTCGCCGCTTCCGTGACTTCCAGCCAGCTGCGCCAGCTTC 2315
 QY 81 ArgValAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
 Db 2316 CGCAAGCGCGCACTTCTTAGAGAGCGTGCAGAACTGGAGTGGCCGAGAGAGGCC 2375
 QY 101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
 Db 2376 ACCAAGACAGCGGCTGCGAGGGCTGTGGCCACTTGTCCAGTCCCTGCCCGGGG 2435
 QY 121 AspProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
 Db 2436 AACCCGACCTTCTTCTAGCGAGCGCTGCGCAAGTGCACAGCGCCACCGACCTGAG 2495
 QY 141 GluLysArgValAlaAlaValThrLeuArgValAlaGluAlaMetAlaPheLeuGlnGlu 160
 Db 2496 GAAGAGCGAGTGGCTGCGAGTACCGCTGCGCAAGGCTAGAGGCTATGCTTCTGAGAG 2555
 QY 161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
 Db 2556 CAGCCCTTAAAGATTTCGACAGCGGCTTCTACGACAAAGTTTCTGAGTGAAGAACTC 2615
 QY 181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
 Db 2616 TTCAGATGTAACGAGTGTGACAGACTTCACTGAGTTCAAGAGTGTGCGGAAAGGT 2675
 QY 201 GlyPheGlyGlu----- 204
 Db 2676 GATTGTGGAGGTAAAGTGTCTCCAGTAGCCAGGCTAGAAAGTGAAGCATAGACATGA 2735
 QY 204----- 204
 Db 2736 AAGGGGGTAATGTGCTTCTTTTAAATCTCAATTACTTAGAACTAATTTAGAC 2795
 QY 204----- 204
 Db 2796 CATATGTGAGGATTTCTAGCCCGTCTCCAGCCCTTCTTTGTGTGTCATGTG 2855
 QY 204----- 204
 Db 2856 TGAATATAAACAAATGCGATGAGAGAGCAAGAAATTATTAATTGCTGCGCAAGACTCT 2915
 QY 204----- 204

Db 2916 GTCATGGCTTCATTAGAGAGTGTCTGAGATGCTTGACACTTCAAGAGATGATGCAA 2975
 QY 204----- 204
 Db 2976 TGTGTACAGAAAGATCTCCGTTTCCCTAAATGTGTATATGAAAGCACTTCAAGAAAA 3035
 QY 204----- 204
 Db 3036 TGGATATTTAAGAAAAATTACTTAAGTACTGAGTGGTGTGATGATGCTGTATGCCAGCT 3095
 QY 204----- 204
 Db 3096 ACTTGGAGGCTGAAGACAGAGATCACTTGAAGCTGGAGGTTGAGGTTGCAATGAGCC 3155
 QY 204----- 204
 Db 3156 AAGATGTGTCCACTGCACTCCAGCTGGGTGACAGACAGACTCAAAAAA 3215
 QY 204----- 204
 Db 3216 AAGAAAGAAAAAAGAAAAAACAATTATCTGAAGTAAAGTTGAGAACCTGTGTTGT 3275
 QY 204----- 204
 Db 3276 ACCAGTGTGTGCCAGCTTCTGTGTTTAAAGTAAATAAATTTACAGTAAATTTG 3335
 QY 204----- 204
 Db 3336 CTGTATTAATAACCTAACCTGTTTAAATGATGATCAATGAGTGGCACTTGGACA 3395
 QY 204----- 204
 Db 3396 AATGCAATGTGGTAAAGCAACCTCAATCTGATTCAGACACTCATACCCCTGT 3455
 QY 204----- 204
 Db 3456 GCCATTAATAGTCTCCCTCCATCCCTCTCTCCAGCCCTGACAACTAGTCCGC 3515
 QY 204----- 204
 Db 3516 TTCTGTCTAGGATTTGCCATTTCTGGGTTTTCACAGATATGTGACTTTGTGT 3575
 QY 204----- 204
 Db 3576 CTGGCTCTTTCACCTAATGAATGTTTGGGCTTCACTACACTGATGATGTCAA 3635
 QY 204----- 204
 Db 3636 TACTCAATCTTTTATGCTGTATTAATTTCCATGATGATGATGATCACTTTCAATG 3695
 QY 204----- 204
 Db 3696 TAGCATTCATCTGTGATGACACTTGGCTGTTTTCACTTTGGCTATGTGTATGG 3755
 QY 204----- 204
 Db 3756 TGTCTATTCATGACAGATATTGTTGAATCTTGTGTTTCACTTCTGTGATTAAT 3815
 QY 204----- 204
 Db 3816 GCCAGAGTGAATTGCTAGGGCAATGATGATGATGATGATGATGATGATGATGATGATG 3875
 QY 204----- 204
 Db 3876 CCAACTTTTCAATTTTATTTTCCACAGCAATGTAAAGTTTGTGATTTCTTCCACA 3935
 QY 204----- 204
 Db 3936 TCCCTGCAACCTGATTAATTTCTGTAATTTTATTAAGGCTGCTAGTGAAGTGA 3995
 QY 204----- 204
 Db 3996 AGAGATGACAGTGTATGCCCACTTTTCTGAGAACTTCTTATTTACAGCTACTC 4055

[illegible]

Qy	7	LeuAspAsnLeuIleAlaSerThrAlaIleTyrLeuGlnIleAlaIleTyrProSerAspCysAsp	26
Db	7	CTGGAAACATCGTGGCCCAACACGGTCTTGTTGAACCCGAGGAGGGCGGAGCAAG	66
Qy	27	SerTyrSGIleuGlnArgArg---ArgArgSerIleuAlaLeuProGlyIleuGlnGlyCys	45
Db	67	CGAAAGGAAAAAGCAGAAAGTGGAAAGAAATCCTGAAGTCCCTCACATTAGCCAGTGT	126
Qy	46	AlaGluIleuArgGlnIleuSerIleuAsnPheHisSerIleuGlnGlnGlnProIle	65
Db	127	GAACACCTCCGAAAGGACCATAGACAGAGATTATCGCAGTTTATGTGACAAACACCAATC	186
Qy	66	GlyArgArgIleuPheArgAspPheIleuAlaThrAlaProThrPheArgIleAlaIleThr	85
Db	187	GGGAGGCTGGTCTTTCCGCAAGTCTTGTGAAACAGAGCCCTGGCTGAGTGTACATTCCG	246
Qy	86	PheIleuGlnAspValGlnAsnTrpGlu-----LeuAlaGluGlnGly	99
Db	247	TTCCTGAGATCCGCTGGCAGAAATATGAAGTACTCCAGATGAAAACTGGAGAGAGAGG	306
Qy	100	ProThrIleuAspSerAlaLeuGlnGlyIleuValAlaThrCysAlaSerAlaProAlaPro	119
Db	307	-----AAGAAATTATAGACCAAGTACCTC-----ACCCCA	336
Qy	120	GlyAsnPro-----GlnProPheIleuSerGlnAlaValAlaIleThr	132
Db	337	AMGTCCTCCCTTTTCATAGCCCAAGTGGCCAGAACTGGTCTCCAGACGAGAGAAAG	396
Qy	133	LysCysGlnAlaIleAlaThrThrGluGluGlnIleArgValAlaIleAlaIleThrIleuArgIleVal	152
Db	397	CTCCTCAAGAAAGCCGTCGAAAGAACTCTTTCTGCTGTGTGACAGTCTGTCCAGAG---	453
Qy	153	GluAlaMetAlaPheIleuGlnGlnGlnGlnProPheLysAspPheValThrSerAlaPheTyr	172
Db	454	-----TACCTAGGGGAGAGAACCATCTCCAGAAATCTGCAGACAGCATGTTTTT	501
Qy	173	AspLysPheIleuGlnTrpLysIleuPheGluMetGlnProValSerAspTyrPheThr	192
Db	502	GACCCCTTCTCCAGTGAAGTGGTGTGAAAAGGCAACCGGTGACCAAAAAACCTTTCAG	561
Qy	193	GlnPheArgValIleuGlyIleuGlyGlyIleuPheGluGlnValCysAlaValGlnValLysAsn	212
Db	562	CAGTATCGAGTGGCTTAGAAAGAGGGGGCTTCGGGAGAGTCTGTGCTGCCAGGTGGAGCC	621
Qy	213	ThrGlyLysMetTyrAlaCysLysLysIleuAspLysLysValGluIleLysIleuGly	232
Db	622	ACGGGTAAATAGTATGCTCGTGAAGCGCTGAGAAAGAGAGAGATCAAAAAAGGAAAGG	681
Qy	233	GlnLysMetAlaIleuIleuGlnLysGluIleIleuGlnLysValSerSerProPheIleVal	252
Db	682	GATCCCAAGGCGCCCATATAGAAAGCAAGTCTCTGAGAAAGTGCACATGCTATTGGTGTC	741
Qy	253	SerLeuAlaTyrAlaPheGluSerTyrThrIleuLysCysLeuValMetSerIleuMetAsn	272
Db	742	AACCTGGCTTATGGCTTACAGACAGAAAGTGCATGTGCTGTGATCTGACATCATGAT	801
Qy	273	GlyGlyAspLeuLysPheHisIleTyrAsnValGlyThrArgGlyIleuAspMetSerArg	292
Db	802	GGGGGTGACGTGAAGTCCACATCTTACAACTGAGGCAACCCGTGGCTTCAGAGAGAGCGG	861
Qy	293	ValIlePheTyrSerAlaGlnIleAlaCysGlyMetLeuHisIleuHisGlyIleuGlyIle	312
Db	862	GCCCTGTGTTTTTGCGGAGATCCTCGCGGCTTGAAAGACCTCCACCGTAGAAACACC	921
Qy	313	ValTyrArgAspMetLysProGlnAsnValIleuIleuAspAspLeuGlyAsnCysArgIleu	332
Db	922	GTCACCGAGATCGAAACCTGAAACATCTGTGTAGATGATTAAGGCGACATTAGATC	981
Qy	333	SerAspLeuGlyIleuAlaValGluMetLysGlyIleuLysProIleThrGlnAlaGlyIle	352
Db	982	TCAAGACTGGGTGGCTGGTGAAGATCCCGAGAGGAGACTGATCCGCGCGGGGTGGCC	1041
Qy	353	ThrAsnGlyTyrMetAlaProGluIleIleuMetGlnLysValSerTyrProVal	372


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Db      1738  TCAAGCTGGGCTTGGCTGTGAAGATCCCGAGGAGACGACTGATCCGCGCGGCTGGCC 1797
Qy      353  ThrasnGLYrMetAlaProGluIleLeuMetGluValSerTySerTyProVal 372
Db      1798  ACTGTGGCTACATGAGCCCCGAGAGCTCTTAACAAACGAG---AGATACGGCTGAGCCCC 1854
Qy      373  AspTrpPheAlaMetGLYCySerTILErGluMetValAlaGLYArGhrProPheLys 392
Db      1855  GACTACTGGGCTTGGCTGCTCATCTATGATGATGATCGAGGGCCAGTGGCGCTTCGCG 1914
Qy      393  AspTyTrpGluValSerTySerGluAspLeuLysGlnArGhrLeuGlnAspGluVal 412
Db      1915  GGCCCTAGAGAGAGGTGAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1974
Qy      413  LysPheGlnHisAspAsnPhrThrGluGluAlaLysAspIleCyArgLeuPheLeuAla 432
Db      1975  GTGTACTCCAC---AAGTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2031
Qy      433  LysLysProGluGlnArgLeuGluSerArgGluLys---SerAspAspProArgLysHis 451
Db      2032  AAGATGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2091
Qy      452  HisPhePheLysThrIleAsnPhrProArgLeuGluAlaGLYLeuIleGluProPhe 471
Db      2092  CCTTCTTCAGAGAACATGAATTCAGAGGCTTGAAGAGCGGAGATGTTGACCTCCCTTC 2151
Qy      472  ValProAspProSerValValTyTrAlaLysAspIleAlaGluIleAspAspPheSerGlu 491
Db      2152  GTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2211
Qy      492  ValArgGLYValGluPheAspAspLysAspLysGluPheLysAsnPheAlaThrGLY 511
Db      2212  GTGAGAGGGGCTCATCTGACACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2271
Qy      512  AlaValProIleAlaThrGluGluGluIleIleGluThrGlyLeuPheGluGluLeuAsn 531
Db      2272  TCTGTCTCATCTCCATGCGCAAAACAGATGATGAAACGAATGCTTTAAGAGCTGAAC 2331
Qy      532  -----AspPro-AsnArg 535
Db      2332  GTGTTTGACCTAATGTGTAACCTCCCGCAATGTCAGAACAAACCACTCCGGAACCG 2391
Qy      535  gPro---ThrGLYCySerGluGluValAsnSerLysSer 547
Db      2392  CCCAAGAAAGGGCTGCTCCAGAGACTCTTCAAGCGGAGCG 2431

RESULT 11
US-09-016-434-1298
; Sequence 1298, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSER: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:

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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1298:
SEQUENCE CHARACTERISTICS:
LENGTH: 2557 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g306804
US-09-016-434-1298

Alignment Scores:
Pred. No.: 6,19e-137 Length: 2557
Score: 1252.50 Matches: 259
Percent Similarity: 63.07% Conservative: 103
Best Local Similarity: 45.12% Mismatches: 162
Query Match: 43.35% Indels: 50
DB: 4 Gaps: 11

US-10-044-205A-2 (1-553) x US-09-016-434-1298 (1-2557)
Qy      7  LeuAspAsnLeuIleAlaAsnThrAlaTyLeuGlnAlaArgLysProSerAspCyAsp 26
Db      227  CTGGAATAACATGCTGCGCCACACCGCTTCCTGCAAGCGAGAGAGAGAGAGAGAGAG 286
Qy      27  SerLysGluLeuGlnArgArg---ArgArgSerLeuAlaLeuProGlyLeuGlnGlyCys 45
Db      287  CGCAAGAGGAAAGCAAGAGATGGAAGAAATCCCTGAAGTTCCCTACATTCGACAGGT 346
Qy      46  AlaGluLeuArgGlnLysLeuSerLeuAsnPhrHisSerLeuCySerGluGlnProIle 65
Db      347  GAAAGACCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 406
Qy      66  GlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThr 85
Db      407  GGGAGGCTGCTTTTCCGACAGTTTGTGAACACGAGCTGGGCTGAGGTGATTCAG 466
Qy      86  PheLeuGluAspValGlnAsnTrpGlu-----LeuAlaGluGluGly 99
Db      467  TTCCCTGAGACTCGGTGGAGAAATATGAGTTACTCCAGATGAAACCTGGGAGAGAGAGG 526
Qy      100  ProThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProIlePro 119
Db      527  -----AAGGAATATGACCAAGTACTC-----ACCCA 556
Qy      120  GlyAsnPro-----GlnProPheLeuSerGlnAlaValAlaThr 132
Db      557  AAGTCCCTGTTTCTATGCCCAAGTTGGCAAGACTGCTCCCAAGAGAGAGAGAGAG 616
Qy      133  LysCySerGlnAlaAlaThrThrGluGluGluArgValAlaAlaValThrLeuArgLysAla 152
Db      617  CTCCTAGAGAGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 673
Qy      153  GluAlaMetAlaPheLeuGlnGluGlnProPheLysAspPheValThrSerAlaPheTy 172
Db      674  -----TACTGAGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 721
Qy      173  AspLysPheLeuGlnTrpLysLeuPheGluMetGlnProValSerAspLysTyTrpPheThr 192
Db      722  GACCGCTTCTCCAGGTGAGAGAGGTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 781
Qy      193  GluPheArgValLeuGluLysGlyGlyPheGlyGluValCysAlaValGlnValLysAsn 212

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QY 177 GlnTrpLysLeuPheGluMetGlnProValSerAspLysTrpPheThrGluPheArgVal 196
 Db 771 CAATGAAATGCGTGGAAAGCAACCGTAAACAAAGAACACATTACATTAAGAGATT 830
 QY 197 LeuGluLysGluValGluValCysAlaValGlnValLysAsnThrGluLysMet 216
 Db 831 CTAGGAAAGCGGATTTGGAGAGGTTGGCTTCAAGTCCAGGCGACAGGAAATG 890
 QY 217 TyrAlaCysLysLysLeuAspLysLysArgLeuLysLysGluLysGluLysMetAla 236
 Db 891 TATGCTCTGCAAAAAGCTCAAAAAAAGATTAAGAGAGAAAGGTAAGCTATGCT 950
 QY 237 LeuLeuGluLysGluLeuGluLysValSerSerProPheLeuValSerLeuAlaTyr 256
 Db 951 CTAATAGAGAAAGAAATCTGGAGAAAGTCAAGATGATGCGATTAAGTTTACCTAC 1010
 QY 257 AlaPheGluSerLysThrHisLeuLysLeuValMetSerLeuMetAsnGluLysAspLeu 276
 Db 1011 GCTTATGAAACCAAAAGATGCTTGGCTGGCTGCTGCTACATTATGATGAGGAGATTG 1070
 QY 277 LysPheHisLysLysValGluLysValGluLysValGluLysValGluLysValGluLys 296
 Db 1071 AAGTTTCAATTACAAACCTGGGCAATCCGGCTTGTATGAGCAGAGAGCGCTTTCTAT 1130
 QY 297 SerAlaGlnIleAlaCysGluMetLeuHisLeuGluLysIleValTyrTrpAsp 316
 Db 1131 GCTGAGAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1190
 QY 317 MetLysProGluLysValLeuLeuAspLysGluLysValGluLysValGluLysValGlu 336
 Db 1191 TTGAAGCTGAGATATTTCTCTGATATGTCGACACATCCGATTTGAGCCCTCGCT 1250
 QY 337 LeuAlaValGluMetLysGluLysProLysThrGlnArgAlaGluLysValGluLysVal 356
 Db 1251 TTGGCAGACAGATCCAGAGAGACAGAGGCTTGAAGAGAGGTTGAGAGAGCGCTAC 1310
 QY 357 MetAlaProGluLysLeuMetGluLysValSerLysTrpProValAspTrpPheAla 376
 Db 1311 ATGGACCTGAGATGTCATTAATATA---AAGTATACGTTTATGCCGATGATGAGGGA 1367
 QY 377 MetGluCysSerLysLysValGluMetValAlaGluLysThrProPheLysAspTyrLysGlu 396
 Db 1368 CTGGCTGCTGATCTTGAATATGATTCAGGAGATTTCTCCATTCAAAAAATCAAGAG 1427
 QY 397 LysValSerLysGluAspLysGluLysGlnArgThrLeuGlnAspGluValLysPheGlnHis 416
 Db 1428 AAGTCAATGGAGAGAGGTCATCAAGAAATCAAGATGATGATGATGATGATGATGATGAT 1484
 QY 417 AspAsnProThrGluGluAlaLysAspLysCysArgLeuPheLeuAlaLysLysProGlu 436
 Db 1485 GAGAGATTTTCAGAGATGCGAATATCTGCGAGATGTTATCAACCAAGATCCAGAC 1544
 QY 437 GlnArgLeuGluSerArg--GluLysSerAspAspProArgLysHisLysPhePheLys 455
 Db 1545 AAGCGCTGCGTGGAGGCGAGGAGGCGGCTGGGTTGAAGAGACCCCGTGTCCAG 1604
 QY 456 ThrIleAsnProThrGluGluAlaGluLysLeuGluProProPheValProAspPro 475
 Db 1605 GACATCACTTCAGAGAGGCTGAGGCAACATGCTGAGAGCCCTTTCTGCTCGATCCT 1664
 QY 476 SerValValTyrAlaLysAspIleAlaGluLysAspPheSerGluValArgVal 495
 Db 1665 CATGCCGTTTACTGTAAAGAGCTGCTGATTCAGAGATTCCTGCGCGCTAAAGGATC 1724
 QY 496 GluPheAspLysAspLysGlnPhePheLysAsnPheAlaThrGluAlaValProIle 515
 Db 1725 TACTGGAACCGCAGAGAAAGACTTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1784
 QY 516 AlaTrpGlnGluGlu 520
 Db 1785 CCCTGGCAGATGAG 1799

RESULT 13
 US-09-614-748A-8
 ; Sequence 8, Application US/09614748A
 ; Patent No. 6660474
 ; GENERAL INFORMATION:
 ; APPLICANT: FELDER, ROBIN A.
 ; APPLICANT: JOSE, PEDRO
 ; TITLE OF INVENTION: G PROTEIN-RELATED KINASE MUTANTS IN ESSENTIAL
 ; TITLE OF INVENTION: HYPERTENSION
 ; FILE REFERENCE: FELDER 3.9-001 CONT
 ; CURRENT APPLICATION NUMBER: US/09/614,748A
 ; PRIORITY FILING DATE: 2000-07-12
 ; PRIORITY APPLICATION NUMBER: PCT/US99/00663
 ; PRIORITY FILING DATE: 1999-01-12
 ; PRIORITY APPLICATION NUMBER: 60/071,199
 ; PRIORITY FILING DATE: 1998-01-12
 ; PRIORITY APPLICATION NUMBER: 60/098,279
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 2017
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-614-748A-8
 Alignment Scores:
 Pred. No.: 4,81e-136 Length: 2017
 Score: 1243.50 Matches: 248
 Percent Similarity: 62.99% Conservative: 89
 Best Local Similarity: 46.36% Mismatches: 145
 Query Match: 43.04% Indels: 53
 DB: Gaps: 8
 US-10-044-205A-2 (1-553) x US-09-614-748A-8 (1-2017)
 QY 7 LeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArgLysProSerAspCysAsp 26
 Db 261 CTCGAGAACCATGCTGGCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 314
 QY 27 SerLysGluLeuGlnArgArgArgSerLeuAlaLeuProGluLeuGlnGluCysAla 46
 Db 314 ----- 314
 QY 47 GluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCysGlnGlnProLysGlu 66
 Db 315 -----TATACAGTCTTTGTGCAAGACAGATAGGA 347
 QY 67 ArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThrPhe 86
 Db 348 AGAGCTCTTTCAGGAGGCTGCTGATGATCCAAACCCACTTAAAGAGGACATGGAATTC 407
 QY 87 LeuGluAspValGlnAsnTrpGluLeuAlaGluGluGluProThrLysAsp----- 103
 Db 408 TTGATGACAGTGGCAGATATGAAATGTTGGCCGATGATGAGACCGAATGTTGGACTG 467
 QY 104 SerAlaLeuGlnGluLeuValAlaThrCysAlaSerAlaProAlaProGluLysProGln 123
 Db 468 TCAATCTTAATGATGATTCCTCAATGATTAAGTGGAGCCCTTATCCAGAAATACCTCCA 527
 QY 124 ProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGluGluGluArg 143
 Db 528 GAT-----GTTGTGACAGAAATGTAATGGGACCTGAAAGAGAGAAC----- 569
 QY 144 ValAlaAlaValThrLeuArgLysAla-----GluAlaMetAlaPhe 157
 Db 570 -----CCTTCAAAAAGCCCTTGGAGAAATGCTAGAGTGGCCATTAATAC 617
 QY 158 LeuGlnGluGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGln 177
 Db 618 CTAGAGGCGACACATTTGAAGATACCAAGAAAGCTCATATTTTCTCAGTTTATACA 677
 QY 178 TrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeu 197

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Db      678  TCGAAGTGGCTGGAAGGCAACCCGTAACAAAGAACCATTTAGACATTACAGAGTTCTA 737
Qy      198  GYLYSGLYGYPHEGNYGVVALCYSAVALGVALYASNTHGYLYSMETLYR 217
Db      738  GGAAGAGGGGATTTGGAGAGTTTGCCTGTCAAGTGGAGCCACAGAAAAATGTAT 797
Qy      218  ALCYLYSLVLSLEASPLYSLSAUGLEULYSLSYGLYGLYLYMETALALEU 237
Db      798  GCTTGCAGAAAGCTACAAAAAAGAAATAGAGAGGAAAGTGAAGCTATAGGCTCTA 857
Qy      238  LEUGLYLLEUGLYLLEUGLYLVSVALSERSEPPROPHETLVALSERLEUALATYRA 257
Db      858  AATGAGAAAAGATTTCTGGAGAAAGTGCAGAAAGTATGATGATGATTAAGGAGGCT 917
Qy      258  PHEGLUSERYLTHRLSLEUCYSLEUVALMETSERLEUMETASNGLYLYASPLEULYS 277
Db      918  TATGAAGCAAGATGCTTGTGCTTGGTGTCAACATTAATGAAGAGGAGGCTTGAAG 977
Qy      278  PHEHSLLEYRAENVALGYTHARGLYLEUSPMETSERARGVALIIEPHERYSER 297
Db      978  TTTCACATTACAACTCGGAGCATCCCGCTTTGATGACAGAGAGCGTTTCTATGCT 1037
Qy      298  ALAGNILEALCYSGLYMETLEUHLISLEUHLISGLULEUGLYLEVALTYRARGAPMET 317
Db      1038  GCAAGAGCTGTGCTGGCTTGAAGATTTACAGAGGAGAAAGATTTGATACAGAGCTTG 1097
Qy      318  LYSFROGLUBANVALLEULEUSPASPLeUGLYASNCYARGLEUSERYLLEUGLYLEU 337
Db      1098  AAGCTGGAATATTCTTCCCTGATGATCGTGAACACATCCGATTTGACAGCTCGGTTG 1157
Qy      338  ALAVALGIMETLYSGLYLYSPROILETHGLARGALAGLYTHRAENGLYRYMET 357
Db      1158  GCCACAGAGATCCAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1217
Qy      358  ALAPROGLULEULEUMETGLUBSVALSERSETYRPROVALAPRTPHEALAMET 377
Db      1218  GCACTGAAAGTTGTCATATATGA---AAGTATACGTTTAAAGTCCGAGTTGGAGGACTT 1274
Qy      378  GLYCYSERILETYRGLIMETVALAGLYARGTHPROPELHYSAPRYLYSGLYLUS 397
Db      1275  GGCTGCTGATCTATGAAATGATTCAGGAGCATTCCTCCATTCMAAAATACMAAGAGAA 1334
Qy      398  VALSERYSGLUSPLeULYSGLINARGTHLEUGLAPGLUVALYSPHEGLINIASP 417
Db      1335  GTCAATGAGAGAGAGGATGATCAAGATCAAGATGATACCGAGGATATCT---GAG 1391
Qy      418  AENPETHRGULUGLUALYASAPILECYARGLEULEUHEUALALYLSYSPROGLUGL 437
Db      1392  AAGTTTCAGAGATCCCAATCTATCTGAGAGATGTTACTCACCAAGATCAAGAGAG 1451
Qy      438  ARGLEUGLYSERARG---GLYLSERASPSPROARGLYSHISPHEPHELYTHR 456
Db      1452  CGGCTGGGCTGAGAGGAGGAGCGGCTGGGCTGAGAGAGAGAGAGAGAGAGAGAGAG 1511
Qy      457  ILEASNPHERPROARGLEUGLUALAGLYLEULILEGLUPROPHPEVALPROASER 476
Db      1512  ATCAACTTCAGAGAGGCTGAGAGCAAACTCTGAGAGAGAGAGAGAGAGAGAGAGAG 1571
Qy      477  VALVALTYRALYASAPILEALAGLULEASAPSPHESEGLUVALARGLYVALGLU 496
Db      1572  GCGCTTACTGTAAGAGAGCTCTCGATATGAGAGAGAGAGAGAGAGAGAGAGAGAG 1631
Qy      497  PHEASAPSPYLSAPLYSGLINPHEPHELYSAENPHEALATHRGYLAVALPROLEA 516
Db      1632  CTGAGACACCGAGATGAGAGACTTCTATGCTCGGTTTGTGTAACGAGGTGTCTCCATCCC 1691
Qy      517  TRYGLINGLUGLULELLEGLUTHRGYLEUPHEGLUGLULEUSN 531
Db      1692  TGGCAGATGATGATGATGATCGGCTGTTTCAAGAGAGAGAGAGAGAGAGAGAGAG 1736

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RESULT 14
US-08-464-954A-2

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; Sequence 2, Application US/08464954A
; Patent No. 6255069
; GENERAL INFORMATION:
; APPLICANT: BENOVIC, JEFFREY L.; GOMEZ, JORGE; KUNAPULI,
; APPLICANT: PRITA
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF G PROTEIN-COUPLED RECEPTOR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: Woodland Falls Corporate Park
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,954A
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/076,084
; FILING DATE: June 11, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: JEFF-0118
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2848
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; ANTI-SENSE: NO
; US-08-464-954A-2

Alignment Scores:
Pred. No.: 2,19e-135 Length: 2848
Score: 1240.00 Matches: 242
Percent Similarity: 65.36% Conservative: 107
Best Local Similarity: 45.32% Mismatches: 165
Query Match: 42.92% Indels: 20
DB: Gaps: 7

US-10-044-205a-2 (1-553) x US-08-464-954A-2 (1-2848)
Qy      7  LEUASPANLEULLEALASNTHRALATYRLEUGLUALARGVSPROSERAPCYSAAP 26
Db      69  CTGGAACATCTGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 128
Qy      27  SERYSGLULEUGLARGARG---ARGARGSERLEUALALEUPROGLYLEUGLNGLYCY 45
Db      129  CGAAGAGGCAAGAAAGCAAGAAATGAGCGAGATGCTCAAGTCCCTCCACATCAGCAGTCC 188
Qy      46  ALAGLULEAUGLNUYLSLEUSERYLEUSNPHEHISERLEUCYSGJUGLNGLINPROLE 65
Db      189  GAAAGAGCTGCGGCTGAGCTTCAGAGGATGATCAATCAAGAGCTTGGAGAGGAGAGGAG 248
Qy      66  GLYARGARGLEUPHEARGASPHELEUALATHYVALPROTHRPHENARGYLSAALATHR 85
Db      249  GGGCGGCTGCTGTTCCAGAGAGTTCTGTGCCAGAGAGGAGGAGGAGGAGGAGGAGGAG 308
Qy      86  PHELEUGLUSAPVALGINSANTPGLULEUALAGLUGLUGLYPROTHRYS----- 102

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Query Match: 42.85% Indels: 20
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 US-10-044-205a-2 (1-553) x US-08-221-817-12 (1-2204)

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 Db 37 CTGAGACATGTCGTAGGACACGTCCTACTCAAGGCCCGGAAAGCTGCGGTGGAAT 96

QY 27 SerLysGluLeuGlnArgArg--ArgArgSerLeuAlaLeuProGlyLeuGlnGlyCys 45
 Db 97 CGCAAGGCGCAAGCAAGAAATGCGCGCGAGTCTCAGTCTCCATGACATGACGATGC 156

QY 46 AlaGluLeuArgGlnLysSerSerLeuAsnIleHisSerLeuGlnGlnProIle 65
 Db 157 GAAGAGCTGCGCTCCAGCTCCGAGCGTCACTATCAAGCTGTCGACGCGACCGCAT 216

QY 66 GlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThr 85
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QY 86 PheLeuGluAspValGlnAsnTrpGluLeuAlaGluGlyProThrLys----- 102
 Db 277 TTCCTGATGGGGTGGCCGAGTATGAGTACCCCGGATGACAGCGAAAGCATGTGG 336

QY 103 AspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGlyAsnPro 122
 Db 337 CGGACGTAACGCAAGATTTCTGAGCCACAGCGGTCTGACCTCATCTCGAGGTCC 396

QY 123 GlnProPheLeuSerGlnAlaValAlaThr-----LysCysGlnAlaAlaThr 138
 Db 397 CGGACGCTGTCGAGCAACTGCAACCGCGGTGGACAGGATCCCTGAAAGACCTTTTC 456

QY 139 ThrGluGluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeu 158
 Db 457 CAGGAACCTCACCCGCGCTG-----ACCACGAGATCTG 489

QY 159 GlnGluGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrp 178
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QY 219 CysLysLysLeuAspLysLysArgLeuLysLysGlyGlyGlyLysMetAlaLeuLeu 238
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QY 259 GluSerLysThrHisLeuLysLeuValMetSerLeuMetAsnGlyLysAspLeuLysPhe 278
 Db 790 GAGACCAAGGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 849

QY 279 HisLysLysAsnValGlyThrArgLysLeuAspMetSerArgValIlePheTyrSerAla 298
 Db 850 CACATCTACCAATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 909

QY 299 GlnIleAlaCysGlyMetLeuHisLeuHisGlnLeuGlyIleValTyrTrpAspMetLys 318
 Db 910 GAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 969

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 Db 1264 TTTTCCCGAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1323

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 Db 1324 CTGGGGTGTGTGGGCGAGTGCCTGCGAGGTGAAGAGACCCCTCTTAAGAGACTG 1383

QY 458 AsnPheProArgLeuGluAlaGlyLeuIleGluProPheValProAspProSerVal 477
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 Db 1444 ATTATCGCAAGAGTGTGCGACATTGAAACAGTTCCTGAGGTCAAGGCGTGGAGCTG 1503

QY 498 AspAspLysAspLysGlnPheLysAsnPheAlaThrGlyAlaValProIleAlaTrp 517
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QY 518 GlnGluGluIleIleGluThrGlyLeuPheGluGluLeuAsn 531
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Search completed: August 13, 2004, 21:12:55
 Job time : 149 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 14:01:20 ; Search time 692.966 Seconds

(without alignments)
15563.146 Million cell updates/sec

Title: US-10-044-205A-1

Perfect score: 2198

Sequence: 1 gaccttaagatgaaggacc.....aacccaggtttatttga 2198

Scoring table:

IDENTITY NUC

Searched:

3225727 seqs, 245303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2008.8	91.4	2249	15 US-10-217-745-5
3	1659	75.5	1659	14 US-10-044-205A-3
4	1658.8	75.5	1662	17 US-10-311-034-45
5	1658.8	75.5	1662	17 US-10-451-168-49
6	1658.4	75.5	1662	15 US-10-217-745-1
7	1657.2	75.4	1662	15 US-09-964-469-1
8	1657.2	75.4	1662	15 US-10-425-962-1
9	1640.8	74.6	1701	13 US-10-072-012-273
10	1046.8	47.6	1062	15 US-10-217-745-3
11	867.4	39.5	36651	9 US-09-964-469-3
12	867.4	39.5	36651	15 US-10-425-962-3
13	418.2	19.0	2848	9 US-09-851-686-2
14	418.2	19.0	2848	10 US-09-873-367C-142

15	418.2	19.0	2848	16 US-10-159-856-4	Sequence 4, Appli
16	401.6	18.3	2817	15 US-10-388-934-621	Sequence 621, App
17	379.4	17.3	2467	15 US-10-084-817-110	Sequence 110, App
18	377.8	17.2	2519	14 US-10-071-766-13	Sequence 13, Appl
19	374.6	17.0	2519	10 US-09-971-392-72	Sequence 72, Appl
20	373	17.0	2511	15 US-10-072-036-60	Sequence 60, Appl
21	373	17.0	2529	15 US-10-072-036-42	Sequence 42, Appl
22	373	17.0	2557	9 US-09-972-694-1	Sequence 7, Appli
23	373	17.0	2557	12 US-10-380-235-7	Sequence 1, Appli
24	373	17.0	2557	16 US-10-305-720-1298	Sequence 1298, Ap
25	368.2	16.8	2557	9 US-09-851-686-1	Sequence 1, Appli
26	320.6	14.6	1737	15 US-10-325-430-2	Sequence 2, Appli
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28	158.4	7.2	493	10 US-09-918-995-37835	Sequence 37835, A
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30	151	6.9	1679	9 US-09-771-161A-25	Sequence 25, Appl
31	151	6.9	2037	13 US-10-087-684-23	Sequence 23, Appl
32	151	6.9	2037	13 US-10-218-779-23	Sequence 47, Appl
33	151	6.9	2070	15 US-10-038-010-47	Sequence 11, Appl
34	151	6.9	3073	13 US-10-029-020-11	Sequence 3, Appli
35	151	6.9	3268	15 US-10-247-671-3	Sequence 482, App
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37	132.8	6.0	2909	12 US-10-152-319A-1465	Sequence 1539, Ap
38	132.4	6.0	2683	12 US-10-152-319A-1539	Sequence 47, Appl
39	132.4	6.0	2683	16 US-10-191-803-38	Sequence 1306, Ap
40	130.8	6.0	2067	16 US-10-305-720-1306	Sequence 38, Appl
41	129.2	5.9	1411	10 US-09-955-999-14	Sequence 14, Appl
42	129.2	5.9	2067	15 US-10-038-010-49	Sequence 49, Appl
43	127.6	5.8	2362	15 US-10-037-270-273	Sequence 273, App
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45	112.4	5.1	1661	13 US-10-087-192-989	Sequence 989, App

ALIGNMENTS

RESULT 1

US-10-044-205A-1

Sequence 1, Application US/10044205A

Publication No. US20020123464A1

GENERAL INFORMATION:

APPLICANT: KAPLELLER, LIBERMAN, ROSA

APPLICANT: BANDARU, RAJASEKHAR

TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Protein

TITLE OF INVENTION: Uses thereof

FILE REFERENCE: 10147-5201

CURRENT APPLICATION NUMBER: US/10/044,205A

CURRENT FILING DATE: 2002-04-19

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: US 60/241,884

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: US 60/241,877

PRIOR FILING DATE: 2000-10-20

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 2198

TYPE: DNA

ORGANISM: Homo sapiens

US-10-044-205A-1

Query Match 100.0%; Score 2198; DB 14; Length 2198;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	1975	CACACAGAGTCCGCGTGAACATATTCCTCAAGATTTCCACGTTGGAATCTGTGAATG	20344

Db 1501 GATAGACGTTCTTCAAAAACCTTGGCAGAGGTCGTCTTCTTACGATGGAGAGAA 1560
 Qy 1851 ATTAGAAGCGGAGCTGTTGAGAGCTGATGACCCCAAGACCTTACGGGTTGTAG 1910
 Db 1561 ATTATGAAAGCGGAGCTGTTGAGAGCTGATGACCCCAAGACCTTACGGGTTGTAG 1620
 Qy 1911 GAGGTAATTCATCCAGCTGCGGTGTTGTTATG 1949
 Db 1621 GAGGTAATTCATCCAGCTGCGGTGTTGTTATG 1659

RESULT 4
 US-10-311-034-45

/ Sequence 45, Application US/10311034
 / Publication No. US20040023242A1
 / GENERAL INFORMATION:

/ APPLICANT: INCYTE GENOMICS, INC.
 / APPLICANT: YUE, Henry
 / APPLICANT: LAL, Preeti
 / APPLICANT: BANDMAN, Olga
 / APPLICANT: BOROMSKI, Mark L.
 / APPLICANT: AU-YOUNG, Janice
 / APPLICANT: LU, Yan
 / APPLICANT: GANDHI, Ameena R.
 / APPLICANT: TRIBOULEY, Catherine M.
 / APPLICANT: CHAWLA, Narinder K.
 / APPLICANT: VAO, Monique G.
 / APPLICANT: LU, Dying Alina M.
 / APPLICANT: GREENWALD, Sara R.
 / APPLICANT: RAMKOMAR, Jayalaxmi
 / APPLICANT: GRIFPIN, Jennifer A.
 / APPLICANT: KEARNEY, Liam
 / APPLICANT: BURFORD, Neil
 / APPLICANT: NGUYEN, Daniel B.
 / APPLICANT: TANG, Y. Tom
 / APPLICANT: BAUGHN, Mariah R.
 / APPLICANT: HE, Ann
 / APPLICANT: THORNTON, Michael
 / APPLICANT: HARELITA, April
 / APPLICANT: ARVIZU, Chandra S.
 / APPLICANT: GURURAJAN, Rajagopal
 / APPLICANT: LO, Terence P.
 / APPLICANT: KHAH, Farrah A.
 / APPLICANT: RECTOR, Shirley A.
 / APPLICANT: AZIMZAI, Yalda
 / APPLICANT: POLICKI, Jennifer L.
 / APPLICANT: DING, Li
 / APPLICANT: GREYER, Megan
 / APPLICANT: ELLIOTT, Vicki S.
 / APPLICANT: THANGANEU, Kavitha
 / APPLICANT: ISON, Craig H.
 / TITLE OF INVENTION: HUMAN KINASES
 / FILE REFERENCE: PI-0125 PCT
 / CURRENT APPLICATION NUMBER: US/10/311,034
 / PRIOR FILING DATE: 2002-12-10
 / PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
 / 60/228,056
 / PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-07-25
 / NUMBER OF SEQ ID NOS: 52
 / SOFTWARE: PERL Program
 / SEQ ID NO 45
 / LENGTH: 1662
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: misc feature
 / OTHER INFORMATION: Incyte ID No. US20040023242A1 7477204CB1
 US-10-311-034-45

Query Match

75.5%; Score 1658.8; DB 17; Length 1662;

Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 291 ATGTGTGACATGGGGGCTTGGACCACTGATGTCACACCGCTTACCTGAGGCCCG 350
 Db 1 ATGTGTGACATGGGGGCTTGGACCACTGATGTCACACCGCTTACCTGAGGCCCG 60
 Qy 351 AAGCCCTGACATGGACAGCAAGAGCTGACAGCGCGCGCGCTTACCTGAGGCCCG 410
 Db 61 AAGCCCTGACATGGACAGCAAGAGCTGACAGCGCGCGCGCTTACCTGAGGCCCG 120
 Qy 411 GGGCTGACAGGGCTGCGCGAGCTCGCCAGAACTGTCCCTGAACTTTCACAGCCGTGT 470
 Db 121 GGGCTGACAGGGCTGCGCGAGCTCGCCAGAACTGTCCCTGAACTTTCACAGCCGTGT 180
 Qy 471 GAGCAGACGCCCTTGGTGGCGCTTTCCTGATCTTCTTACGACAGTGGCCAGTTTC 530
 Db 181 GAGCAGACGCCCTTGGTGGCGCTTTCCTGATCTTCTTACGACAGTGGCCAGTTTC 240
 Qy 531 CGCAAGGCGGCACTTCTTACGACAGTGGCAACTGGAGCTGGCCGAGAGGAGCC 590
 Db 241 CGCAAGGCGGCACTTCTTACGACAGTGGCAACTGGAGCTGGCCGAGAGGAGCC 300
 Qy 591 ACCAAAGACAGCGCGCTGAGGGCTGTGGCCACTTGTGAGAGTGGCCCTGCGCGCG 650
 Db 301 ACCAAAGACAGCGCGCTGAGGGCTGTGGCCACTTGTGAGAGTGGCCCTGCGCGCG 360
 Qy 651 AACCCGCAACCTTCTTCTGACAGCGCGCTGTGGCCAGCAAGTGGCCAGCACTGAG 710
 Db 361 AACCCGCAACCTTCTTCTGACAGCGCGCTGTGGCCAGCAAGTGGCCAGCACTGAG 420
 Qy 711 GAGAGGAGGTGGCTGAGTGGAGTGGCCAGAGTGGAGTGGCTTCTTGGAAAG 770
 Db 421 GAGAGGAGGTGGCTGAGTGGAGTGGCCAGAGTGGAGTGGCTTCTTGGAAAG 480
 Qy 771 CAGCCCTTAAAGATTTGTGACACAGCGCTTCTTACGCAAGTGTGGAGTGGAAATC 830
 Db 481 CAGCCCTTAAAGATTTGTGACACAGCGCTTCTTACGCAAGTGTGGAGTGGAAATC 540
 Qy 831 TTGAGATGCAACAGTGTGACAGCAAGTGTGACAGTGTGAGTGGAGTGGAAAGT 890
 Db 541 TTGAGATGCAACAGTGTGACAGCAAGTGTGACAGTGTGAGTGGAGTGGAAAGT 600
 Qy 891 GATTGGGAGGATGTGCGGTGACAGTGGAAACACTGGAAATGTATGCTGTAG 950
 Db 601 GATTGGGAGGATGTGCGGTGACAGTGGAAACACTGGAAATGTATGCTGTAG 660
 Qy 951 AAACCTGACAGAGCGCTGAGAGAAAGTGGAGAGTGGCTGTGGAAAG 1010
 Db 661 AAACCTGACAGAGCGCTGAGAGAAAGTGGAGAGTGGCTGTGGAAAG 720
 Qy 1011 GAAATCTTGGAGAGTGTGACAGCCCTTCAATGTCTCTGTGGCTATGCTTGGAGAC 1070
 Db 721 GAAATCTTGGAGAGTGTGACAGCCCTTCAATGTCTCTGTGGCTATGCTTGGAGAC 780
 Qy 1071 AAGACCATCTGCTGTGTGATGAGCTGATGAAATGGGGAGACTTAACTTGCATC 1130
 Db 781 AAGACCATCTGCTGTGTGATGAGCTGATGAAATGGGGAGACTTAACTTGCATC 840
 Qy 1131 TACAGGTGGAGCAGCGCTGAGACATGAGCGGGTGAATTTTACTGGGCGAGATA 1190
 Db 841 TACAGGTGGAGCAGCGCTGAGACATGAGCGGGTGAATTTTACTGGGCGAGATA 900
 Qy 1191 GCGTGGAGAGTGTGACCTCATTAATGCGGATGCTGTATGAGAGATGAGAGCTGAG 1250
 Db 901 GCGTGGAGAGTGTGACCTCATTAATGCGGATGCTGTATGAGAGATGAGAGCTGAG 960
 Qy 1251 AATGTCTTGTGATGACCTGAGCACTGAGAGTGTATCTGACTTGGGCTGGCGTGAAG 1310
 Db 961 AATGTCTTGTGATGACCTGAGCACTGAGAGTGTATCTGACTTGGGCTGGCGTGAAG 1020
 Qy 1311 ATGAAGGCTGGCAAGCCATCAAGAGGCTGAAACCAATGATGTATGATGCTGAG 1370


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Db      901  GCGTGGGATGCTGCACTTCATGAACTCGGCACTGATGGGACATGAACTGGAG 960
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Db      961  AATGTCCTTCTGGAAGACCTTCGCACTCGAGTTATCTGACCTGCGGCTGCGCTGAG 1020
Qy      1311  ATGAAGGCTGGCAAGCCCATCCAGAGAGGCTGGAACCAATGTTATCATGCTCTGAG 1370
Db      1021  ATGAAGGCTGGCAAGCCCATCCAGAGAGGCTGGAACCAATGTTATCATGCTCTGAG 1080
Qy      1371  ATCCATATGAAAAGTTAGTTATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1430
Db      1081  ATCCATATGAAAAGTTAGTTATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1140
Qy      1431  ATTTATGAATGTTGCTGCAAGACCACTTCAAGATTACAGAAAAGTCACTAA 1490
Db      1141  ATTTATGAATGTTGCTGCAAGACCACTTCAAGATTACAGAAAAGTCACTAA 1200
Qy      1491  GAGATCTGAAGCAAAAGACCTGCAAGAGGCTCAATTCAGCATGATTAATCTACA 1550
Db      1201  GAGATCTGAAGCAAAAGACCTGCAAGAGGCTCAATTCAGCATGATTAATCTACA 1260
Qy      1551  GAGAAAGCAAAAGATATTGCAAGGCTCTTCTGCTAGAAACAGAGCAAGCTTAGA 1610
Db      1261  GAGAAAGCAAAAGATATTGCAAGGCTCTTCTGCTAGAAACAGAGCAAGCTTAGA 1320
Qy      1611  AGAGAGAAAGTCTGATGATCCAGAAACATCATTTCTTAAACAGATCACTTCTCT 1670
Db      1321  AGAGAGAAAGTCTGATGATCCAGAAACATCATTTCTTAAACAGATCACTTCTCT 1380
Qy      1671  CCGCTGAAGCTGGCCCAATTAAGACCCCACTTGGCAAGCCCTTATGCTTATGCC 1730
Db      1381  CCGCTGAAGCTGGCCCAATTAAGACCCCACTTGGCAAGCCCTTATGCTTATGCC 1440
Qy      1731  AAAAGCATCGCTGAAATGATGATTTCTGAGGTTGCGGAGGCTGGAATTTAGCA 1790
Db      1441  AAAAGCATCGCTGAAATGATGATTTCTGAGGTTGCGGAGGCTGGAATTTAGCA 1500
Qy      1791  GATTAAGCATCTTCTGAAAACTTTGCAAGGCTGCTGCTTCTATAGATGAGAGAA 1850
Db      1501  GATTAAGCATCTTCTGAAAACTTTGCAAGGCTGCTGCTTCTATAGATGAGAGAA 1560
Qy      1851  ATTATGAAGCGGGACTGTTGAGGAATGATGATGATGATGATGATGATGATGATG 1910
Db      1561  ATTATGAAGCGGGACTGTTGAGGAATGATGATGATGATGATGATGATGATGATG 1620
Qy      1911  GAGGTAATTCATCCAAAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1952
Db      1621  GAGGTAATTCATCCAAAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1662

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; ORGANISM: homo sapiens
US-10-217-745-1
Query Match      75.5%; Score 1658.4; DB 15; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1659; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      291  ATGTGACATGAGGAGGCTGGAACATCTGATTCGCAACATCCGCTTACTGAGGCTGG 350
Db      1  ATGTGACATGAGGAGGCTGGAACATCTGATTCGCAACATCCGCTTACTGAGGCTGG 60
Qy      351  AAGCCTTGAGCTGAGCAAGCAAGAGCTGCAAGGCTGAGGCTGAGGCTGAGGCTG 410
Db      61  AAGCCTTGAGCTGAGCAAGCAAGAGCTGCAAGGCTGAGGCTGAGGCTGAGGCTG 120
Qy      411  GGGCTGAGAGGCTGCGCGAGAGCTCCGCAAGAGCTGCTGCAATCTTCAAGCTGCT 470
Db      121  GGGCTGAGAGGCTGCGCGAGAGCTCCGCAAGAGCTGCTGCAATCTTCAAGCTGCT 180
Qy      471  GAGCAGAGCCATGAGTGGCGGCTCTTCTGATCTTCTGATCTTCTGATCTTCTGAT 530
Db      181  GAGCAGAGCCATGAGTGGCGGCTCTTCTGATCTTCTGATCTTCTGATCTTCTGAT 240
Qy      531  CGAAGGCGGCAACCTTCTGAGAGAGCTGCAAGAGCTGAGGCTGAGGAGGAGGCC 590
Db      241  CGAAGGCGGCAACCTTCTGAGAGAGCTGCAAGAGCTGAGGAGGAGGAGGCC 300
Qy      591  ACCAAGACAGGCGCTGCAAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 650
Db      301  ACCAAGACAGGCGCTGCAAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 360
Qy      651  AACCCGCAACCTTCTGAGAGAGCTGCAAGGCTGAGGCTGAGGCTGAGGCTGAGG 710
Db      361  AACCCGCAACCTTCTGAGAGAGCTGCAAGGCTGAGGCTGAGGCTGAGGCTGAGG 420
Qy      711  GAAAGCAGAGTGGCTGAGAGAGCTGCAAGGCTGAGGCTGAGGCTGAGGCTGAGG 770
Db      421  GAAAGCAGAGTGGCTGAGAGAGCTGCAAGGCTGAGGCTGAGGCTGAGGCTGAGG 480
Qy      771  CAGCCTTTAAGATTTGAGACAGGCTTCTGACAGAGCTTCTGACAGAGCTTCTGAC 830
Db      481  CAGCCTTTAAGATTTGAGACAGGCTTCTGACAGAGCTTCTGACAGAGCTTCTGAC 540
Qy      831  TTGAGATGCAACAGTGTGAGCAAGATCTTCACTGATCTGATCTGATCTGATCTG 890
Db      541  TTGAGATGCAACAGTGTGAGCAAGATCTTCACTGATCTGATCTGATCTGATCTG 600
Qy      891  GGTGTTGGAGAGTATGCTGCTGCAAGGCTGAAAAACATGAGGAGATGATGCTGTA 950
Db      601  GGTGTTGGAGAGTATGCTGCTGCAAGGCTGAAAAACATGAGGAGATGATGCTGTA 660
Qy      951  AATCTGCAAGAGAGGCTGAAAGAAAGAGTGGGAGAGATGCTCTTCTGGAAG 1010
Db      661  AATCTGCAAGAGAGGCTGAAAGAAAGAGTGGGAGAGATGCTCTTCTGGAAG 720
Qy      1011  GAAATCTGAGAGAGTCAAGGCTTCTGATGCTGATGCTGATGCTGATGCTGATG 1070
Db      721  GAAATCTGAGAGAGTCAAGGCTTCTGATGCTGATGCTGATGCTGATGCTGATG 780
Qy      1071  AAGACCATCTTCTGCTTCTGATGAGCTGATGATGATGATGATGATGATGATGATG 1130
Db      781  AAGACCATCTTCTGCTTCTGATGAGCTGATGATGATGATGATGATGATGATGATG 840
Qy      1131  TAAACGTTGAGAGGCTGAGGCTGCAATGAGCGGAGTATCTTCTGAGCCAGATA 1190
Db      841  TAAACGTTGAGAGGCTGAGGCTGCAATGAGCGGAGTATCTTCTGAGCCAGATA 900
Qy      1191  GCGTGGAGTGTGCACTGCACTGCAATGAGCTGAGTGTGAGTGTGAGTGTGAGT 1250
Db      901  GCGTGGAGTGTGCACTGCACTGCAATGAGCTGAGTGTGAGTGTGAGTGTGAGT 960
Qy      1251  AATGCTCTTCTGATGACTGCGCACTGAGGTTATCTGACCTGAGGCTGAGGCTGAG 1310

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Db 961 AATGCTCTGTGATGACCTTGGCACTCAGGTTATCTGACTGGGGCTGGCCGTGGAG 1020
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 Db 1021 ATGAAGGGTGGCAAGCCCATCACCAGAGGGCTGGAAACAATGGTTACATGGCTTGGAG 1080
 QY 1371 ATCTTAATGAAAAAGTAATTTCTTATCTCTGAGCTGCTTGGCAATGGAGTGAAGC 1430
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 QY 1731 AAAGCATCGCTGAATATGATATTTCTGAGAGTTGGGGGGTGGAAATTTGATGACAA 1790
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 QY 1851 ATTATGAAACGGGAGCTGTTTGAAGAGTGAATGACCCCAACAGACTTACGGTGTGAG 1910
 Db 1561 ATTATGAAACGGGAGCTGTTTGAAGAGTGAATGACCCCAACAGACTTACGGTGTGAG 1620
 QY 1911 GAGGTAATTCATCAAGTGTGAGCTGTTGTTTATGTAA 1952
 Db 1621 GAGGTAATTCATCAAGTGTGAGCTGTTGTTTATGTAA 1662
 RESULT 7
 US-09-964-469-1
 ; Sequence 1, Application US/09964469
 ; Patent No. US20020034803A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GUGLER, Karl et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: CLO000636D1V
 ; CURRENT APPLICATION NUMBER: US/09/964,469
 ; PRIOR FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: 60/208,331
 ; PRIOR FILING DATE: 2000-06-01
 ; PRIOR APPLICATION NUMBER: 09/738,894
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO: 1
 ; LENGTH: 1662
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-964-469-1
 Query Match 75.4%; Score 1657.2; DB 9; Length 1662;
 Best Local Similarity 99.8%; Pred. No. 0;

Matches 1659; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 291 ATGTGGAAGATGGGGGCGCTGAGCAACCTGATGCGCAACACCGCTTACCTGAGCGCCG 350
 Db 1 ATGTGGAAGATGGGGGCGCTGAGCAACCTGATGCGCAACACCGCTTACCTGAGCGCCG 60
 QY 351 AAGCCCTGGAAGTGCAGCAGCAAGAAAGCTGAGCGCGCGCTGAGCGCTGAGCGCCG 410
 Db 61 AAGCCCTGGAAGTGCAGCAGCAAGAAAGCTGAGCGCGCGCTGAGCGCTGAGCGCCG 120
 QY 411 GGGCTGCAAGGCTGCGGAGAGCTCCGCGCAAGAGTGTCTTGAATTCACAGCTGTGT 470
 Db 121 GGGCTGCAAGGCTGCGGAGAGCTCCGCGCAAGAGTGTCTTGAATTCACAGCTGTGT 180
 QY 471 GAGCAGAGCCCATCGGTGCGCGCTCTTCCGTGATCTTCTTGAAGCAAGTGCACGTTG 530
 Db 181 GAGCAGAGCCCATCGGTGCGCGCTCTTCCGTGATCTTCTTGAAGCAAGTGCACGTTG 240
 QY 531 CGCAAGCGCGCAACCTTCTTAAGAGAGCTGCAAACTGGAGCTGGCTGAGAGAGAGCC 590
 Db 241 CGCAAGCGCGCAACCTTCTTAAGAGAGCTGCAAACTGGAGCTGGCTGAGAGAGAGCC 300
 QY 591 ACCAAGAGACAGCGCTGCAAGGCGCTGAGCGCTGAGCGCTGAGCGCTGAGCGCG 650
 Db 301 ACCAAGAGACAGCGCTGCAAGGCGCTGAGCGCTGAGCGCTGAGCGCTGAGCGCG 360
 QY 651 AACCGGCAACCCCTTCTCAGCCAGCGCGCTGAGCGCTGAGCGCTGAGCGCGCTGAG 710
 Db 361 AACCGGCAACCCCTTCTCAGCCAGCGCGCTGAGCGCTGAGCGCTGAGCGCGCTGAG 420
 QY 711 GAAAGCAGTGGCTGAGTGAAGCTGCGCAAGGCTGAGCGCTTCTTTCAGAGAG 770
 Db 421 GAAAGCAGTGGCTGAGTGAAGCTGCGCAAGGCTGAGCGCTTCTTTCAGAGAG 480
 QY 771 CAGCCCTTAAAGATTTGCGAGCAAGCGCTTCTTAAAGATTTGCGAGTGAATCT 830
 Db 481 CAGCCCTTAAAGATTTGCGAGCAAGCGCTTCTTAAAGATTTGCGAGTGAATCT 540
 QY 831 TTGAGATGCAACAGTGTGAGCAAGAGTCTTCACTGATGTTGAGAGTGTGAGAGAGT 890
 Db 541 TTGAGATGCAACAGTGTGAGCAAGAGTCTTCACTGATGTTGAGAGTGTGAGAGAGT 600
 QY 891 GATTTTGGGAGGTATGTCGCTGAGTGAAGAAACCTGAGAAATGTATGCTGTAG 950
 Db 601 GATTTTGGGAGGTATGTCGCTGAGTGAAGAAACCTGAGAAATGTATGCTGTAG 660
 QY 951 AAACCTGAGCAAGAGCGCTGAGAAAGAGTGGCGAGAGATGCTCTTGGAGAAAG 1010
 Db 661 AAACCTGAGCAAGAGCGCTGAGAAAGAGTGGCGAGAGATGCTCTTGGAGAAAG 720
 QY 1011 GAATCTTGAAGAGGTGAGCAGCGCTTCACTTGTCTCTGAGCTATGCTTGAAGC 1070
 Db 721 GAATCTTGAAGAGGTGAGCAGCGCTTCACTTGTCTCTGAGCTATGCTTGAAGC 780
 QY 1071 AAGACCATCTTCTGCTTGTGATGAGCTGATGATGAGGAGAGCTCAAGTTCACATC 1130
 Db 781 AAGACCATCTTCTGCTTGTGATGAGCTGATGATGAGGAGAGCTCAAGTTCACATC 840
 QY 1131 TACAACTGGGAGCGGAGCGCTGAGCATGAGCGGAGTATCTTTACTGCGCCAGATA 1190
 Db 841 TACAACTGGGAGCGGAGCGCTGAGCATGAGCGGAGTATCTTTACTGCGCCAGATA 900
 QY 1191 GCGTGTGAGAGTGTGAGCACTTCAAGAACTGGAGTGTATGCGGAGCATGAAGCTTGA 1250
 Db 901 GCGTGTGAGAGTGTGAGCACTTCAAGAACTGGAGTGTATGCGGAGCATGAAGCTTGA 960
 QY 1251 AATGCTTCTGATGATCTGCGCAACTGCAAGGTTATCTGAGCTGGGGCTGGCCGTGAG 1310
 Db 961 AATGCTTCTGATGATCTGCGCAACTGCAAGGTTATCTGAGCTGGGGCTGGCCGTGAG 1020
 QY 1311 ATGAAGGGTGGCAAGCCCATCACCAGAGGGCTGGAACCAATGTTACATGCTCTGAG 1370
 Db 1021 ATGAAGGGTGGCAAGCCCATCACCAGAGGGCTGGAACCAATGTTACATGCTCTGAG 1080

QY 1371 ATCTATGAGAAAGGATGATATCTATCTGATGAGCTGTTGGCAATGGATGACG 1430
DB 1081 ATCTATGAGAAAGGATGATATCTATCTGATGAGCTGTTGGCAATGGATGACG 1140
QY 1431 ATTATGAAATGGTTGCTGAGACGACACCATTCAGAAATTCAGAAAGGATGACG 1490
DB 1141 ATTATGAAATGGTTGCTGAGACGACACCATTCAGAAATTCAGAAAGGATGACG 1200
QY 1491 GAGGATCTGAGCAAGAACTCTGCAAGACGAGGTCATTCAGATGATTAAGTTCAC 1550
DB 1201 GAGGATCTGAGCAAGAACTCTGCAAGACGAGGTCATTCAGATGATTAAGTTCAC 1260
QY 1551 GAGGATCTGAGCAAGAACTCTGCAAGACGAGGTCATTCAGATGATTAAGTTCAC 1610
DB 1261 GAGGATCTGAGCAAGAACTCTGCAAGACGAGGTCATTCAGATGATTAAGTTCAC 1320
QY 1611 AGCAGAGAAAGTCTGATGATCCAGAAACATCATTCCTTAAAGCATCACTTCT 1670
DB 1321 AGCAGAGAAAGTCTGATGATCCAGAAACATCATTCCTTAAAGCATCACTTCT 1380
QY 1671 CGCTGGAAGCTGCTGATTAATGAACCCCATTTGTCAGACCTTCAGTGTATGCG 1730
DB 1381 CGCTGGAAGCTGCTGATTAATGAACCCCATTTGTCAGACCTTCAGTGTATGCG 1440
QY 1731 AAAGCATGCTGATTAATGAATTCCTGATGATTCGAGGCTGAGATTTGATGAAA 1790
DB 1441 AAAGCATGCTGATTAATGAATTCCTGATGATTCGAGGCTGAGATTTGATGAAA 1500
QY 1791 GATAGCATGCTTCAAAAACCTTTGCAAGCTGCTGCTGATGATGAGCAAGAA 1850
DB 1501 GATAGCATGCTTCAAAAACCTTTGCAAGCTGCTGCTGATGATGAGCAAGAA 1560
QY 1851 ATTATGAAAGGAGCTGTTGAGCAATGATGATGATGATGATGATGATGATGAT 1910
DB 1561 ATTATGAAAGGAGCTGTTGAGCAATGATGATGATGATGATGATGATGATGAT 1620
QY 1911 GAGGATTAATTCATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1952
DB 1621 GAGGATTAATTCATCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1662

RESULT 8

US-10-425-962-1
; Sequence 1, Application US/10425962
; Publication No. US20030180786A1
; GENERAL INFORMATION:
; APPLICANT: GIBBS, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C000636D1Y2
; CURRENT APPLICATION NUMBER: US/10/425,962
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 09/964,469
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-425-962-1

Query Match 75.4%; Score 1657.2; DB 15; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1659; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 291 ATGTGACATGAGGAGCCCTGAGCAACCTGATCGCCAAACGCGCTCACTGAGGCCCG 350

DB 1 ATGTGACATGAGGAGCCCTGAGCAACCTGATCGCCAAACGCGCTCACTGAGGCCCG 60
QY 351 AAGCCCTGAGATGCTGCAACGCAAGAGCTGCAAGGAGCTGAGGAGCTGAGGAGGAG 410
DB 61 AAGCCCTGAGATGCTGCAACGCAAGAGCTGCAAGGAGCTGAGGAGCTGAGGAGGAG 120
QY 411 GAGGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGGAG 470
DB 121 GAGGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGGAG 180
QY 471 GAGGAGGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGGAG 530
DB 181 GAGGAGGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGGAG 240
QY 531 GAGGAGGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGGAG 590
DB 241 GAGGAGGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGGAG 300
QY 591 ACCAAGAGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGGAG 650
DB 301 ACCAAGAGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGGAG 360
QY 651 AACCCGCAACCTTCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGGAG 710
DB 361 AACCCGCAACCTTCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGGAG 420
QY 711 GAGGAGGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGGAG 770
DB 421 GAGGAGGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGGAG 480
QY 771 GAGGAGGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGGAG 830
DB 481 GAGGAGGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGGAG 540
QY 831 TTGAGATGCAACGAGTGTGAGCAAGTACTTCACTGATGATGATGATGATGATGAT 890
DB 541 TTGAGATGCAACGAGTGTGAGCAAGTACTTCACTGATGATGATGATGATGATGAT 600
QY 891 GGTGTTGGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 950
DB 601 GGTGTTGGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 951 AAACCTGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1010
DB 661 AAACCTGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 1011 GAAATCTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1070
DB 721 GAAATCTTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 1071 AAGACCTATCT 1130
DB 781 AAGACCTATCT 840
QY 1131 TACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1190
DB 841 TACAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
QY 1191 GCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1250
DB 901 GCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
QY 1251 AATGCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1310
DB 961 AATGCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1311 ATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1370
DB 1021 ATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
QY 1371 ATCTAATGAGAAAGGATTAATCTATCTGATGATGATGATGATGATGATGATGAT 1430

Db 1081 ATCTATATGGAAGTAAGTATTCCTATCTCTGACCTGTTTCCATGAGTACGAGC 1140
 QY 1431 ATTATGAAATGTTGCTGACGACAAACATTCAGAAAGTATTAAGGAAAGGTCATGAAA 1490
 Db 1141 ATTATGAAATGTTGCTGACGACAAACATTCAGAAAGTATTAAGGAAAGGTCATGAAA 1200
 QY 1491 GAGGATCTGAAGCAAAAGCTCTGCAAGACGAGTCAAAATTCAGACATGATTAACCTGACA 1550
 Db 1201 GAGGATCTGAAGCAAAAGCTCTGCAAGACGAGTCAAAATTCAGACATGATTAACCTGACA 1260
 QY 1551 GAGGATCTGAAGCAAAAGCTCTGCAAGACGAGTCAAAATTCAGACATGATTAACCTGACA 1610
 Db 1261 GAGGATCTGAAGCAAAAGCTCTGCAAGACGAGTCAAAATTCAGACATGATTAACCTGACA 1320
 QY 1611 AGCAGAGAAAAGCTCTGATGATCCAGAGAAACATCATTTCTTTAAAGATCACTTTCTCT 1670
 Db 1321 AGCAGAGAAAAGCTCTGATGATCCAGAGAAACATCATTTCTTTAAAGATCACTTTCTCT 1380
 QY 1671 GCGCTGAGAGCTGCTTAATTTGAACCCCTTTTGGCCAGACGCTTCAAGTGTATGACC 1730
 Db 1381 GCGCTGAGAGCTGCTTAATTTGAACCCCTTTTGGCCAGACGCTTCAAGTGTATGACC 1440
 QY 1731 AAGGACATGCTGATTAATGATGATTTCTGAGGTTGCGGCGGTGGAATTTGATGACAAA 1790
 Db 1441 AAGGACATGCTGATTAATGATGATTTCTGAGGTTGCGGCGGTGGAATTTGATGACAAA 1500
 QY 1791 GATAAGCAGTCTTCAAAAACCTTTGCGACAGGTGCTTTCTTATGATGCGACAGGAAAGAA 1850
 Db 1501 GATAAGCAGTCTTCAAAAACCTTTGCGACAGGTGCTTTCTTATGATGCGACAGGAAAGAA 1560
 QY 1851 ATTATAGAAAGGAGACTGTTTGAAGAACTGAAAGACCCCAAGACCTCAAGGTTGTGAG 1910
 Db 1561 ATTATAGAAAGGAGACTGTTTGAAGAACTGAAAGACCCCAAGACCTCAAGGTTGTGAG 1620
 QY 1911 GAGGATATTCATCAAGTCTGCGTGTGTTTGTATTTGTA 1952
 Db 1621 GAGGATATTCATCAAGTCTGCGTGTGTTTGTATTTGTA 1662

RESULT 9
 US-10-072-012-273
 ; Sequence 273, Application US/10072012
 ; Publication No. US2004003493A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tchehnev, Velizar
 ; APPLICANT: Spylek, Kimberly
 ; APPLICANT: Zerhusen, Bryan
 ; APPLICANT: Patlurajan, Meera
 ; APPLICANT: Shimkele, Richard
 ; APPLICANT: Li, Li
 ; APPLICANT: Gangoli, Esha
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Miller, Charles E.
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Taupier Jr, Raymond J.
 ; APPLICANT: Gusev, Vladimir Y.
 ; APPLICANT: Coleman, Steven D.
 ; APPLICANT: Wolenc, Adam R.
 ; APPLICANT: Pena, Carol E. A
 ; APPLICANT: Furtak, Katarzyna
 ; APPLICANT: Grose, William M.
 ; APPLICANT: Alsbrook II, John P.
 ; APPLICANT: Lepley, Denise M.
 ; APPLICANT: Rieger, Daniel K.
 ; APPLICANT: Burgess, Catherine E.
 ; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-258
 ; CURRENT APPLICATION NUMBER: US/10/072.012
 ; PRIORITY FILING DATE: 2002-01-31
 ; PRIORITY APPLICATION NUMBER: 60/265,102
 ; PRIORITY FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: 60/265,514
 ; PRIOR FILING DATE: 2001-01-31
 ; PRIOR APPLICATION NUMBER: 60/265,517
 ; PRIOR FILING DATE: 2001-01-31
 ; PRIOR APPLICATION NUMBER: 60/265,412
 ; PRIOR FILING DATE: 2001-01-31
 ; PRIOR APPLICATION NUMBER: 60/265,395
 ; PRIOR FILING DATE: 2001-01-31
 ; PRIOR APPLICATION NUMBER: 60/266,406
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: 60/266,767
 ; PRIOR FILING DATE: 2001-02-05
 ; PRIOR APPLICATION NUMBER: 60/267,057
 ; PRIOR FILING DATE: 2001-02-07
 ; PRIOR APPLICATION NUMBER: 60/266,975
 ; PRIOR FILING DATE: 2001-02-07
 ; PRIOR APPLICATION NUMBER: 60/267,459
 ; PRIOR FILING DATE: 2001-02-08
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 1391
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 273
 ; LENGTH: 1701
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-072-012-273
 Query Match 74.6%; Score 1640.8; DB 13; Length 1701;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 1693; Conservative 0; Mismatches 2; Indels 21; Gaps 3;
 QY 273 TGCGCCCGGTGTCAGCCATGTTGATGATGAGGAGGCTTGTGACAACTGATGCGCAACCC 332
 Db 1 TGCGCCCGGTGTCAGCCATGTTGATGATGAGGAGGCTTGTGACAACTGATGCGCAACCC 60
 QY 333 GCTTACCTGAGGCGCGGAGGCGCTGCGACATGCGCAAGAGTGTGCGCGG 392
 Db 61 GCTTACCTGAGGCGCGGAGGCGCTTGTGACATGCGCAAGAGTGTGCGCGG 120
 QY 393 GGTAGCTGAGGCTGCGGAGGCTGCGGAGGCTGCGGAGGCTGCGGAGGCTGCGGAGGCTGCGG 452
 Db 121 GGTAGCTGAGGCTGCGGAGGCTGCGGAGGCTGCGGAGGCTGCGGAGGCTGCGGAGGCTGCGG 180
 QY 453 AACTTCACAGCTGTGTGAGCAGACCCATCGTGTGCGGCTTGTGAGTCTCTA 512
 Db 181 AACTTCACAGCTGTGTGAGCAGACCCATCGTGTGCGGCTTGTGAGTCTCTA 240
 QY 513 GCGACAGTGCACCTTCCGCAAGGCGGCAACCTTCTAGAGACGTGCAAGTGGAG 572
 Db 241 GCGACAGTGCACCTTCCGCAAGGCGGCAACCTTCTAGAGACGTGCAAGTGGAG 300
 QY 573 CTGCGCAGAGGAGGAGCCCAACCAAGACAGGCGCTGCAAGGCTGTGTGCGG 632
 Db 301 CTGCGCAGAGGAGGAGCCCAACCAAGACAGGCGCTGCAAGGCTGTGTGCGG 360
 QY 633 AGTGCCTTCCGCGGAGGAGCCCAACCTTCTAGAGACGTGCAAGTGGAG 692
 Db 361 AGTGCCTTCCGCGGAGGAGCCCAACCTTCTAGAGACGTGCAAGTGGAG 420
 QY 693 CAAAGACGACCACTGAGGAGAGAGGAGGCTGCAAGTGGAGGCTGCAAGTGGAG 752
 Db 421 CAAAGACGACCACTGAGGAGAGAGGAGGCTGCAAGTGGAGGCTGCAAGTGGAG 480
 QY 753 ATGGCTTCTTTCAGAGAGGAGGCTTTCAGAGTGTGACCAAGGCTTTCAGAGAG 812
 Db 481 ATGGCTTCTTTCAGAGAGGAGGCTTTCAGAGTGTGACCAAGGCTTTCAGAGAG 540
 QY 813 TTTCTGAGTGAAGTCTTTCAGAGTGAACAGTGTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAG 872
 Db 541 TTTCTGAGTGAAGTCTTTCAGAGTGAACAGTGTGCAAGTGAAGTGAAGTGAAGTGAAGTGAAG 600
 QY 873 AGAGGCTGAGGAGGAGTGTGAGGAGGAGTGTGAGGAGGAGTGTGAGGAGGAGTGTGAGGAGGAG 932

Db 601 AGAGTCTGGGAGAAAGTGTGTTTGGGAGGTA-----AAAAACACTGGG 645
 QY 933 AAGATGATGCTCTGTATAGAACTGACAAAGAGCGGCTGAAAGAAAGAGTGGGAGAG 992
 Db 646 AAGATGATGCTCTGTATAGAACTGACAAAGAGCGGCTGAAAGAAAGAGTGGGAGAG 705
 QY 993 ATGCTCTCTTGGAAAGAAATCTTGGAGAGTCAAGAGCCCTTCAATGTCCTG 1052
 Db 706 ATGCTCTCTTGGAAAGAAATCTTGGAGAGTCAAGAGCCCTTCAATGTCCTG 765
 QY 1053 GCTATGCTCTTGGAGAGAGAGCCATCTCTGCTCTGTCAAGCTGATGATGAGGGA 1112
 Db 766 GCTATGCTCTTGGAGAGAGAGCCATCTCTGCTCTGTCAAGCTGATGATGAGGGA 825
 QY 1113 GACCTCAATGCTCAATCTCAAGAGTGGGAGCGGCTGAGCATGAGCGGCTGATC 1172
 Db 826 GACCTCAATGCTCAATCTCAAGAGTGGGAGCGGCTGAGCATGAGCGGCTGATC 885
 QY 1173 TTTTACTGGCCGAGATAGCTGTGGAGTGTGACCTCTCATGAACTGGGCTGCTAT 1232
 Db 886 TTTTACTGGCCGAGATAGCTGTGGAGTGTGACCTCTCATGAACTGGGCTGCTAT 945
 QY 1233 CGGGAATGAGAGCTGAGATGTGCTTGTGATGACCTGGGCACTGAGGTTATCTGAC 1292
 Db 946 CGGGAATGAGAGCTGAGATGTGCTTGTGATGACCTGGGCACTGAGGTTATCTGAC 1005
 QY 1293 CTGGGAGTGGGCTGAGATGAAAGGTTGGAGCGCATACCCAGAG--GGCTGAGAC 1349
 Db 1006 CTGGGAGTGGGCTGAGATGAAAGGTTGGAGCGCATACCCAGAGCGGCTGAGAC 1065
 QY 1350 AATGCTTACATGCTCTCTGAGATCTTATGAGAAAGTAAATTCCTTCTGCTGAGAC 1409
 Db 1066 AATGCTTACATGCTCTCTGAGATCTTATGAGAAAGTAAATTCCTTCTGCTGAGAC 1125
 QY 1410 TGGTTTGCATGAGTATGACGCTTTATGAAATGTTGCTGAGAGCAACCATTTCAAGAT 1469
 Db 1126 TGGTTTGCATGAGTATGACGCTTTATGAAATGTTGCTGAGAGCAACCATTTCAAGAT 1185
 QY 1470 TACAGAGAAAGTCACTGAAAGAGATCTTAACAAAGATCTTGCAGAGAGTCAAA 1529
 Db 1186 TACAGAGAAAGTCACTGAAAGAGATCTTAACAAAGATCTTGCAGAGAGTCAAA 1245
 QY 1530 TTCCAGATGATTAATCTTCAAGAGAGCAAAAGATATTTGACAGGCTCTTGTGCTAAG 1589
 Db 1246 TTCCAGATGATTAATCTTCAAGAGAGCAAAAGATATTTGACAGGCTCTTGTGCTAAG 1305
 QY 1590 AACCCAGAGCAAGCTTGAAGAG--AGGAAAGTCTGATGATCCAGAGAAATCAT 1646
 Db 1306 AACCCAGAGCAAGCTTGAAGAGAGGAAAGTCTGATGATCCAGAGAAATCAT 1365
 QY 1647 TTCTTAAACGATCAACTTCTGCTGCTGAGAGCTGCTAATTGAACCCCATTTGTG 1706
 Db 1366 TTCTTAAACGATCAACTTCTGCTGCTGAGAGCTGCTAATTGAACCCCATTTGTG 1425
 QY 1707 CCAAGCTTCAAGTGTATGATCCAAAGACATGCTGAAATGATGATTTCTGAGAGT 1766
 Db 1426 CCAAGCTTCAAGTGTATGATCCAAAGACATGCTGAAATGATGATTTCTGAGAGT 1485
 QY 1767 CGGGGGTGGAAATTTGATGACAAAGATTAAGCATTTTCAAAAATTGCGACAGTGTCT 1826
 Db 1486 CGGGGGTGGAAATTTGATGACAAAGATTAAGCATTTTCAAAAATTGCGACAGTGTCT 1545
 QY 1827 GTTCTTATGATGAGAGAGAAATTAAGAAAGAGAGCTGTTTGAAGAACTGATGAC 1886
 Db 1546 GTTCTTATGATGAGAGAGAAATTAAGAAAGAGAGCTGTTTGAAGAACTGATGAC 1605
 QY 1887 CCCAAGACCTTACAGGTTGTGAGAGAGTAAATCATCAAGCTGAGGCTGCTGTTGTA 1946
 Db 1606 CCCAAGACCTTACAGGTTGTGAGAGAGTAAATCATCAAGCTGAGGCTGCTGTTGTA 1665
 QY 1947 TTGTAATGCTCTCTTTACAGAGCAAGCAAGCAAGA 1982
 Db 1666 TTGTAATGCTCTCTTTACAGAGCAAGCAAGCAAGA 1701

RESULT 10
 US-10-217-745-3
 ; Sequence 3, Application US/10217745
 ; Publication No. US20030004328A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Walke, D. Wade
 ; APPLICANT: Wilganowski, Nathaniel L.
 ; TITLE OF INVENTION: No. US20030004328A1 Human G-Coupled Protein Receptor Kinases and
 ; TITLE OF INVENTION: Polynucleotides
 ; FILE REFERENCE: Encoding the Same
 ; CURRENT APPLICATION NUMBER: US/10/217,745
 ; PRIOR FILING DATE: 2002-08-12
 ; PRIOR FILING DATE: US/09/802,117
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1062
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-10-217-745-3
 Query Match 47.6%; Score 1046.8; DB 15; Length 1062;
 Best Local Similarity 99.8%; Pred. No. 1.7e-308;
 Matches 1048; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 291 ATGATGACATGGGAGCCCTGAGCAACCTGATCCGCAACCGCTTACTGAGAGCCCG 350
 Db 1 ATGATGACATGGGAGCCCTGAGCAACCTGATCCGCAACCGCTTACTGAGAGCCCG 60
 QY 351 AAGCCTTGAGCTGAGCAGCAAGAGAGTGAAGCGGAGCGGAGTGAAGCTGAGAGCCCG 410
 Db 61 AAGCCTTGAGCTGAGCAGCAAGAGAGTGAAGCGGAGCGGAGTGAAGCTGAGAGCCCG 120
 QY 411 GGGCTGAGAGGCTGCGGAGCTCGGCAAGGCTGCTGCAAGCTTCCCTGCAAGCTGTGT 470
 Db 121 GGGCTGAGAGGCTGCGGAGCTCGGCAAGGCTGCTGCAAGCTTCCCTGCAAGCTGTGT 180
 QY 471 GAGCAGAGCCATGCTGAGCGGCTTCCGTAATCTTCTGAGAGTGTGCGAGGCTGCGAG 530
 Db 181 GAGCAGAGCCATGCTGAGCGGCTTCCGTAATCTTCTGAGAGTGTGCGAGGCTGCGAG 240
 QY 531 CGCAAGCGGCAACTTCTTGAAGAGCTGAGCAACTGAGAGCTGCGAGAGGAGGCC 590
 Db 241 CGCAAGCGGCAACTTCTTGAAGAGCTGAGCAACTGAGAGCTGCGAGAGGAGGCC 300
 QY 591 ACCAAGACAGCGGCTGAGAGGCTGAGCACTTGTGAGAGTGTGCGAGGCTGCGAGG 650
 Db 301 ACCAAGACAGCGGCTGAGAGGCTGAGCACTTGTGAGAGTGTGCGAGGCTGCGAGG 360
 QY 651 AACCCGAACTTCTTCAAGAGCGGCTGAGCAACTGAGAGCTGAGAGGAGGAGCC 710
 Db 361 AACCCGAACTTCTTCAAGAGCGGCTGAGCAACTGAGAGCTGAGAGGAGGAGCC 420
 QY 711 GAAAGAGAGTGTGAGTGAAGCTGAGCAAGCTGAGAGGCTGAGAGGCTTCTTGAAGAG 770
 Db 421 GAAAGAGAGTGTGAGTGAAGCTGAGCAAGCTGAGAGGCTGAGAGGCTTCTTGAAGAG 480
 QY 771 GAGCCCTTAAAGATTTGTGAGCAGAGCTTCAAGCAAGTTTCTGAGAGAACTC 830
 Db 481 GAGCCCTTAAAGATTTGTGAGCAGAGCTTCAAGCAAGTTTCTGAGAGAACTC 540
 QY 831 TTGAGATGAGCAAGTGTGAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 890
 Db 541 TTGAGATGAGCAAGTGTGAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 600
 QY 891 GGTTTTGGGAGGTATGTGCGCTCAAGTGAAGAAACAATGAGAAAGATGATGCTGTAAG 950
 Db 601 GGTTTTGGGAGGTATGTGCGCTCAAGTGAAGAAACAATGAGAAAGATGATGCTGTAAG 660

```

RESULT 11
US-09-964-469-3
Sequence 3, Application US/09964469
Patent No. US20020034803A1
GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEROPF
FILE REFERENCE: CU000636D1V
CURRENT APPLICATION NUMBER: US/09/964,469
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/208,331
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: 09/728,894
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 36651
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(36651)
OTHER INFORMATION: n = A,T,C or G
US-09-964-469-3

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Query Match	39.5%	Score 867.4	DB: 9	Length 36651
Best Local Similarity	95.1%	Pred. No. 1.1e-252		
Matches	895	Conservative	0	Mismatches 46; Indels 0; Gaps 0;
Qy	1	GACCTPAAGTAAAGGACCTCACTATAGGGCTGAGACGGCCGCCCGGAGGAGGCTTC	60	
Db	1786	GACCTPAAGTAAAGGACCAAGTGGAGGAGTGGCCCCCGGAGGCTTCACGACGCTTTC	1845	
Qy	61	GCTTGGCAGGTGGAGCATGACCTATGCTGTCGATTTCTGCGGGCTATATACATAGCA	120	
Db	1846	GCTTGGCAGGTGGAGCATGACCTATGCTGTCGATTTCTGCGGGCTATATACATAGCA	1905	
Qy	121	GTCAAAGCTTCTTACAAAGAAAGCTTTTCACACCTTCACAGGGGCCACCGCACAGGCC	180	
Db	1906	GTCAAAGCTTCTTACAAAGAAAGCTTTTCACACCTTCACAGGGGCCACCGCACAGGCC	1965	

QY	181	ACGAGCACTACCTGTAATCCCTTGGACGTTCTCAACCGGAAAGGAAACACACCGACA	240
Db	1966	ACGAGCACTACCTGTAATCCCTTGGACGTTCTCAACCGGAAAGGAAACACACCGACA	2025
QY	241	GCCCTCAACCCCTCTTGTGCTTCCCTGGAGATGCGCCCTGCTGCTGACATGATGGACA	300
Db	2026	GCCCTCAACCCCTCTTGTGCTTCCCTGGAGATGCGCCCTGCTGCTGACATGATGGACA	2085
QY	301	TGGGGGCGCTTGGACAACTGATGCGCAACACCGCTACCTGACAGGCGCGGAAAGCCCTCG	360
Db	2086	TGGGGGCGCTTGGACAACTGATGCGCAACACCGCTACCTGACAGGCGCGGAAAGCCCTCG	2145
QY	361	ACTGCGACAGCAAAAGCTGAGGCGGCGGCGCTACCTGCGCCCTGCGCGGCTGCAAG	420
Db	2146	ACTGCGACAGCAAAAGCTGAGGCGGCGGCGCTACCTGCGCCCTGCGCGGCTGCAAG	2205
QY	421	GCTGCGGAGGCTCGCGCAGAGAGCTGCTCCCTGAACCTTGCACAGCTGTGTGAGACGAGC	480
Db	2206	GCTGCGGAGGCTCGCGCAGAGAGCTGCTCCCTGAACCTTGCACAGCTGTGTGAGACGAGC	2265
QY	481	CCATCGGTGCGCGCTCTTCCGTGACCTTCTTACGACAGGCCACAGTTCGCGCAAGCGG	540
Db	2266	CCATCGGTGCGCGCTCTTCCGTGACCTTCTTACGACAGGCCACAGTTCGCGCAAGCGG	2325
QY	541	CAACCTTCCAGAGGACGTCGAGAACTGAGGAGCTGAGCGCAGAGAGGAGCCACCAAGACA	600
Db	2326	CAACCTTCCAGAGGACGTCGAGAACTGAGGAGCTGAGCGCAGAGAGGAGCCACCAAGACA	2385
QY	601	GCGCGCTGCAAGGGGCTGTGTGCACTTGTGCGAGTGCCTTCCCGGGGAAACCGCGAAC	660
Db	2386	GCGCGCTGCAAGGGGCTGTGTGCACTTGTGCGAGTGCCTTCCCGGGGAAACCGCGAAC	2445
QY	661	CCCTTCTTGAACCAAGCGCGTGTGCAACAAATGGCCAAAGCACAACCTGAGAGAGCGAG	720
Db	2446	CCCTTCTTGAACCAAGCGCGTGTGCAACAAATGGCCAAAGCACAACCTGAGAGAGCGAG	2505
QY	721	TGGCGTGAAGTACGCTGCGCAGAGGCTGAGGCGCATGTGCTTCTTGCAGAGCAGCCCTT	780
Db	2506	TGGCGTGAAGTACGCTGCGCAGAGGCTGAGGCGCATGTGCTTCTTGCAGAGCAGCCCTT	2565
QY	781	AGGATTTGTGACCAAGCGCTTCTTACGACAAATTTTGTGAGTGAAGAACTTTGAGATGC	840
Db	2566	AGGATTTGTGACCAAGCGCTTCTTACGACAAATTTTGTGAGTGAAGAACTTTGAGATGC	2625
QY	841	AACCACTGTCAGACAAATCTTCACTGAGTTTCAGAGGCTGGGGAAGAGTGTGTTTGAGG	900
Db	2626	AACCACTGTCAGACAAATCTTCACTGAGTTTCAGAGGCTGGGGAAGAGTGTGTTTGAGG	2685
QY	901	AGGTATGTGCGCTCAGGTGAAGAAACACTGTGGAAGATGAT	941
Db	2686	AGGTATGTGCTCTCCCACTAGCCAGGCTGAAGTGAAGCAT	2726

RESULT 12
 US-10-425-962-3
 ; Sequence 3, Application US/10425962
 ; Publication No. US20030180786A1
 ; GENERAL INFORMATION:
 APPLICANT: GUGELER, Karl et al
 TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 TITLE OF INVENTION: THERBOF
 FILE REFERENCE: C1000636DIV2
 CURRENT APPLICATION NUMBER: US/10/425, 962
 CURRENT FILING DATE: 2003-04-30
 PRIOR APPLICATION NUMBER: 09/964, 469
 PRIOR FILING DATE: 2001-09-28
 PRIOR APPLICATION NUMBER: 09/738, 894
 PRIOR FILING DATE: 2000-12-18
 PRIOR APPLICATION NUMBER: 60/208, 331
 PRIOR FILING DATE: 2000-06-01
 NUMBER OF SEQ ID NOS: 4

QY	1	GACCCCTAATAATGAAGGACCTCACTATAGAGCTGAGAGCGCCGCCGGGAGAGTGCCTTTC	60
Db	1786	GACCCCTAATAATGAAGGACCAATGAGGAGAGAGTGGCCGCCGAGAGTGTCCAGCAGCTTTC	1845
QY	61	GCCCTTGGCAGTGGGAGCATGACCTATGCTGTGGAGAGTCTCTTGGCGGAGTATACATYAGCCA	120
Db	1846	GCCCTTGGCAGTGGGAGCAATGACCTATGCTGTGGAGTCTCTTGGCGGAGTATACATYAGCCA	1905
QY	121	GTAAAGCTTCTTCAAAAGAAACCTCTTTACAACCTCCACAGAGTGTCCACCAAGAGCC	180
Db	1906	GTCAAAAGCTCTTCAAGAGAAACCTCTTTACAACCTCCACAGAGTGTCCACCAAGAGCC	1965
QY	181	ACAGAGCTCACGTAAATCCCTTGGACGTTGTCAACCCGGGAAAGGAAAGCCGACGA	240
Db	1966	ACAGAGCTCACGTAAATCCCTTGGACGTTGTCAACCCGGGAAAGGAAAGCCGACGAGA	2025
QY	241	GCCCTCAAGCCTCTTGTGTCTCCCTTGGAGTGGCCGCCGAGCTCAAGGCCATGTGGACA	300
Db	2026	GCCCTCAAGCCTCTTGTGTCTCCCTTGGAGTGGCCGCCGAGCTCAAGCCATGTGGACA	2085
QY	301	TGGGGGCCCTTGGACAACCTGATGCGAACATGCTCCCTCACTGAGAGCCGGAAACCTCGG	360
Db	2086	TGGGGGCCCTTGGACAACCTGATGCGAACACGCTCACTGAGAGCCGGAAACCTCGG	2145
QY	361	ACTGGAAGCAAAAGAGCTGACGAGGAGGAGGAGGAGTACCTTGGCTTGCCTGGCTGACG	420
Db	2146	ACTGGAAGCAAAAGAGCTGACGAGGAGGAGGAGGAGTACCTTGGCTTGCCTGGCTGACG	2205
QY	421	GCTGCGGAGAGCTCGGCCAAGAGCTGTCCCTGAACTTCAACAGCTGTGTGACGACGAC	480
Db	2206	GCTGCGGAGAGCTCGGCCAAGAGCTGTCCCTGAACTTCAACAGCTGTGTGACGACGAC	2265
QY	481	CCATGGAGTGGGCGCTCTTCCGTGACTTCTTACCAAGTGCCTCCAGCTTCCGACAGCGG	540
Db	2266	CCATGGAGTGGGCGCTCTTCCGTGACTTCTTACCAAGTGCCTCCAGCTTCCGACAGCGG	2325
QY	541	CAACCTTCTTAAAGACGTGCAAACTGGGAGCTGGCCAGAGGAGACCCACAAAGACA	600
Db	2326	CAACCTTCTTAAAGACGTGCAAACTGGGAGCTGGCCAGAGGAGACCCACAAAGACA	2385
QY	601	GCGGCGCTGACGAGGCTGTGTGCCACTTGTGTGAGTGGCCCTGCCCCGGAGAACCCGAC	660
Db	2386	GCGGCGCTGACGAGGCTGTGTGGCCACTTGTGTGAGTGGCCCTGCCCCGGAGAACCCGAC	2445
QY	661	CCCTTCTCAAGCCAGGCGGTGGCCACAAGTGGCAAGCAGGCCACACTGAGGAAAGAGGAG	720
Db	2446	CCCTTCTCAAGCCAGGCGGTGGCCACAAGTGGCAAGCAGGCCACACTGAGGAAAGAGGAG	2505
QY	721	TGGCTGAGTGAAGCTGTGGCAAGCTTGAAGGCATGAGCTTCTTGGAAAGAGAGCCCTTAA	780
Db	2506	TGGCTGAGTGAAGCTGTGGCAAGCTTGAAGGCATGAGCTTCTTGGAAAGAGAGCCCTTAA	2565
QY	781	AGGATTTGCGTACAGGCCCTTCTAAGACAAGATTTCTGCAGTGAAACTCTTCCAGATGC	840
Db	2566	AGGATTTGCGTACAGGCCCTTCTAAGACAAGATTTCTGCAGTGAAACTCTTCCAGATGC	2625
QY	841	AACCAATGTCAACAAGTACTTCACTGAGCTTCAAGAGTCTGGGAAAGAGTGTGTTGGG	900

535 CGACIACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAACTGGCTGGAAAGGCA 598

Db 539 GCCAGTACCAAAAAACCTTTCAGGCATACGAGTCCCTGGCAAAAGTGGCTTTGGGCA 658
 QY 902 GGTATGCGCCGTCAGGAGGAAAAACCTGGGAAGATGATGCTGTAAAGAACTGGACA 961
 Db 659 GGTGTGCGCTCCAGGAGGCGCCACAGATTAAGATGATGCTGTAAAGAACTGGACA 718
 QY 962 GAAGCGGCTGAAGAAAGAGTGGCGCAAGAGTGGCTGTGGAAAGAAAGAACTTTGA 1021
 Db 719 AAAGCGGATCAAGAAAGGGAAGGGAAGGCCATGAGCCCTTAACGAGAAAGAGATCTGGA 778
 QY 1022 GAAGGTACAGACCCCTTTCATGTCTCTGCGCTATGACCTTTGAGAGACAGCCATCT 1081
 Db 779 GAAAGTGAACAGTAGATTTGATGAGCTTGGCTTAAGCTATGAGACAGAGCGCT 838
 QY 1082 CTGCTTTGATGAGCCCTGATGATGAGGAGAGACCTTAAGTTCATCTTACAGCTGGG 1141
 Db 839 GTGCTGTGCTGACACTGATGAAACGAGGAGGAGACCTTAAGTTCATCTTACAGCTGGG 898
 QY 1142 CAGCGTGGCTGACATGAGCCGAGGTATCTTTTACTGCGGCGCAGATAGCTTGTGGAT 1201
 Db 899 CAGGCTGGCTTCCCCAGAGCGGAGCGCTCTTCTAGCGCGCGAGATCTGTGTGGCT 958
 QY 1202 GCTGACCTTCATGAACTCGGCATGCTCTATCGGACATGAGAGCTGAGATGTGCTTCT 1261
 Db 959 GAGAGACCTGACCCGAGAGCGCATGCTGTACAGGAGACCTGAGCCCGAGAACATCTTGT 1018
 QY 1262 GATATGCTCGGCAACGAGAGTATCTGACTTGGGCTGCGCGCTGAGATGAGAGGTGG 1321
 Db 1019 GATATGACAGCGCCACATCGCATCTGACTTGGAGATGAGCTGTGATGTGCGGAGGG 1078
 QY 1322 CAGGCCATTCACCCAGAGGCTGGAAGCAATGTTATCATGCTGCTGATGATCTTATGAA 1381
 Db 1079 CAGAGCATCAAAAGGCGGTGTGGGACCGTGGGTTACATGAGTCTGGAG---GTGGTGA 1135
 QY 1382 AAAAGTAAATTTCTTATCTGATGATGATGATGATGATGATGATGATGATGATGAT 1441
 Db 1136 GATATGACGATACAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 1195
 QY 1442 GGTGCTGAGAGCAACACTTCAAGATTTCAAGAAAGTCAAGAAAGTCAAGAAAGTCAAG 1501
 Db 1196 GATGCGAGGCGGAGTGGCTTCAAGAGAGAAAGAAATCAAGAGGAGAGAGTGGGA 1255
 QY 1502 GCAGAGAACTCTGCAAGACGAGGTCAAAATTCAGCATGATTAATTTCAAGAGAGCAAA 1561
 Db 1256 GCGGCTGTGTAAGAGAGTCCCGAGAGATTTCCAGGCGTTTCCCGAGAGCGCGCTC 1315
 QY 1562 AATATTTTGAAGGCTTCTTGGCTAAAGAAACGAGAGACGCTTGAAGAGAGAGAA 1621
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 QY 1622 GTCTGATGATCCAGAGAAACATCTTTTAAAGCATCACTTCTCTGCTTGAAGC 1681
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 QY 1682 TGCGCTTATGAAACCCCATTTGTGCGAGACCTTCAAGTGGTTTATGCGAAGACATCG 1741
 Db 1436 TGCGATCTGAGAGCGCGCTTCAAGCTTGAACCCCGAGCATTTTACGTAAGAGTGTCT 1495
 QY 1742 TGAATTTGATGATTTCTGAGGTTGCGGAGGAGTGAATTTGATGAGAAAGATTAAGCACT 1801
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 QY 1802 CTGAAAACTTTGAGAGAGTGTGTTCTTATGACATGCGAGAGAGAAATTAAGAAAC 1861
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 QY 1862 GAGACTGTTTGAAGAACTGAATGAC 1886
 Db 1616 GAGTGTCTTCAAGAGCTGAATGTC 1640

; Sequence 4, Application US/10159856
 ; Publication No. US20030228689A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Susan M. Freier
 ; APPLICANT: Kenneth W. Dobie
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPRE
 ; FILE REFERENCE: RUS-0365
 ; CURRENT APPLICATION NUMBER: US/10/159,856
 ; CURRENT FILING DATE: 2002-05-31
 ; NUMBER OF SEQ ID NOS: 134
 ; SEQ ID NO 4
 ; LENGTH: 2848
 ; TYPE: DNA
 ; ORGANISM: H. sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (63) ... (1793)
 US-10-159-856-4

Query Match 19.0%; Score 418.2; DB 16; Length 2848;
 Best Local Similarity 56.2%; Pred. No. 4, 2e-116;
 Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;

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 QY 365 CGACAGCAAG---AGCTGACAGCGCGCGGAGTGAAGCTGAGCCCTGCGGCTGACAGG 421
 Db 125 AATTCGAAAGGCAAAAGCAAAAGAAATGGCGAGATGCTCAAGTCCCTGACATCAAGCA 184
 QY 422 CTGCGGAGAGCTCCCGCAGAAAGTGTCTTAACTTCAAGCTGTGTGAGCAGAGCC 481
 Db 185 GTGGAAGAGCTGCGGCTGAGCTTCAAGGTGATCAAGCTGTGCGAGCGGACCG 244
 QY 482 CATGCTGCGCCCTCTTCCGTGATCTTCTGACATGCGACAGTGGCCGAGTTCGCGAGAGGCG 541
 Db 245 CATTTGGCGCCCTGCTGTTCGAGAGATTTCTGTGCAAGAGCGAGAGTGAAGCTGAGCTGCT 304
 QY 542 AACCTTCTGAAGAGAGCTGCAAGACTGAGAGCTGAGAGAGAGAGAGAGAGAGAGAG 601
 Db 305 CGGCTTCTGATGAGGAGTGGCGCGAGATGAGAGTGAAGTGAAGAGAGAGAGAGAGAG 364
 QY 602 CGGCTGAGAGAGAGAGTGGCGAGCTTGTGAGAGTGGCTTGTGCGGAGAGAGAGAGAGAG 661
 Db 365 TGGAGCGGACG---TAAGCAAGATTTTCTGAGCAACAGGAGTCTGACCTCAATCCCTGA 421
 QY 662 CTTCCTGAG 721
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 QY 722 GGTGAGTGAAG 781
 Db 481 ACCCTTTCAG 538
 QY 782 GATTTTTCAG 841
 Db 539 GATTTTTCAG 598
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QY 1202 GCTGACCTTCATGAGACTGCGCATGCTCTATCGGACATGAAAGCTGAGATGTCTTCT 1261
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QY 1802 CTTCAAAAATTGCGACAGGTGCTGTCTTAATGACATGCGAGAGAAATTAAGAAC 1861
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QY 1862 GCGACTGTTGAGAACTGAATGAC 1886
Db 1616 CGAGTCTTCAAGAGCTGAATGTC 1640

Search completed: August 13, 2004, 19:06:08
Job time : 698.966 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 12:57:35 ; Search time 3850.63 Seconds

(without alignments)
17045.794 Million cell updates/sec

Title: US-10-044-205a-1

Perfect score: 2198
Sequence: 1 gacccaagatgaaggagacc.....aacaccaggtatttga 2198

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

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1: em_estba:*
2: em_esthm:*
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14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
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24: em_gss_pro:*
25: em_gss_rtd:*
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27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	398.6	18.1	2978	AK051405	AK051405 Mus muscu
2	376	17.1	2989	BC057206	BC057206 Mus muscu
3	311.8	14.2	1201	BX404586	BX404586 BX404586
4	311.6	14.2	2329	BC027597	BC027597 Homo sapi

C	5	307	14.0	917	13	EX392018	EX392018 BX392018
	6	304.6	13.9	1721	29	AY406080	AY406080 Homo sapi
	7	300.2	13.7	1058	13	BQ057469	BQ057469 AGENCOURT
	8	299.2	13.6	1019	13	BQ061148	BQ061148 AGENCOURT
	9	295	13.4	1721	29	AY406082	AY406082 Mus muscu
	10	281.8	12.8	934	13	BQ526699	BQ526699 AGENCOURT
	11	280.6	12.8	903	13	BQ146436	BQ146436 AGENCOURT
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	17	269.2	12.2	857	13	BQ527897	BQ527897 AGENCOURT
	18	268.8	12.2	968	13	BQ066445	BQ066445 AGENCOURT
	19	267	12.1	1028	13	BQ063841	BQ063841 AGENCOURT
C	20	265.6	12.1	696	10	BE677821	BE677821 AGENCOURT
	21	265.4	12.1	998	13	BQ057613	BQ057613 AGENCOURT
	22	264.8	12.0	1032	12	BM472080	BM472080 AGENCOURT
	23	264.4	12.0	1034	10	BE568334	BE568334 AGENCOURT
	24	264.2	12.0	851	13	BQ230423	BQ230423 AGENCOURT
	25	264.2	12.0	1622	29	AY406081	AY406081 Pan trogl
	26	263.6	12.0	826	12	BG828886	BG828886 602725869
	27	263	12.0	777	10	BE795217	BE795217 601592482
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	34	252.4	11.5	838	13	BX849055	BX849055 BX849055
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	36	249	11.3	676	9	AI640213	AI640213 wa30e01.x
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	38	244.4	11.1	660	13	BQ520195	BQ520195 NISC n103
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	40	240.2	10.9	995	13	BQ056240	BQ056240 AGENCOURT
	41	239.4	10.9	569	12	BM712420	BM712420 UI-E-DWI-
C	42	239.4	10.9	658	9	AI738477	AI738477 w332d04.x
C	43	239.2	10.9	724	13	BM014695	BM014695 BM014695
	44	238.6	10.9	942	10	BE727456	BE727456 60150667
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ALIGNMENTS

RESULT 1
LOCUS AK051405
DEFINITION Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:DI30046K22 product:6 PROTEIN-COUPLED RECEPTOR KINASE GNRK6 (EC 2.7.1.1-) homolog [Mus musculus], full insert sequence.
ACCESSION AK051405
VERSION AK051405.1 GI:26094516
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
1 Carinci, P., and Hayashizaki, Y.
Normalisation and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

REFERENCE
1 Carinci, P., and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)

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AUTHORS Carinci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shiota, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374

PUBMED 11042159
 SHIBAHARA, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Kono, H., Akiyama, T., Nishi, K., Katsunuma, T., Tashiro, H., Itoh, M.,
 Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, T., Izawa, M., Ohara, E., Matsuda, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system - 384-format
 sequencing pipeline with 384 multichannel sequencer
 Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL 20530913
 MEDLINE 11076861

REFERENCE 4
 The RIKEN Genome Exploration Research Group Phase II Team and the
 PANTOM Consortium
 Functional annotation of a full-length mouse cDNA collection
 Nature 409, 685-690 (2001)

REFERENCE 5
 The PANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

JOURNAL 6 (bases 1 to 2978)
 AUTHORS Fukuda, S., Furuno, M., Akiyama, T., Arakawa, T., Bono, H., Carninci, P.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiroaki, T., Hirozane, T.,
 Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Konda, M.,
 Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ono, M., Ohsato, N.,
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahita, S.,
 Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://fantom.gsc.riken.go.jp/
 Location/Qualifiers

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 /organism="Mus musculus"
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 /strain="C57BL/6J"
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 /db_xref="WGI:2419686"
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 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="12 days embryo"
 misc_feature 256..1893
 /note="G PROTEIN-COUPLED RECEPTOR KINASE GRK5 (EC 2.7.1.-)
 homolog [Mus musculus] (SWISSPROT|O70293, evidence: PASTY,
 100%ID, 96.9%length, match=1714)
 putative"

ORIGIN

Query Match 18.1%; Score 398.6; DB 11; Length 2978;
 Best Local Similarity 55.5%; Pred. No. 3.3e-77;
 Matches 892; Conservative 0; Mismatches 659; Indels 8; Gaps 3;

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 508 TCCCTAGCCAGAGTCCGACGCTTCCGAAAGGCGGAACTTCTTCAAGAGAGGAGGAGGAGG 567
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 783 CAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 842
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Db 1440 ACCGTCTGAGAGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1499

QY 1648 TCTTTAAAGCATCACTTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1707

Db 1500 TTTTCAGAGAACTGATTTTCAAGCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1589

QY 1708 CAGACCTTCAGAGGTGTTATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1767

Db 1560 CTGATCCCGAGGCTATTATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1619

QY 1768 GGGGGGTGATTTGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1827

Db 1620 AAGGTGTGATCTGAG 1679

QY 1828 TTCTTAAGCATGAG 1886

Db 1680 TGTCCATCCCTGAG 1738

RESULT 2
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LOCUS BC057206 Mus musculus G protein-coupled receptor kinase 6, mRNA (CDNA clone IMAGE:5328461), containing frame-shift errors.
ACCESSION BC057206
VERSION BC057206.1 GI:34784381
KEYWORDS HNC.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Dege, J.G., Klausner, R.D., Collins, F.S., Wagner, K.H., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stieplet, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loguellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McMan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.D., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Meyers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Small, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12479332

REFERENCE 2 (bases 1 to 2989)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (29-AUG-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer

REMARK
COMMENT Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: gcgaps-remail.nih.gov
Tissue Procurement: Lotmar Hennighausen Ph.D., Priscilla Forth Ph.D.

CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LINT)
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Ahter, N., Ayala, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantrop, S., Thomas, P.D., Touchman, J.W., Tsurgou, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H., and Green, E.D.

FEATURES
source
1..2989
/organism="Mus musculus"
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/strain="NMRI"
/db_xref="taxon:10090"
/clone="IMAGE:5328461"
/tissue_type="Mammary tumor. MAP-Tag model. 5 months old, gross tissue."
/clone_1ib="NCI_CGAP_Mam4"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 17.1%; Score 376; DB 11; Length 2989;
Best Local Similarity 54.8%; Pred. No. 3.3e-72;
Matches 883; Conservative 0; Mismatches 700; Indels 27; Gaps 6;

QY 280 CTTGCTCAGCCATGCTGAGCATGAGGAGGCGCTGAGCAACTGATGCGCAACCGCTACC 339

Db 145 CGGACCGGAGCGGCGCTGAGCGCCATGAGAGCTCGAGAAATGCTAGCAACACGCTCTAC 204

QY 340 TGCAGGCGCGAGAGCCCTGAGCTGCGACAGCAAG--AGCTGAGCGGCGGCGCTA 396

Db 205 TCAAGCGCGGAGAGAGTGTGCGGAGATGCAAGAGCAAGAGCAAGATGCGCGCAGA 264

QY 397 GCGTGCCTCCCGCGGAGCTGAGAGCGGCTGAGAGAGTCCGCCAAGACTGCTTGAAGT 456

Db 265 TGTCTCAATTTCCCATATCAGCAGAGTGAAGAGTGTGACTGAGCTTGAAGCTGAGT 324

QY 457 TCCACAGCTGTGTGAGAGAGAGCCCATGAGTGCCTGCTTCTGAGCTTCTGAGCA 516

Db 325 ACCACAGCTATGTGAGCGCAGCCCATTTGGGCGCTGTATTTTCGAGATTTGTGCTA 384

QY 517 CAGTCCCGAGCTTCCGAGAGGCGCAACTTCTTGAAGAGAGTGCAGAGTGCAGAGCTGG 576

Db 385 CGAGACTGAGCTGAGCCCGGTGTACTGCTTCTGAGATGCGGTGTCTGAATATGAGTGA 444

QY 577 CCGAGAGAGAGCCCAAGAGAGAGCGGCTGAGAGGCTGTGCGCCTGCTGAGAGT 636

Db 445 CCGCTGATGAG 501

QY 637 CCGCTGCGCGGAG 696

Db 502 ACACGGTCTCTAAGCTTACCTTGAAGTTCCAGCGACCTGTGTAGTAAAC--TGTGCCAG 560
 QY 697 CAGCCACACTGAGAGAGAGCGAGTGTCTGCAGTACGCTGCGCAAGCTGAGGCATG 756
 Db 561 CGGCTAGAGAGAGAGCGCTGCAAGACCTCTTCCAGAGCTGACCGGGCTGA--CCACG 618
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 Db 619 AGTACTGAGACGAGCGCCCTTTTGCAGACTACTGAGAGCATCTTCAACCGTTTTC 678
 QY 817 TGGAGTGAAGAACTCTTCCAGATGCAACAGTGTCAACAATGACTTCACTGAGTTCAAG 876
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 QY 937 TGTATGCTGTGAAGAACTGCAACAAGCGGTGTAAGAAAGAGTGTGCGAGAGATGG 996
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 Db 1024 ATGCTGTGAGATGTGTGTGTGCTGCAAGACCTGACCGGGAAGGATGTGTACAGG 1083
 QY 1237 ACATGAAGCTGAGAAATGTGCTTGTGATGACCTCGGCAATGCAAGTTATCTGACCTGG 1296
 Db 1084 ATCTMAAGCAGAGAAATCTTCTGTATGACATGAGCAATTCGAGATCTCGAGACTGG 1143
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 Db 1681 CTTGCGCAAGATGATGTGTGAGACCGAGTGTCTTCAAGAACTCAATGTCT 1730
 RESULT 3
 BX404586 1201 bp mRNA linear EST 13-MAY-2003
 LOCUS BX404586 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
 DEFINITION CS0DA004YM05 3-PRIME, mRNA sequence.
 ACCESSION BX404586
 VERSION BX404586.1 GI:30648023
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 Li, W.-B., Gruber, C., Tesse, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seq@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 3090.f For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DA004YM05&cluster=3090.f. Contact :
 Feng Liang Email: fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Paraday Avenue Genoscope sequence ID : CS0DA004YM05NPL.
 Location/Qualifiers
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 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."

ORIGIN

Query Match 14.2%; Score 311.8; DB 13; Length 1201;
 Best Local Similarity 59.8%; Pred. No. 4.6e-58;
 Matches 539; Conservative 1; Mismatches 358; Indels 3; Gaps 1;

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 QY 872 CAGAGTCTGGGAAAGGTGTTTGGGAGAGTATGTGCTCCAGTGAAGAAACATCGG 931
 Db 944 CGAGTCTGGGCAAGGTGTGCTTTGGGAGAGTGTGCGCTGCGAGGTGCGGCGCACAG 885
 QY 932 GAAGTATGATCTCTTGAAGAACTGCAACAAGCGGTGCAAGAGAGTGTGCGAGAA 991
 Db 884 TTAGTATGATCTCTTGAAGAGCTAGAGAAAGCGATCAAGAGCGAGAGAGGAGGC 825
 QY 992 GATGCTCTCTTGAAGAAAGTCTTGAAGAGTGTGAGAGTGTGAGAGTGTGAGTGTCTCT 1051
 Db 824 CATGGCTGAAAGAGAGCAATCTGAGAGAAAGTAAAGTGTGTGTGTGTGAGCTT 765

QY 1052 GGCTATGCTTGGAGAGACCAACCATCTGCTTGTGATGAGCCGTGATGAGGAG 1111
 DB 764 GGCTATGCTTGGAGAGACCAACCATCTGCTTGTGATGAGCCGTGATGAGGAG 705
 QY 1112 AGACTGAAATTTGACATCTCAACAGTGGGACCGTGGCTGAGCATGAGCCGGTAT 1171
 DB 704 CGACTCAAGTTTCAACATCTCAACAGTGGGACCGTGGCTGAGCATGAGCCGGTAT 645
 QY 1172 CTTTATCTGCGCCCAATGAGTGGGATCTGCACTTCCTGATGAACTGCGATCTTA 1231
 DB 644 CTTTATCTGCGCCCAATGAGTGGGATCTGCACTTCCTGATGAACTGCGATCTTA 585
 QY 1232 TCAGGACATGAAAGCTGAGATGCTTCTGAGTACCTGCGCACTGCAAGTTATCTGA 1291
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 QY 1412 GTTTCCTGAGGATGAGCACTTATGAAATGTTGCTGAGCAACCATTAAGATTA 1471
 DB 407 GTTTCCTGAGGATGAGCACTTATGAAATGTTGCTGAGCAACCATTAAGATTA 348
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 DB 227 TTTCCGAGGCTTTTCCCGAGGCGCCCTCATCTTGTCTACAGCTCTCTGCAAGAGACC 168
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 DB 167 TAAAGCATCACTTCTGCTGCTGAGAGGCTGCTTAATGAAACCCCAATTTGAGCA 108
 QY 1712 C 1712
 DB 107 C 107
 RESULT 4
 LOCUS BC027597 2329 bp mRNA linear HTC 01-MAY-2002
 DEFINITION Homo sapiens, similar to G protein-coupled receptor kinase 2-like
 (Drosophila), clone IMAGE:4830673, mRNA.
 VERSION BC027597.1 GI:20379554
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2329)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (08-APR-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 REMARK
 COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabp-remail.nih.gov
 Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (MGBRI) & Shireki

Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 contact: amadan@systemsbiology.org
 Anup Madan, Jessica Fahy, Erin Helton, Mark Ketterman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/BLINL at: <http://image.lnl.gov>
 Series: IRAC Plate: 34 Row: 1 Column: 14
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 4883346
 This clone has the following problem: frame shifted.

FEATURES
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ORIGIN
 Query Match 14.2%; Score 311.6; DB 11; Length 2329;
 Best Local Similarity 57.4%; Pred. No. 5.9e-58;
 Matches 623; Conservative 0; Mismatches 454; Indels 9; Gaps 3;

QY 767 AGAGCAGCCCTTTAAGATTCGTGACAGGCGCTTCTGCAAGTTCTGCAAGGAA 826
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 QY 827 ACTCTTGAGATGCAACAGTGTGACAGACATCTTCACTGAGTTCAAGAGTCTGAGAA 886
 DB 981 ATGGCTGAAAGGCAACCGTTAAACAAAGACATTTAGACATTAAGAGTTCTAGAAA 1040
 QY 887 AGGTGTTTGGGAGATGATGCGCTGAGAGTAAACCTGGAAGATGATGCTG 946
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 QY 947 TAAAGACTGCAAGAGAGGCTGAAAGAAAGGTGGCGAAGATGCTCTGGA 1006
 DB 1101 CAAAAGCTACAAAAAAGAAATTAAGAGAGAAAGTGAAGCTATGCTTAATGA 1160
 QY 1007 AAGAGAAATCTTGAAGAGTCAAGAGCCCTTTCATTGTCTCTGSCCTATGCTTGA 1066
 DB 1161 GAAAGAAATCTTGAAGAGTCAAGAGTGAAGTTGATGATTTAGCTTACCTTATGA 1220
 QY 1067 GAGCAAGACCATCTGCTGTGATGAGCTGATGAGTGAATGGGAGACTCAAGTTCCA 1126
 DB 1221 AACCAAGATGCTTGTGCTGTGCTGCTACCATTTAAGATGAGGAGTTGAAGTTCA 1280
 QY 1127 CATCTACACGCTGGGACCGTGGCTGAGCATGAGCCGGGATCTTTTACTGCGGCCCA 1186
 DB 1281 CATTTAGAACCTGGGAAATCCCGGCTTTGATGAGAGAGCCGTTTCTATGCTGAGA 1340
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 DB 1401 TGAGATGATGCTTGTGATGACCTGCGCACTGCAAGTTATCTGACCTGGAGCTGGCCGT 1460
 QY 1307 GGAATGAAAGGCTGCAAGCCATCAACCAAGGCTGAAACCAATGTTATGAGCTCC 1366
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 QY 1367 TGAGATCTTATGAAAGATGATTTCTTATCTGATGAGCTGATGAGCTGATGAGGATG 1426
 DB 1521 TGAGATGATCA--ATAATGAAAGATTAAGTTAGTCCGATGAGTGGGAGCTTGGCTG 1577

QY 1427 CAGCATTTATGAAATGTTGCTGAGCAACACCATTCAGAAATTCAGAGAAAGGTCAG 1486
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 DB 1755 GGGCTGAGGGGCGAGAGAGCGGCTGGGATGAAGAGACCCGCTGTTTCAAGAGATCA 1814
 QY 1664 CTTCCTGCTGAGAAAGTGGCTTAATTAACCCCATTTGTCAGACCCCTTCAGTGT 1723
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 QY 1724 TTATGCCAAAGATGCTGAATTTGATGATTTCTGAGGTTGCGGGGCTGAAATTTGA 1783
 DB 1875 TTACTGTAAGAGCTGCTGAGATTCAGAGAGTTCTTGCGGGTGAAGAGATCTACCTGA 1934
 QY 1784 TGACAAAGATAGCACTTCTTCAAAAATTGCGAGAGTCTGTTCTATAGCATGCA 1843
 DB 1935 CACCGAGATGAAGATCTTATGCTCGGTTTGCTACCGGGTGTGTCTTCATCCCTGCA 1994
 QY 1844 GGAAGA 1849
 DB 1995 GAATGA 2000

RESULT 5

BX392018/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BX392018 917 bp mRNA linear EST 13-MAY-2003
 BX392018 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
 Homo sapiens cDNA clone CSOD1010YD11 3-PRIME, mRNA sequence.
 BX392018
 BX392018.1 GI:30607809
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 917)
 La,W.B., Gruber,C., Jessee,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 3090.f For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CSDBAI046ZH12_CS04416_1&cluster=3090.f.
 Contact: Peng Liang Email: fliang@lifetech.com URL:
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID: CSDBAI046ZH12_CS04416_1.
 Location/Qualifiers
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 /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)

ORIGIN

primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match

14.0%; Score 307; DB 13; Length 917;

Best Local Similarity

63.8%; Pred. No. 5e-57;

Matches

482; Conservative 0; Mismatches 270; Indels 3; Gaps 1;

QY 749 GGCATGCTCTTCTTGCAAGACACCCCTTTAAGATTTGCGACCGAGCCCTTACGA 808
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 QY 809 CAGTTTCTGAGTGAAGAACTCTGAGATGACCAAGTGCAGCAATGATCTCACTGA 868
 DB 736 CGCTTTCTGAGTGAAGTGGCTGGAAGGCGACGAGCAAAAAACCTTCAGGCA 677
 QY 869 GTTCAAGTGTGAGGAAAGTGTGTTTGGGAGAGTATGTCCTCCAGGTGAAAAACAC 928
 DB 676 ATACGAGTCTGGGCAAGGTGCTTGGGAGAGTGTGCGCTCCAGGTGCGGCGCAC 617
 QY 929 TGGGAAGATGATGCTGTAAGAACTGGAAGAGCGGCTGAAGAGAAAGGTGCGCA 988
 DB 616 AGGTAAAGATGATGCTGCAAGAGCTAGAGAAAGAGGATCAAGAGCGGAAGGGA 557
 QY 989 GAAGATGCTCTTGGAAAGAAATCTTGAAGAGGTGAGAGCCCTTCATTTCTTC 1048
 DB 556 GGCATGCGGCTGACAGAGAGAGATCTGGAAGAAAGTGAAGATGATGAGTGA 497
 QY 1049 TCTGCTATGCTTTGAGAGCAAGACCATCTGCTGTTGATGACCTGATGATAG 1108
 DB 496 CTGGCTACAGCTATGAGACAGAGAGCGCTGTGCTGAGTGTGACATGATGAG 437
 QY 1109 GGGAGACCTCAAGTTTCAATCTACATCAAGCTGAGCAAGCTGAGCATGAGCCGAGT 1168
 DB 436 GGGGACCTCAAGTTTCAATCTACATCAAGCTGAGCAAGCTGAGCATGAGCCGAGT 377
 QY 1169 GATCTTTTACCTGAGCCGAGATGACCTGAGGATGCTGACCTTCATGAATCTGAGATCGT 1228
 DB 376 GGTCTTCTAGAGCGCGAGATCTGCTGAGTGTGCTGAGGATCTGACCGGAGCGCATCGT 317
 QY 1229 CTATCGGACATGAGAGCTGAGAGATGCTGTTGATGATGATCTGCGGACATGCAAGTATC 1288
 DB 316 GTACAGGACCTGAGAGCCGAGAGATCTTGTGATGATGACAGGCGCATGCTCATCTC 257
 QY 1289 TGACCTGGGCGTGGCGTGAAGTGAAGGAGTGAAGCCCATCAAGAGGCGTGAAGC 1348
 DB 256 TGACCTGGGCGTGGCGTGAAGTGAAGGAGTGAAGCCCATCAAGAGGCGTGAAGC 197
 QY 1349 CAATGTTACATGCTCTCTGAGATCTTAATGAGAAAGTAAATTTATCTATCTGTGA 1408
 DB 136 CGTGGTTACATGCTCTCTGAG---GTGGTGAAGAAATGAACGTTACACCTTCAGCCTGA 140
 QY 1409 CTGCTTTGCCATGAGATGACATTTATGAATGTTGTTGCGAGCAACCATTCAGAA 1468
 DB 139 CTGGTGGGCGCTGCGCTGCTCTGTAAGAGTATGCAAGGCGAGTCCGCTTCACGA 80
 QY 1469 TTAACAGAAAGGTCAATTAAGAGATCTGAAGC 1503
 DB 79 GAGAGAGAGAGATCAAGCGGAGAGAGTGAAGC 45

RESULT 6

AY406080

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AY406080 1721 bp DNA linear GSS 15-DEC-2003
 Homo sapiens GPRK3 gene, VIRUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 AY406080
 AY406080.1 GI:39762054
 GSS.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
AUTHORS
JOURNAL
PUBMED
AUTHORS
COMMENT
FEATURES
SOURCE
ORIGIN
Query Match
Best Local Similarity
Matches 559; Conservative 0; Mismatches 561; Indels 9; Gaps 3;

1 (bases 1 to 1721)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Perrera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 1721)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Perrera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment
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13.9%; Score 304.6; DB 29; Length 1721;
Pred. No. 2e-56;
Matches 559; Conservative 0; Mismatches 561; Indels 9; Gaps 3;

759 TTCTTGAAGAAGAGAGCCCTTTAAGATTGCTGACAGCGCTCTCAACAAGATTG 818
402 TACCTGAGGGAGAACATTCACGATATCTGAGACACATGTTTGAACCGCTTTC 461
819 CAGTGGAACTCTTCAAGATGCAACAGTCTCAACAAGTCTTCACTGAGTCAAGT 878
462 CAGTGGAAAGTGTGGAAGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 521
879 CTGGGGAAGGTGTTTGGGAGGTATGTGCGCTCCAGGTGAAAAACCTGGAAATG 938
522 NNN 581
939 TATGCTGTAAAGAACTGACACAGACGCTGAGAGAAAGGTGGCGAAGATGCT 998
582 TATGCTGAAAGCGCTTGGAGAGAGAGATCAAAAAGGAAAGGAGATGCTGACC 641
999 CTCTTGAAGAAAGAAATCTTGAAGAGTCAAGACCCCTTCAATGTTCTCTG 1058
642 CTCAATGAAAGCAATCTCTGAGAGGTCAAGTCAAGTGTGCTCAACCTGGCTTA 701
1059 GCTTTGAGAGCAAGACCACTCTGCTTGCATGAGCTGATGATGAGGAGACCTG 1118
702 GCTTGAAGACCAAGATGCACTGTGCTTGTGCTGACATCAATGATGAGGAGAT 761
1119 AAGTTCACATCTACACAGTGGGACGCTGCTGACATGACATGAGGAGATCTT 1178
762 AAGTTCACATCTACACAGTGGGACGCTGCTGACATGAGGAGATCTT 821
1179 TCGGCGCAATAGCTGTGGAGTGTGCACTCAATGAACTGGCACTGTCTATG 1238
822 GCGGCAAGATCTCTGCGCTTGAAGACCTCCACCGTGAACACGCTTACCGAG 881
1239 ATGAAGCTGAGATGAGTCTTCTGATGACCTCGGCACTGCAAGTATCTGACT 1298
882 CTGAAGCTGAGAAATCTCTTGAATGATTTATGAGCACTTGAATCTGACACT 941
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942 TTGGCTGATGATCCCGAGGAGACCTGATCCGCGCGGAGTGGGAGCTGTTGCT 1001

1359 ATGCTCTCTAGATCTTAATGAAAAAGTAAGTATTCTTATCTCTGAGTGGTTGCC 1418
1002 ATGCTCTCTAGAGTCTCC--TGAACACCAAGAGTACGCGCTGAGCCCCCACTAGCGG 1058
1419 ATGAGTACAGCATTTATGAAATGCTTGTGAGCAACACATTTCAAAATTTACAGAA 1478
1059 CTGAGTCTCTCATCTATGAGATGATCGAGGCGAGTGGCTTCCGCGGCGCAAGAG 1118
1479 AAGTTCACATCTACACAGTGGGACGCTGACATCTGCAACAGAGTCAAAATTCAGCAT 1538
1119 AAGTTCACATCTACACAGTGGGACGCTGACATCTGCAACAGAGTCAAAATTCAGCAT 1178
1539 GATTAATCTACACAGAGAAAGAAAGTATTTCAGAGCTCTTCTTGGCTTAAGAACTGAG 1598
1179 ---AAGTTCCTCGAGAGAGCCCAAGTCCATCTGCAAGTGTGCTCAAGAAAGTCCAG 1235
1599 CAAGGCTTGAAGAGCAAGAAA---GTCTGATGATCCAGAAACATCATTTCTTAA 1655
1236 CAGAGGCTGGCTGCGCAGAGAGAGGAGGCTGCAAGAGTCAAGACACCCCTTCTTAA 1295
1656 ACATCACTTCTCTGCTGAGAGTGTGCTTAAATGAAACCCCAATTTGTCAGACCT 1715
1296 AAGTTCACATCTACACAGTGGGACGCTGACATCTGCAACAGAGTCAAAATTCAGCAT 1355
1716 TCAGTGTATGCAAGAAAGATCCGCTGAATGATGATTTCTCTGAGGTTGGGAGT 1775
1356 NNN 1415
1776 GAATTTGATGACAAAGTAAAGAGTCTTCAAAAACCTTGCACAGTGTGTTCTATA 1835
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1836 GATGCGAGAGAAATTTATGAAACGAGACTTTGAGGAACTGATG 1884
1476 NNN 1524

RESULT 7
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DEFINITION B0057469 1058 bp mRNA linear EST 29-MAR-2002
ACCESSION AGENCOURT_6739297 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5813090
VERSION B0057469
KEYWORDS B0057469.1 GI:19816809
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.
1 (bases 1 to 1058)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
AUTHORS Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaabs-remail.nih.gov
Tissue Procurement: Lou Straut
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILMI)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILMI at:
<http://image.llnl.gov>
Plate: LICK2064 row: j column: 03
High quality sequence stop: 631.
Location/Qualifiers
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/mol_type="mRNA"
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/clone="IMAGE:5813090"
/tissue_type="Lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"

ORIGIN

/clone_11b="NIH_MGC_99"
 /note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 library."

Query Match 13.7%; Score 300.2; DB 13; Length 1058;
 Best Local Similarity 63.9%; Pred. No. 1.7e-55;
 Matches 471; Conservative 0; Mismatches 263; Indels 3; Gaps 1;

749 GGCCATGAGCTTTCTGCAAGACAGCCCTTAAAGATTTCGTGACCAAGGCGCTTCTACGA 808
 5 GACCCAGAGTACTAGAGGTGGCCCTTTTGGCCGACTACTGACAGCATCTACTCA 64
 QY 809 CAAGTTCTGACATGAGAACTCTTGAAGATGACACCAAGTGTGACATCTTACTGA 868
 Db 65 CCGTTCTGACATGAGAACTCTTGAAGATGACACCAAGTGTGACATCTTACTGA 124
 QY 869 GTTCAAGATGCTGGGAGAAAGGTGTTTGGGAGGATATGTCGCTCCAGTGAAGAAACAC 928
 Db 125 ATACCGAGTCTTGGGAGAAAGGTGTTTGGGAGGATATGTCGCTCCAGTGAAGAAACAC 184
 QY 929 TGGGAAGATGATGCTCTGTAAGAACTGACCAAGAGCGCTGAAAGAAAGGTGCGA 988
 Db 185 AGTAAAGTATGATGCTCTGTAAGAACTGACCAAGAGCGCTGAAAGAAAGGTGCGA 244
 QY 989 GAAGATGCTCTCTTGGAAAGAAATCTTGAAGAGTGTGACAGGCTTCACTGTCTC 1048
 Db 245 GGCCATGAGCGCTGAAAGAGAAAGTCTTGAAGAGTGTGACAGGCTTCACTGTCTC 304
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 Db 365 GGGAGACTCAAGTTCACATCTACAGTGGGCAAGCGCTGAGCATGAGCGGCT 424
 QY 1169 GATCTTTTACTGAGCCCAATAGCTGTGAGATGTCGACCTTCACTGATGATG 1228
 Db 425 CGTCTTCTAGCGCCGAGATCTGCTGTGAGGAGCACTGACCGGAGCGATGCT 484
 QY 1229 CTATGGGAGCATGAAAGCTGAGATGCTTCTGAGATGACCTGAGCAACTGAGATG 1288
 Db 485 GTACAGGAGCATGAAAGCTGAGATGCTTCTGAGATGACCTGAGCAACTGAGATG 544
 QY 1289 TGACCTGAGGCTGAGCCCTGAGATGAGAGGTGCAAGCCCATCACCGAGGCTGAAAC 1348
 Db 545 TGACCTGAGGATGATGCTGATGATGATGATGATGATGATGATGATGATGATG 604
 QY 1349 CAATGTGATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1408
 Db 605 CGTGGTATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 661
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 Db 662 CTGCTTGTGATGAGGATGAGATGATGATGATGATGATGATGATGATGATGATG 721
 QY 1469 TTACAGAGAAAGTCA 1485
 Db 722 GAGAGAGAGAGATCA 738

RESULT 8
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 LOCUS
 DEFINITION AGNCOURT_6862941 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5920180

5', mRNA sequence.
 B0061148
 B0061148.1 GI:19884933
 EST.
 Homo sapiens (human)
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1019)
 NIH-MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Lou Staudt
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LINC2083 row: h column: 05
 High quality sequence stop: 704.
 Location/Qualifiers

FEATURES

source

1..1019
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 /note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 library."

ORIGIN

Query Match 13.6%; Score 299.2; DB 13; Length 1019;
 Best Local Similarity 63.8%; Pred. No. 2.7e-55;
 Matches 470; Conservative 0; Mismatches 264; Indels 3; Gaps 1;

749 GGCCATGAGCTTTCTGCAAGACAGCCCTTAAAGATTTCGTGACCAAGGCGCTTCTACGA 808
 5 GACCCAGAGTACTAGAGGTGGCCCTTTTGGCCGACTACTGACAGCATCTACTCA 64
 QY 809 CAAGTTCTGACATGAGAACTCTTGAAGATGACACCAAGTGTGACATCTTACTGA 868
 Db 65 CCGTTCTGACATGAGAACTCTTGAAGATGACACCAAGTGTGACATCTTACTGA 124
 QY 869 GTTCAAGATGCTGGGAGAAAGGTGTTTGGGAGGATATGTCGCTCCAGTGAAGAAACAC 928
 Db 125 ATACCGAGTCTTGGGAGAAAGGTGTTTGGGAGGATATGTCGCTCCAGTGAAGAAACAC 184
 QY 929 TGGGAAGATGATGCTCTGTAAGAACTGACCAAGAGCGCTGAAAGAAAGGTGCGA 988
 Db 185 AGTAAAGTATGATGCTCTGTAAGAACTGACCAAGAGCGCTGAAAGAAAGGTGCGA 244
 QY 989 GAAGATGCTCTCTTGGAAAGAAATCTTGAAGAGTGTGACAGGCTTCACTGTCTC 1048
 Db 245 GGCCATGAGCGCTGAAAGAGAAAGTCTTGAAGAGTGTGACAGGCTTCACTGTCTC 304
 QY 1049 TCTGAGCTTATGCTTTGAGAGCAAGCACTCTGCTGTGTCATGAGCTGATGATG 1108
 Db 305 CTGGGCTTATGCTTTGAGAGCAAGCACTCTGCTGTGTCATGAGCTGATGATG 364
 QY 1109 GGGAGACTCAAGTTCACATCTACAGTGGGCAAGCGCTGAGCATGAGCGGCT 1168

[illegible]

Insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."

ORIGIN

Query Match 12.4%; Score 280.6; DB 13; Length 903;
Best Local Similarity 62.6%; Pred. No. 3.5e-51;
Matches 455; Conservative 0; Mismatches 269; Indels 3; Gaps 1;

QY 759 TTCTTGCAAGAGAGCCCTTTAGGATTTCTGACAGAGCCCTTACGACAAAGTTCTG 818
DB 93 TACCTGAGGGAGAGACCATTCACCAATATGTGACAGCATTTTGTACCGCTTCTC 152
QY 819 CAGTGGAAACCTTCCAGATGCAACCATGTGACAGCAAGTACTTCTGAGTTGAGAGTG 878
DB 153 CAGTGGAAAGGTGTGGAAAGGCAACGGGTGCAAAAACATTTACAGGAGTGTAGAGTG 212
QY 879 CTGGGAAAGGTGTGGGAGGTATGTCGCTGACAGTTGAAAAACATGGGAAAGTG 938
DB 213 CTAGGAAAGGGGCTCTTGGGAGAGTCTGTGCTGACAGTTCTGGGCAAGGTTAAATG 272
QY 939 TATGCTTTAAAGAACTGACACAGAGCGCTGAGAGAAAGGTTGGGCAAGAGTGCT 998
DB 273 TATGCTGCAAGCGCTTGGAGAAAGAGGATCAAAAAGGAAAGGAGTTCATGGCC 332
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DB 333 CTCAATGAGAGAGATCTCTGAGAGAGTCAACAGTCAGTTGTGTCAACCTGCTGCTAT 392
QY 1059 GCCTTTGAGAGCAAGACCATCTGCTGCTGACAGAGCCCTGATGATGAGGAGAGAGCTC 1118
DB 399 GCTTACGAGACAGAGATGCACTGTGCTGTGCTGACATCATGATGAGGAGTACCTG 452
QY 1119 AAGTTCAATCTTACAGCGTGGAGCGCTGCTGAGCATGAGCGGAGTATCTTTAC 1178
DB 453 AAGTTCAATCTTACAGCGTGGAGCGCTGAGCATGAGCGGAGTATCTTTAC 512
QY 1179 TCGGCGCAATGAGCTGTGGAGATCTGACATCTTCAATGAACTGCAATCTGATGAGAC 1238
DB 513 GCGGAGAGATCTCTGCGGCTTGAAGACCTCCAGCTGAGAAACCGTCTACCGAGAT 572
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QY 1359 ATGCTCTGAGATCTTATGAGAAAGTAAATTTCTTATCTGTTGAGCTGTTGCTC 1418
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DB 750 CTGGCTGCTCATTTATGATGATGAGGAGGCAAGTCCGCTTCCGCGCGGAGAG 809
QY 1479 AAGGTCA 1485
DB 810 AAGGTCA 816

RESULT 12

BM794145

LOCUS

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Homo sapiens

cdna clone

S22SNUI6n1-37-D08

560 bp

mrna

linear

EST 05-MAR-2002

5', mRNA sequence.

BM794145

ACCESSION

BM794145.1

GI:19142377

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

TITLE

21C Frontier Korean EST Project 2001

JOURNAL

Unpublished (2002)

COMMENT

Contact: Kim YS

FEATURES

source

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Location/Qualifiers

High quality sequence stop: 560.

Location/Qualifiers

1..560

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/note="Organ: Stomach; Vector: pT73-Pac; Site: 1; Ecoli; Site 2; Note: The S22SNUI6 library was contributed by the Soares Laboratory and it was constructed as described by Bonaldi, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cells of SNU-16 culture. SNU-16 cell was obtained from Korean Cell Line Bank (KCLB). SNU-16 was established from ascitic fluids of Korean patients by Park J.G. et al. (1990), Cancer Res 50: 2773-2780."

ORIGIN

Query Match 12.4%; Score 272.2; DB 12; Length 560;
Best Local Similarity 68.0%; Pred. No. 2.3e-49;
Matches 379; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

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QY 936 ATGATGCTGTAAAGAACTGAGCAAGAGCGCTGAAGAAAGTGGCGAGAGAGTG 995
DB 121 ATGATGCTGTGAAGAGCTAGAGAAAGCGATCAAGAAAGCGAGAGGCGCATG 180
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DB 301 CTCAAGTTCACTTACAGTGGGAGCGCTGGCTTCCCGAAGCGGCGCTCTTC 360
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 QY 1236 GGGCTGCGCGTGGAGATGAAAGGGTGGCAAGCCATTCACCCAGAGGGCTGGAACCATGTG 1355
 DB 481 GGACTGACTGTGATGCTCCCGAGAGCCAGACCATCAAGAGGCGTGTGGGCAAGCGGGGT 540
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 VERSION BM697499
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 601)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548
 COMMENT Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@iowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).
 Seq primer: M13 Reverse.
 Location/Qualifiers
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 /note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
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 tissue(s): fetal eyes. The library was constructed
 according to Bonaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pT73-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is AGATTAAGA. This library
 was created for the program, Gene Discovery in the Visual
 System, supported by National Eye Institute (NEI)."
 ORIGIN

Query Match 12.4%; Score 272.2; DB 12; Length 601;
 Best Local Similarity 67.5%; Pred. No. 2.3e-49;
 Matches 382; Conservative 0; Mismatches 184; Indels 0; Gaps 0;
 QY 816 CTGCAATGGAAGTCTTCTGAGATGCAACAGTGTGACAGAGTCTCACTGATGTTCA 875
 DB 1 CTGCAGTGGAGATGCTGAGAAAGGACCGATGACCAAAAACACTTTCAGGCAATACCGA 60
 QY 876 GTGCTGGGAAAAGTGTGTTGGGAGATATGTGCGCTTCAGGTGAAAACACTGGAG 935
 DB 61 GTCTGGGCAAAAGTGTGTTGGGAGTGTGCGCTTCAGGTGCGGCAAGTGAAG 120
 QY 936 ATGTATGCTGTAAAGAACTGGAACAAGACGCTGGAAGAAAGTGGCAGAAATG 995
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 QY 996 GCTCTCTGGAAGAAAGTGTGGAAGAGTGAAGAGCCCTTTCATTTCTCTGCGCC 1055
 DB 181 GCGCTGAAGGAAAGGATCTTGAAGAAAGTGAAGAGTGTGATGATGAGCTTGGCC 240
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 DB 301 CTCAAGTTCACATCTTCAACTGCTGGCAGCGTGGCTGGAATGAGCGGATCTTT 360
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 DB 421 GACCTGAAAGCCGAGAAACATCTTGATGATGACACGCGCAATCCGATCTCTGACTG 480
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 DB 541 TACATGCTCTCTGAGAT 557
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 VERSION B0061150.1 GI:19884936
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1017)
 AUTHORS NIH-MGC http://img.ncbi.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Lou Staudt
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
 http://image.jnl.gov
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 High quality sequence strop: 697.
 Location/Qualifiers

ORIGIN

source

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```

ORIGIN

```

Query Match      12.4%; Score 272.2; DB 13; Length 1017;
Best Local Similarity 58.8%; Pred. No. 2.6e-49;
Matches 526; Conservative 0; Mismatches 359; Indels 9; Gaps 3;

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QY 1711 ACCCTCAATGCTTTATGCGAAAGACATGCTGAATGATTTCTCTGAGGTTGGG 1770

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DB 775 GGGTGAATTTGACCAACAGACAGACACTTCTACTTCAAGTCTTCCAGGGCTGTGCT 834
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RESULT 15
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KINASE GRK5 (HUMAN);, mRNA sequence.
A1934968
A1934968.1 GI:5673838
EST.
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 815)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-remail.nih.gov
This clone is available royalty-free through LINT; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Location/Qualifiers
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/lab_host="DH10B"
/clone_id="Soares_NRL_T-GBC_S1"
/note="Organ: pooled; Vector: pT73D-Pac (pharmacia) with
a modified polyLinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBH19W, testis NHT, and B-cell
NCI CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687223,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."

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ORIGIN

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Query Match      12.3%; Score 270.6; DB 9; Length 815;
Best Local Similarity 62.3%; Pred. No. 5.7e-49;
Matches 439; Conservative 0; Mismatches 263; Indels 3; Gaps 1;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 13:15:49 ; Search time 114.544 Seconds

(Without alignments)
10648.983 Million cell updates/sec

Title: US-10-044-205A-1

Perfect score: 2198
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1657.2	75.4	1662	4	US-09-964-469-1
5	1046.8	47.6	1062	4	US-09-802-117-3
6	867.4	39.5	36651	4	US-09-738-894A-3
7	867.4	39.5	36651	4	US-09-964-469-3
8	419.8	19.1	2848	3	US-08-464-954A-2
9	418.2	19.0	2204	1	US-08-221-817-12
10	418.2	19.0	2204	1	US-08-454-439-12
11	418.2	19.0	2204	5	PCT-US94-10487-12
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26	311.6	14.2	1975	4	US-09-614-748A-9
27	253.2	11.5	1305	4	US-09-614-748A-12

28	251.6	11.4	1420	4	US-09-614-748A-11	Sequence 11, Appl
29	130.8	6.0	2067	4	US-09-016-434-1306	Sequence 1306, Ap
30	127.6	5.8	2362	4	US-09-620-312D-273	Sequence 273, App
31	116.4	5.3	294	1	US-08-221-817-9	Sequence 9, Appl1
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35	112	5.1	1788	4	US-09-417-197-68	Sequence 68, Appl
36	110.8	5.0	1191	4	US-09-841-683-10	Sequence 10, Appl
37	110.8	5.0	1224	4	US-09-841-683-8	Sequence 8, Appl1
38	110.8	5.0	1485	4	US-09-801-876B-1	Sequence 1, Appl1
39	110.8	5.0	1485	4	US-10-254-869-1	Sequence 1, Appl1
40	110.8	5.0	1675	4	US-09-841-683-12	Sequence 12, Appl
41	110.8	5.0	2244	3	US-09-094-714A-48	Sequence 48, Appl
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ALIGNMENTS

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Sequence 5, Application US/09802117									
Patent No. 644456									
GENERAL INFORMATION:									
APPLICANT: Walke, D. Wade									
APPLICANT: Wilgowski, Nathaniel L.									
APPLICANT: Turner, C. Alexander Jr.									
TITLE OF INVENTION: No. 644456el Human G-Coupled Protein Receptor Kinases and Polymu									
FILE REFERENCE: LEX-0147-USA									
CURRENT APPLICATION NUMBER: US/09/802,117									
CURRENT FILING DATE: 2001-03-08									
PRIOR APPLICATION NUMBER: US 60/188,449									
PRIOR FILING DATE: 2000-03-10									
NUMBER OF SEQ ID NOS: 5									
SOFTWARE: FastSeq for Windows Version 4.0									
SEQ ID NO 5									
LENGTH: 2249									
TYPE: DNA									
ORGANISM: homo sapiens									
US-09-802-117-5									
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 ; Sequence 1, Application US/09802117
 ; Patent No. 6444456
 ; GENERAL INFORMATION:
 ; APPLICANT: Walke, D. Wade
 ; APPLICANT: Wiganowski, Nathaniel L.
 ; APPLICANT: Turner, C. Alexander Jr.
 ; TITLE OF INVENTION: No. 6444456 Human G-Coupled Protein Receptor Kinases and Polymuc
 ; TITLE OF INVENTION: Encoding the Same
 ; FILE REFERENCE: LEX-0147-USA
 ; CURRENT APPLICATION NUMBER: US/09/802,117
 ; PRIOR FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: US 60/188,449
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1662
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; US-09-802-117-1

Query Match 75.5%; Score 1658.4; DB 4; Length 1662;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1659; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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 QY 351 AAGCCTTCGAGCTGCGACAGCAAGAGCTGCGAGCGGCGGCTGAGCCTGCGCC 410

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Qy      1371  ATCCATATGAAAAGTGAATGTTATCTTCTGAGTGTGAGTGTGAGTGTGAGTGT 1430
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Qy      1431  ATTTATGAATGTTGTGAGACACATTCAAAGTTTACAAGGAAAAGTGTAGTAA 1490

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Db      1441  AAAGACATGCTGAATTTGATGATTTCTGTGAGGTTGCGGAGGAGTGAATTTGAT 1500
Qy      1791  GATPACAGTCTTCAAAAACCTTGGACAGAGTCTGTCTTATAGCATGGCAGAGAA 1850
Db      1501  GATPACAGTCTTCAAAAACCTTGGACAGAGTCTGTCTTATGATGGCAGAGAA 1560
Qy      1851  ATTTATGAAGGAGAGTGTGAGAACTGAATGATCCCAACAGCTTAAGGTTGTAG 1910
Db      1561  ATTTATGAAGGAGAGTGTGAGAACTGAATGATCCCAACAGCTTAAGGTTGTAG 1620
Qy      1911  GAGGTAAATTCATCAAGTGTGCGTGTGTTGTTATGTA 1952
Db      1621  GAGGTAAATTCATCAAGTGTGCGTGTGTTGTTATGTA 1662

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RESULT 3
US-09-738-894A-1
; Sequence 1, Application US/09738894A
; Patent No. 6331423
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C100636
; CURRENT APPLICATION NUMBER: US/09/738, 894A
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-09-738-894A-1

```

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Query Match      75.4%; Score 1657.2; DB 4; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1659; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      291  ATGTGAGCATGAGGAGCCCTGAGCAACCTGATGCCCAACAGCTTACCTGAGAGCCG 350
Db      1  ATGTGAGCATGAGGAGCCCTGAGCAACCTGATGCCCAACAGCTTACCTGAGAGCCG 60
Qy      351  AAGCCCTGAGCATGAGGAGCCCTGAGCAACCTGATGCCCAACAGCTTACCTGAGAG 410
Db      61  AAGCCCTGAGCATGAGGAGCCCTGAGCAACCTGATGCCCAACAGCTTACCTGAGAG 120
Qy      411  GGGCTGCGAGGCTGCGGAGAGCTCCGCGAAGAGTGTCCCTGAAGTTCACAGCTGTGT 470
Db      121  GGGCTGCGAGGCTGCGGAGAGCTCCGCGAAGAGTGTCCCTGAAGTTCACAGCTGTGT 180
Qy      471  GAGCAGAGCCCATCGGTGCGCGCTCTTCCCTGATCTTCCAGCAAGTGGCCAGCTTC 530

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Db 181 GAGCAGACGCCCATGCTGCGCCCTTCCTGCTGACCTTCAGCCAGAGTCCACGCTTC 240
 QY 531 CGCAGAGCGGCAACCTTCCTAGAGAGCGTGCAGAACTGCGAGCTGGCCGAGAGGACCC 590
 Db 241 CGCAGAGCGGCAACCTTCCTAGAGAGCGTGCAGAACTGCGAGCTGGCCGAGAGGACCC 300
 QY 591 ACCAAGACGCGCGCTGAGAGGCGCTGCGACCTGCTGCGAGTGGCCCTCCCGCGGG 650
 Db 301 ACCAAGACGCGCGCTGAGAGGCGCTGCGACCTGCTGCGAGTGGCCCTCCCGCGGG 360
 QY 651 AACCCGCAACCTTCCTGAGCCAGCGCGTGGCCACCAAGTCCCAAGAGCCACCACTGAG 710
 Db 361 AACCCGCAACCTTCCTGAGCCAGCGCGTGGCCACCAAGTCCCAAGAGCCACCACTGAG 420
 QY 711 GAAAGCGAGTGGCTGCACTGACGCTGCGCAAGGCTGAGGCCATGCTTTCTTGCAAG 770
 Db 421 GAAAGCGAGTGGCTGCACTGACGCTGCGCAAGGCTGAGGCCATGCTTTCTTGCAAG 480
 QY 771 CAGCCCTTAAAGATTTCTGACCAAGGCGCTTCGACAGAGTTCTGCAAGTGAACCTC 830
 Db 481 CAGCCCTTAAAGATTTCTGACCAAGGCGCTTCGACAGAGTTCTGCAAGTGAACCTC 540
 QY 831 TTCGAGATGCAACCAAGTGCAGACCAAGTACTTCACTGAGTTCAAGTGTCTGCGAAAGT 890
 Db 541 TTCGAGATGCAACCAAGTGCAGACCAAGTACTTCACTGAGTTCAAGTGTCTGCGAAAGT 600
 QY 891 GGTTCGAGAGTATGTCCTGCTGAGTGAACCACTGCGAAGATGTTGCTGCTGAG 950
 Db 601 GGTTCGAGAGTATGTCCTGCTGAGTGAACCACTGCGAAGATGTTGCTGCTGAG 660
 QY 951 AACCTGCAAGAAAGGCGCTGAAAGAAAGTGGCGAAGATGCTCTCTTGCAAAAG 1010
 Db 661 AACCTGCAAGAAAGGCGCTGAAAGAAAGTGGCGAAGATGCTCTCTTGCAAAAG 720
 QY 1011 GAAATCTTGAGAAAGTGCAGAGCCCTTAATGTCTCTCTGCGCTATGCTTGAAGC 1070
 Db 721 GAAATCTTGAGAAAGTGCAGAGCCCTTAATGTCTCTCTGCGCTATGCTTGAAGC 780
 QY 1071 AAGACCATCTCTGCTGCTGATGAGCTGATGATGCGGAGACCTCAAGTTCACATC 1130
 Db 781 AAGACCATCTCTGCTGCTGATGAGCTGATGATGCGGAGACCTCAAGTTCACATC 840
 QY 1131 TACAACGTGGCAACGCGTGGCTGCAATGAGCGGAGTATCTTTTCTGCGCCAGATA 1190
 Db 841 TACAACGTGGCAACGCGTGGCTGCAATGAGCGGAGTATCTTTTCTGCGCCAGATA 900
 QY 1191 GCTGTGGAGATGCTGACCTGCAATCACTGCGCATGCTATGCGGACATGAAGCTGAG 1250
 Db 901 GCTGTGGAGATGCTGACCTGCAATCACTGCGCATGCTATGCGGACATGAAGCTGAG 960
 QY 1251 AATGTCTTCTGATGACCTGCGCACTGCGAGTATCTGACCTTGGGGCTGGCGCTGAG 1310
 Db 961 AATGTCTTCTGATGACCTGCGCACTGCGAGTATCTGACCTTGGGGCTGGCGCTGAG 1020
 QY 1311 ATGAAGGTGGAGGCCATCAACCAAGAGGCTGGAACCAATGTTACATGCTCTGAG 1370
 Db 1021 ATGAAGGTGGAGGCCATCAACCAAGAGGCTGGAACCAATGTTACATGCTCTGAG 1080
 QY 1371 ATCTTAATGAAAAGGTATATCTTCTATCTGCTGAGCTGTTTGCATGGAGTCAAC 1430
 Db 1081 ATCTTAATGAAAAGGTATATCTTCTATCTGCTGAGCTGTTTGCATGGAGTCAAC 1140
 QY 1431 ATTTATGAATGTGCTGAGAGACCACTTCAAGATTTACAAAGAAAAGTCAATAA 1490
 Db 1141 ATTTATGAATGTGCTGAGAGACCACTTCAAGATTTACAAAGAAAAGTCAATAA 1200
 QY 1491 GAGGATCGAAGCAAGCACTGCAAGCAAGGCTCAAAATTCAGCATGATTAATTCA 1550
 Db 1201 GAGGATCGAAGCAAGCACTGCAAGCAAGGCTCAAAATTCAGCATGATTAATTCA 1260
 QY 1551 GAGGAGCAAAAGATTTGAGGCTCTTCTTGCTAAGAAACAGAGCAACGCTTAGA 1610
 Db 1261 GAGGAGCAAAAGATTTGAGGCTCTTCTTGCTAAGAAACAGAGCAACGCTTAGA 1320

QY 1611 AGCAGAAAAGTCTATGATCCAGAAAACATCATTTCTTTAAACGATCAACTTCT 1670
 Db 1321 AGCAGAAAAGTCTATGATCCAGAAAACATCATTTCTTTAAACGATCAACTTCT 1380
 QY 1671 CGCTGGAAGCTGCGCTAATTAACCCCATTTGTGCGACACCTTCAAGTGTATGCC 1730
 Db 1381 CGCTGGAAGCTGCGCTAATTAACCCCATTTGTGCGACACCTTCAAGTGTATGCC 1440
 QY 1731 AAGGACATGCTGAATATGATATTTCTGAGGTTGCGGGGCTGAATTTGATGACAA 1790
 Db 1441 AAGGACATGCTGAATATGATATTTCTGAGGTTGCGGGGCTGAATTTGATGACAA 1500
 QY 1791 GATTAAGTCTTCAAAAACCTTTCGACAGTGTCTGTTCTATAGATGCGAGAAAG 1850
 Db 1501 GATTAAGTCTTCAAAAACCTTTCGACAGTGTCTGTTCTATAGATGCGAGAAAG 1560
 QY 1851 ATTATGAAGCGGACGCTTTGAGAACTGAATGACCCCAAGACCTACGGGTGAG 1910
 Db 1561 ATTATGAAGCGGACGCTTTGAGAACTGAATGACCCCAAGACCTACGGGTGAG 1620
 QY 1911 GAGGTAAATCAATCCAGTCTGCGGTGTTGTTATTTGA 1952
 Db 1621 GAGGTAAATCAATCCAGTCTGCGGTGTTGTTATTTGA 1662

RESULT 4
 US-09-964-469-1
 ; Sequence 1, Application US/09964469
 ; Patent No. 6579709
 ; GENERAL INFORMATION:
 ; APPLICANT: GUEGLER, Karl et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: C1000636D1V
 ; CURRENT APPLICATION NUMBER: US/09/964,469
 ; PRIOR FILING DATE: 2001-09-28
 ; PRIOR APPLICATION NUMBER: 60/208,331
 ; PRIOR FILING DATE: 2000-06-01
 ; PRIOR APPLICATION NUMBER: 09/738,894
 ; PRIOR FILING DATE: 2000-12-18
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 1662
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-964-469-1

Query Match 75.4%; Score 1657.2; DB 4; Length 1662;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1659; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 291 ATGTGAGCATGCGGCGCTTGAACACTGATGCGCAACCGCTTACTGAGGCCCGG 350
 Db 1 ATGTGAGCATGCGGCGCTTGAACACTGATGCGCAACCGCTTACTGAGGCCCGG 60
 QY 351 AAGCCCTGCGACCTGCGACAGCAAGAGCTGACGCGGCGGCTGAACCTTCAAGCTGAG 410
 Db 61 AAGCCCTGCGACCTGCGACAGCAAGAGCTGACGCGGCGGCTGAACCTTCAAGCTGAG 120
 QY 411 GGGCTGAGGGGCTGCGAGCTCGCGCAAGAGCTGCTCTGAACCTTCAAGCTGAGT 470
 Db 121 GGGCTGAGGGGCTGCGAGCTCGCGCAAGAGCTGCTCTGAACCTTCAAGCTGAGT 180
 QY 471 GAGCAGAGCCCATGCGTGGCTGCTTCTGCTGACCTTCAAGCAAGTGCACAGTTC 530
 Db 181 GAGCAGAGCCCATGCGTGGCTGCTTCTGCTGACCTTCAAGCAAGTGCACAGTTC 240
 QY 531 CGCAGAGCGGCAACCTTCTAGAGAGCGTGCAGAACTGCGAGCTGGCCGAGAGGACCC 590
 Db 241 CGCAGAGCGGCAACCTTCTAGAGAGCGTGCAGAACTGCGAGCTGGCCGAGAGGACCC 300

QY 591 ACCAAGACAGGCGCTGCAAGGAGCTGTGCTCACTTGTGCAAGTGCCTTGCCTGCGG 650
 Db 301 ACCAAGACAGGCGCTGCAAGGAGCTGTGCTCACTTGTGCAAGTGCCTTGCCTGCGG 360
 QY 651 AACCGCAACCTTCTCAGCAGGCGGCGCAACCAAGTGCAGGCGCACCACATGAG 710
 Db 361 AACCGCAACCTTCTCAGCAGGCGGCGCAACCAAGTGCAGGCGCACCACATGAG 420
 QY 711 GAAGACGAGTGTGCTGCAAGTGCAGTGCAGGCGCTGAGGCGCTTCTTTCAGAG 770
 Db 421 GAAGACGAGTGTGCTGCAAGTGCAGTGCAGGCGCTGAGGCGCTTCTTTCAGAG 480
 QY 771 CAGCCTTTAAAGATTTCTGACAGGCGCTTCTTACGACAAATTTCTGCAAGTGC 830
 Db 481 CAGCCTTTAAAGATTTCTGACAGGCGCTTCTTACGACAAATTTCTGCAAGTGC 540
 QY 831 TTGAGATGCAACCAAGTGCAGCAAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 890
 Db 541 TTGAGATGCAACCAAGTGCAGCAAGTGCAGTGCAGTGCAGTGCAGTGCAGTGC 600
 QY 891 GGTGTTGAGGAGTATGTCCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 950
 Db 601 GGTGTTGAGGAGTATGTCCTGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 660
 QY 951 AAACCTGCAAGAAAGCGGCTGAAGAAAGTGCAGAGATGCTCTTTCAGAAAG 1010
 Db 661 AAACCTGCAAGAAAGCGGCTGAAGAAAGTGCAGAGATGCTCTTTCAGAAAG 720
 QY 1011 GAAATCTTGAAGAGTCAAGCAGCCTTCTCACTTGTCTGCTGCTGCTGCTGAGC 1070
 Db 721 GAAATCTTGAAGAGTCAAGCAGCCTTCTCACTTGTCTGCTGCTGCTGAGC 780
 QY 1071 AAGACCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1130
 Db 781 AAGACCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 QY 1131 TACACGTTGAGCAGGCTGCTGCACTGCACTGCACTGCACTGCACTGCACTGCA 1190
 Db 841 TACACGTTGAGCAGGCTGCTGCACTGCACTGCACTGCACTGCACTGCACTGCA 900
 QY 1191 GCTGTGAGGATGCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 1250
 Db 901 GCTGTGAGGATGCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 960
 QY 1251 AATGTCTTGTGATGACTGCGCACTGCACTGCACTGCACTGCACTGCACTGCACT 1310
 Db 961 AATGTCTTGTGATGACTGCGCACTGCACTGCACTGCACTGCACTGCACTGCACT 1020
 QY 1311 ATGAAGGTGCAAGCCCATCAACCAAGGCTGCAACCAATGCTTCACTGCTCTGAG 1370
 Db 1021 ATGAAGGTGCAAGCCCATCAACCAAGGCTGCAACCAATGCTTCACTGCTCTGAG 1080
 QY 1371 ATCTAATGCAAAAGTATGTTATCTATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1430
 Db 1081 ATCTAATGCAAAAGTATGTTATCTATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 QY 1431 ATTTATGAAATGCTGCTGCAAGCACTTCAAAAGTATCAAGAAAGTCACTGTA 1490
 Db 1141 ATTTATGAAATGCTGCTGCAAGCACTTCAAAAGTATCAAGAAAGTCACTGTA 1200
 QY 1491 GAGATCTGAAGCAAGAACTTGAAGCAAGTGCAGTGCAGTGCAGTGCAGTGCAG 1550
 Db 1201 GAGATCTGAAGCAAGAACTTGAAGCAAGTGCAGTGCAGTGCAGTGCAGTGCAG 1260
 QY 1551 GAGAGCAAAAGATTTTGAAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1610
 Db 1261 GAGAGCAAAAGATTTTGAAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
 QY 1611 AGCAGAGAAAGTCTGATGATCCAGAGAACTATCTTCTTAAAGATCACTTCTCT 1670
 Db 1321 AGCAGAGAAAGTCTGATGATCCAGAGAACTATCTTCTTAAAGATCACTTCTCT 1380

QY 1671 GCCTGGAAGCTGACCTATTTGAACCCCATTTGTGCAAGCCCTTCACTGATTTATGCC 1730
 Db 1381 GCCTGGAAGCTGACCTATTTGAACCCCATTTGTGCAAGCCCTTCACTGATTTATGCC 1440
 QY 1731 AAAGACATGCTGAAATTTGATTTCTGAGGTTGCGGAGGTTGGAATTTGATGACAAA 1790
 Db 1441 AAAGACATGCTGAAATTTGATTTCTGAGGTTGCGGAGGTTGGAATTTGATGACAAA 1500
 QY 1791 GATAGCAATTTCTTCAAAAATTTTGGACAGGTTGCTGCTTCTATACATGCGAGAGAA 1850
 Db 1501 GATAGCAATTTCTTCAAAAATTTTGGACAGGTTGCTGCTTCTATACATGCGAGAGAA 1560
 QY 1851 ATTATGAAACGAGACTGTTTGAAGAACTGATGACCCCAAGACCTTACGAGGTTGAG 1910
 Db 1561 ATTATGAAACGAGACTGTTTGAAGAACTGATGATGACCCCAAGACCTTACGAGGTTGAG 1620
 QY 1911 GAGGTATTTATTCAGACTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1952
 Db 1621 GAGGTATTTATTCAGACTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1662

RESULT 5
 US-09-802-117-3
 ; Sequence 3, Application US/09802117
 ; Patent No. 644456
 ; GENERAL INFORMATION:
 ; APPLICANT: Walke, D. Wade
 ; APPLICANT: Milgromski, Nathaniel L.
 ; APPLICANT: Turner, C. Alexander Jr.
 ; TITLE OF INVENTION: No. 644456 Human G-Coupled Protein Receptor Kinases and Polymu
 ; FILE REFERENCE: LEX-0147-USA
 ; CURRENT FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: US 60/188,449
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 1062
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; US-09-802-117-3

Query Match 47.6%; Score 1046.8; DB 4; Length 1062;
 Best Local Similarity 99.8%; Pred. No. 2.7e-248;
 Matches 1046; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 291 ATGTGGAATGAGGAGGCTGCAAACTGATGCGCAACCGCTTACCTGCAAGGCGCG 350
 Db 1 ATGTGGAATGAGGAGGCTGCAAACTGATGCGCAACCGCTTACCTGCAAGGCGCG 60
 QY 351 AAGCCTTGAAGTGCAGACAGCAAAAGCTGCAAGGCGGCGGCTGAGCTTGCCTGCGC 410
 Db 61 AAGCCTTGAAGTGCAGACAGCAAAAGCTGCAAGGCGGCGGCTGAGCTTGCCTGCGC 120
 QY 411 GGGCTGAGGAGTGCAGGAGCTCGGCAAGCTGCTGAACTGCTGCTGCTGCTGCTGCT 470
 Db 121 GGGCTGAGGAGTGCAGGAGCTCGGCAAGCTGCTGAACTGCTGCTGCTGCTGCTGCT 180
 QY 471 GAGACAGACCCATGCTGCGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 530
 Db 181 GAGACAGACCCATGCTGCGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
 QY 531 CGAAGGCGCAACTTCTTGAAGACTGCAAACTGCAAGCTGCGCGAGGAGGAGCC 590
 Db 241 CGAAGGCGCAACTTCTTGAAGACTGCAAACTGCAAGCTGCGCGAGGAGGAGCC 300
 QY 591 ACCAAGACAGGCGCTGCAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 650
 Db 301 ACCAAGACAGGCGCTGCAAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 QY 651 AACCGCAACCTTCTCAGCAGGCGGCGCAACCAAGTGCAGGCGCACCACATGAG 710

Db 361 AACCGACACCTTCTCTGACGACGCGTGGCCACCAAGTCCAGACCACTGAG 420
 Qy 711 GAAGAGCAGTGTGCTGACGACGCTGCGACGCTGAGGCGCTTCTTGGCAAG 770
 Db 421 GAAGAGCAGTGTGCTGACGCTGCGACGCTGAGGCGCTTCTTGGCAAG 480
 Qy 771 CAGCCCTTAAAGATTTGTGACGAGGCTTCTTAAAGATTTGTGACGAGTTC 830
 Db 481 CAGCCCTTAAAGATTTGTGACGAGGCTTCTTAAAGATTTGTGACGAGTTC 540
 Qy 831 TTGAGATGACCAACGAGTGCAGACAGTCTTCACTGAGTTCAGAGTGGGAAAAGT 890
 Db 541 TTGAGATGACCAACGAGTGCAGACAGTCTTCACTGAGTTCAGAGTGGGAAAAGT 600
 Qy 891 GGTTCGAGGAGTATGTCCTCCAGGTGAAAAACATCGAGAGATGATGCTGTAG 950
 Db 601 GGTTCGAGGAGTATGTCCTCCAGGTGAAAAACATCGAGAGATGATGCTGTAG 660
 Qy 951 AAACGTGACAAAGAGGCTGAAAGAAAGGTGGGAGAGATGCTTCTTGGAAAAG 1010
 Db 661 AAACGTGACAAAGAGGCTGAAAGAAAGGTGGGAGAGATGCTTCTTGGAAAAG 720
 Qy 1011 GAAATCTTGAAGAGGTGACGAGCCCTTCACTGCTCTGAGCTATGCTTGAAGC 1070
 Db 721 GAAATCTTGAAGAGGTGACGAGCCCTTCACTGCTCTGAGCTATGCTTGAAGC 780
 Qy 1071 AAGACCATCTCTGCTCTGATGAGCTGATGATGAGGAGACCTGAACTTCACTC 1130
 Db 781 AAGACCATCTCTGCTCTGATGAGCTGATGATGAGGAGACCTGAACTTCACTC 840
 Qy 1131 TACACGTGGGACAGGCTGCTGACATGACCGGGGTATCTTTTACCTGCGCCAGATA 1190
 Db 841 TACACGTGGGACAGGCTGCTGACATGACCGGGGTATCTTTTACCTGCGCCAGATA 900
 Qy 1191 GCCTGGGATGCTGACCTCCATGATGATGATGATGATGATGATGATGATGATG 1250
 Db 901 GCCTGGGATGCTGACCTCCATGATGATGATGATGATGATGATGATGATGATG 960
 Qy 1251 AATGCTCTTGTGATGACCTGCGCACTGCAAGTTATCTGACCTGGGCTGGCGTGA 1310
 Db 961 AATGCTCTTGTGATGACCTGCGCACTGCAAGTTATCTGACCTGGGCTGGCGTGA 1020
 Qy 1311 ATGAGGGTGGCAAGCCCATCACCAAGG 1340
 Db 1021 ATGAGGGTGGCAAGCCCATCACCAAGG 1050

RESULT 6
 US-09-738-894A-3
 ; Sequence 3, Application US/09738894A
 ; Patent No. 6331423
 ; GENERAL INFORMATION:
 ; APPLICANT: GUEGLER, Karl et al
 ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
 ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 ; FILE REFERENCE: CL000636
 ; CURRENT APPLICATION NUMBER: US/09/738,894A
 ; CURRENT FILING DATE: 2000-12-18
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 36651
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(36651)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-738-894A-3

Query Match 39.5%, Score 867.4, DB 4, Length 36651,

Best Local Similarity 95.1%, Pred. No. 1.8e-203;
 Matches 895; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 1 GACCTTAAGATGAAGGACCTCACTATAGGCTGAGCGCGCCCGGCGAGTGTTC 60
 Db 1786 GACCTTAAGATGAAGGACCTCACTATAGGCTGAGCGCGCGCGGCGAGTGTTC 1845
 Qy 61 GCCTTGAGGAGGAGCATGACCTATGCTGAGTTCCTGGCGGAGTATATAGCA 120
 Db 1846 GCCTTGAGGAGGAGCATGACCTATGCTGAGTTCCTGGCGGAGTATATAGCA 1905
 Qy 121 GTCAAGCTTCTTAAGAAAGAAACCTTTTCAACCTTCACCGGCTCCACAGGCT 180
 Db 1906 GTCAAGCTTCTTAAGAAAGAAACCTTTTCAACCTTCACCGGCTCCACAGGCT 1965
 Qy 181 ACAGACTACCTGTAATTCCTTGAACCTTTCACCGGCTCCACAGGCTCCACAG 240
 Db 1966 ACAGACTACCTGTAATTCCTTGAACCTTTCACCGGCTCCACAGGCTCCACAG 2025
 Qy 241 GCCCTCAGCCCTCTTGTGCTTCCCTGAGAGTCCGCGCTCCAGCATGCTGACA 300
 Db 2026 GCCCTCAGCCCTCTTGTGCTTCCCTGAGAGTCCGCGCTCCAGCATGCTGACA 2085
 Qy 301 TGCGGAGCTTGAACAACCTGATGCAACACCGCTTACCTGAGGCTCCGAAAG 360
 Db 2086 TGCGGAGCTTGAACAACCTGATGCAACACCGCTTACCTGAGGCTCCGAAAG 2145
 Qy 361 ACTGCGACGCAAAAGAGTGCAGGCGGCGGCGGAGCTGAGCTGCGCGGCTGAG 420
 Db 2146 ACTGCGACGCAAAAGAGTGCAGGCGGCGGCGGAGCTGAGCTGCGCGGCTGAG 2205
 Qy 421 GCTGCGGAGAGTCCGCGCAAGAGCTGCTCCGAACTTCAACAGCTGTGAGAGAG 480
 Db 2206 GCTGCGGAGAGTCCGCGCAAGAGCTGCTCCGAACTTCAACAGCTGTGAGAGAG 2265
 Qy 481 CCATGCGTGCCTGCTTCCGTAATTCCTTGAACCTTCAACAGCTGTGAGAGAG 540
 Db 2266 CCATGCGTGCCTGCTTCCGTAATTCCTTGAACCTTCAACAGCTGTGAGAGAG 2325
 Qy 541 CAACCTTCTTAAGAGAGCTGCAAGAGCTGAGGAGCTGAGGAGGAGGAGGAG 600
 Db 2326 CAACCTTCTTAAGAGAGCTGCAAGAGCTGAGGAGCTGAGGAGGAGGAGGAG 2385
 Qy 601 GCGGCTGACAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAG 660
 Db 2386 GCGGCTGACAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAG 2445
 Qy 661 CTTCTCAGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAG 720
 Db 2446 CTTCTCAGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAG 2505
 Qy 721 TGGCTGAGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAG 780
 Db 2506 TGGCTGAGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAG 2565
 Qy 781 AGATTTGTGACAGGAGCTTCTTCAAGCAAGTTCTGCACTGAGGAGGAGTTC 840
 Db 2566 AGATTTGTGACAGGAGCTTCTTCAAGCAAGTTCTGCACTGAGGAGGAGTTC 2625
 Qy 841 AACCAAGTGTGACAGGAGCTTCTTCAAGCAAGTTCTGCACTGAGGAGGAGTTC 900
 Db 2626 AACCAAGTGTGACAGGAGCTTCTTCAAGCAAGTTCTGCACTGAGGAGGAGTTC 2685
 Qy 901 AGTATGAGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 941
 Db 2686 AGTATGAGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2726

RESULT 7
 US-09-964-469-3
 ; Sequence 3, Application US/09964469
 ; Patent No. 6579709
 ; GENERAL INFORMATION:

/ APPLICANT: GUEGLER, Karl et al
 / TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEIN, NUCLEIC
 / TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
 / FILE REFERENCE: THEREOF
 / CURRENT APPLICATION NUMBER: US/09/964,469
 / PRIOR FILING DATE: 2001-09-28
 / PRIOR APPLICATION NUMBER: 60/208,331
 / PRIOR FILING DATE: 2000-06-01
 / PRIOR APPLICATION NUMBER: 09/738,894
 / NUMBER OF SEQ ID NOS: 4
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 3
 / LENGTH: 36651
 / TYPE: DNA
 / ORGANISM: Human
 / FEATURE:
 / NAME/KEY: misc feature
 / LOCATION: (1)..(36651)
 / OTHER INFORMATION: n = A,T,C or G
 / US-09-964-469-3

Query Match 39.5%; Score 867.4; DB 4; Length 36651;

Best Local Similarity 95.1%; Pred. No. 1.0e-203;

Matches 895; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Db 1 GACCTTAATGAAAGGAACTTCACTATAGGCTCGAGAGGCGCCGCGAGGTCTTTC 60
 Qy 1786 GACCTTAATGAAAGGAACTTCACTATAGGCTCGAGAGGCGCCGCGAGGTCTTTC 1845
 Db 61 GCTTTGGAGAGTGGAGCATCTATCTGTGTGAGTCTTCTGCGGCTATATACATAGCA 120
 Qy 1846 GCTTTGGAGAGTGGAGCATCTATCTGTGTGAGTCTTCTGCGGCTATATACATAGCA 1905
 Db 121 GTCAAGCTTCTTACAAAAGAACTCTTTCACACCTTCACAGGCTTCACCCCAAGGCC 180
 Qy 1906 GTCAAGCTTCTTACAAAAGAACTCTTTCACACCTTCACAGGCTTCACCCCAAGGCC 1965
 Db 181 ACAAGACTCACTGTAAATCCCTTGAAGTGTCTCAACCGGGAAGGAAAGACGACGACA 240
 Qy 1966 ACAAGACTCACTGTAAATCCCTTGAAGTGTCTCAACCGGGAAGGAAAGACGACGACA 2025
 Db 241 GGCCTCCAGGCTCTTGTGCTTTCCCTGGAGTGGCGCCGCTGCTACGCTATGTGAGCA 300
 Qy 2026 GGCCTCCAGGCTCTTGTGCTTTCCCTGGAGTGGCGCCGCTGCTACGCTATGTGAGCA 2085
 Db 301 TGGGAGGCTCTGACAACTGATCGCAACACGCTTACCTGAGGCGCCGGAAGCCCTCGG 360
 Qy 2086 TGGGAGGCTCTGACAACTGATCGCAACACGCTTACCTGAGGCGCCGGAAGCCCTCGG 2145
 Db 361 ACTGCGACAGCAAAAGAGCTGACGCGGCGGCGTGAAGCTTGCCTGCGCGGCTGAGG 420
 Qy 2146 ACTGCGACAGCAAAAGAGCTGACGCGGCGGCGGCGTGAAGCTTGCCTGCGCGGCTGAGG 2205
 Db 421 GCTGCGGAGAGCTCGCGCAAGAGTGTCTTCAACAGCTCTGTGTGAGCAGCAGC 480
 Qy 2206 GCTGCGGAGAGCTCGCGCAAGAGTGTCTTCAACAGCTCTGTGTGAGCAGCAGC 2265
 Db 481 CCATCGGTGCGCGCTCTTCCGTGATCTTCTGTGCAACAGTGGCCCAAGTTCGCGCAAGCGG 540
 Qy 2266 CCATCGGTGCGCGCTCTTCCGTGATCTTCTGTGCAACAGTGGCCCAAGTTCGCGCAAGCGG 2325
 Db 541 CAACCTTCTTGAAGAGCTGCAAGACTGAGAGCTGAGCGAGGAGGAGCCCAACCAAGACA 600
 Qy 2326 CAACCTTCTTGAAGAGCTGCAAGACTGAGAGCTGAGCGAGGAGGAGCCCAACCAAGACA 2385
 Db 601 GCGGCTGCGAGGAGCTGTGTGCACTTGTGCAAGTGTGCTGCTGCGGAGGAAACCGGCAAC 660
 Qy 2386 GCGGCTGCGAGGAGCTGTGTGCACTTGTGCAAGTGTGCTGCTGCGGAGGAAACCGGCAAC 2445
 Db 661 CCTTCTCAAGCAGGCTGTGCGCAACAGTGTGCAAGCAGCAACCTGTGAGGAAAGAGGAG 720

Db 2446 CCTTCTCAAGCAGGCTGTGCGCAACAGTGTGCAAGCAGCAACCTGTGAGGAAAGAGGAG 2505
 Qy 721 TGGCTGAGTGAAGCTGTGCGCAAGCTGAGGCTTCTTGTGCAAGCAGGCTTTA 780
 Db 2506 TGGCTGAGTGAAGCTGTGCGCAAGCTGAGGCTTCTTGTGCAAGCAGGCTTTA 2565
 Qy 781 AGATTTCTGACAGGAGCTTCTTACAGCAAGTTCCTGAGTGAAGCTTCTGAGAGTGC 840
 Db 2566 AGATTTCTGACAGGAGCTTCTTACAGCAAGTTCCTGAGTGAAGCTTCTGAGAGTGC 2625
 Qy 841 AACAGTGTCAAGCAAGTCTTCACTGAGTTCAGAGTGTGCGGAAAGGTGTGTTGCGG 900
 Db 2626 AACAGTGTCAAGCAAGTCTTCACTGAGTTCAGAGTGTGCGGAAAGGTGTGTTGCGG 2685
 Qy 901 AGTATGTGCTTCCAGGTGAAAAACCTGCGGAAGTGT 941
 Db 2686 AGTATGTGCTTCCAGGTGAAAAACCTGCGGAAGTGT 2726

RESULT 8

US-08-464-954A-2

/ Sequence 2, Application US/08464954A

/ Patent No. 6255069

/ GENERAL INFORMATION:

/ APPLICANT: BENOVIC, JEFFREY L.; GOMEZ, JORGE; KUNAPULI,

/ APPLICANT: PRIYA

/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

/ TITLE OF INVENTION: MODULATING THE ACTIVITY OF G PROTEIN-COUPLED RECEPTOR

/ NUMBER OF SEQUENCES: 12

/ CORRESPONDENCE ADDRESS:

/ ADDRESSER: Jane Massey Licata, Esq.

/ STREET: Woodland Falls Corporate Park

/ STREET: 210 Lake Drive East, Suite 201

/ CITY: Query Hill

/ STATE: NJ

/ COUNTRY: USA

/ ZIP: 08002

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE

/ OPERATING SYSTEM: PC-DOS

/ SOFTWARE: WORDPERFECT 5.1

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/464,954A

/ FILING DATE: Herewith

/ CLASSIFICATION: 435

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: 08/076,084

/ FILING DATE: June 11, 1993

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Jane Massey Licata

/ REGISTRATION NUMBER: 32,257

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (609) 779-2400

/ TELEFAX: (609) 779-8488

/ INFORMATION FOR SEQ ID NO: 2:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 2848

/ TYPE: NUCLEIC ACID

/ STRANDEDNESS: SINGLE

/ TOPOLOGY: LINEAR

/ ANTI-SENSE: NO

/ US-08-464-954A-2

Query Match 19.1%; Score 419.8; DB 3; Length 2848;

Best Local Similarity 56.2%; Pred. No. 1.1e-93;

Matches 891; Conservative 0; Mismatches 682; Indels 12; Gaps 5;

Qy 305 GGCCTTGAACAACCTGATGCAACACCGCTTACCTGAGGCGCGGAAGCCCTCGAGCTG 364
 Db 65 GGAGCTGGAACATCTGTAGGAAACGAGTGTACTCAAGGCTCCGGAAGGTGCGGTGG 124

QY 365 CGACAGCAAG--AGCTCAGCGCGCGCGCTAGCCTGACCTCCCTGCGCGCTGCAAGG 421
 Db 125 AAATCGCAAGGCAAGCAAGAAATGCGCGAGATGCTCAAGTTCCCTCAGCATCAGCA 184
 QY 422 CTGGCGGAGACTCCGCGCAAGAGCTGCTCCCTGAATTCCACAGCTGTGTGACAGCAGCC 481
 Db 185 GTGCAAGAGCTCGGCTCAGCTCAGCTGACGTATACAGCTGTGTGAGAGCGCAAGC 244
 QY 482 CATCGTGTGCGGCTCTTCTGCTGACCTTCTGACCAAGTGTCCAGCTTCCGCAAGCGCC 541
 Db 245 CATGGGCGCTGCTCTTCTGCTGAGATTCTGTGCAAGAGCGCGAGCTGAGCGCTGTGCT 304
 QY 542 AACCTTCTGAGAGAGTGTGCAAGAACTGTGAGCTGTGCGCAAGAGAGCAACCAAGAGAG 601
 Db 305 CGCTCTCTGAGATGAGGAGTGTGCGAGTATGAGAGTATGAGAGTATGAGAGAGAGAG 364
 QY 602 CGCGCTGAGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 661
 Db 365 TGAGCGGAGAG--TAAAGAGATTTTCTGAGAGCAAGAGTCTGAGCTGAGCTGAGCTG 421
 QY 662 CTTCCTGAGCG 721
 Db 422 GGTCCCGCGAGTGTGTGAGCAAC-TGCAAGCGCGCTGAGCAAGAGTCTGCTGCAAG 480
 QY 722 GGTCTGAGTACGCTGCGAGAGCTGAGGCTGAGGCTTCTTGTGCAAGAGAGCTTGA 781
 Db 481 ACCCTTTCAGAGAACTACCGCGCTGA--CCAGAGTACCTGAGCGCTGCTGCTGCTGCT 538
 QY 782 GATTTTGTGAGAGCGCTTCTAGCAAGATTTCTGAGAGTGTGAGAACTTCTGAGAGTGA 841
 Db 539 CGACTACTGAGAGATCTTCTTCAACCTTCTGAGAGTGTGAGAGTGTGAGAGTGTGAG 598
 QY 842 ACCAGTCTGAGAGAGTCTTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 901
 Db 599 GCGAGTACCAAAACACCTTCAGAGCAATACAGAGTCTGAGCAAGAGTGTGAGTGTGAG 658
 QY 902 GGTATGTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 961
 Db 659 GGTGTGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 718
 QY 962 GAAGCGGCTGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1021
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 QY 1022 GAAGTGTGAG 1081
 Db 779 GAAGTGTGAG 838
 QY 1082 CTGCTGTGATGAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1141
 Db 839 GTGCTGTGATGAGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 898
 QY 1142 CAGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1201
 Db 899 CAGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 958
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 QY 1322 CAGGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1381
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 QY 1382 AAGGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1441
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QY 1442 GGTGCTGAG 1501
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 QY 1502 GCAAG 1561
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 Db 1376 TGCGCGAG 1435
 QY 1682 TGCGCTATGAG 1741
 Db 1436 TGCGATGCTGAG 1495
 QY 1742 TGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1801
 Db 1496 GATGATGAG 1555
 QY 1802 CTTCAG 1861
 Db 1556 CTACAG 1615
 QY 1862 GAGAGCTTTGAG 1886
 Db 1616 CGAGTCTTCAG 1640

RESULT 9

US-08-221-817-12
 ; Sequence 12, Application US/08221817
 ; Patent No. 5532151
 ; GENERAL INFORMATION:
 ; APPLICANT: Chantry, David
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Hoeksma, Merle F.
 ; TITLE OF INVENTION: A No. 5532151el G Protein-Coupled Receptor
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/221,817
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/123,932
 ; FILING DATE: 17 SEP 1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5532151and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 31981
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
 LENGTH: 2204 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 31..1758
 US-08-221-817-12

Query Match 19.0%; Score 418.2; DB 1; Length 2204;
 Best Local Similarity 56.2%; Pred. No. 2.5e-93;
 Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;

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QY 305 GGCCTTGACAACTGATGCGCAAGCCGCTACGACGCGCCGGAAGCCCTCGACATG 364
DB 33 GGAGCTCGAGAAACATGCTAGCGAACAAGTGTCTACTACAGCCCGGAAGAGTGGCGTGG 92
QY 365 CGACAGCAAG--AGCTGAGCGCGCGCGCGCTAGCCCTGCGCCCGCGCGCTGAGAG 421
DB 93 AATGCGCAAGCGCAAGCAAGAAATGCGCGAGATGCTCCAGTTCCTCATCAGCA 152
QY 422 CTGCGGAGGCTCGCGCAAGAGCTGCTCCGTAACCTTCCACAGCTGTGTGAGAGAGCC 481
DB 153 GTGCGAAGAGCTGCGGCTGAGCGCTGAGCGCTGATCAAGCTGTGCGAGCGGACCG 212
QY 482 CATGCGTCCGCGCTCTTCCGTAACCTTCCAGCAAGTCCCAAGTTCGCGAAGCGCGC 541
DB 213 CATGCGGCGCTGCTGCTGCGAGAGTCTGTGCGCAAGAGCGCGAGCTGAGCGCGCTG 272
QY 542 AACCTTCTAGAGAGCTGCAAGATGAGAGCTGCGCGAGCGCGAGAGAGAGCAAGAGAG 601
DB 273 GCGCTTCTGAGTGGAGTGGCGCGAGTATGAGAGTCCCGAGTACAAAGCGAGAGCATG 332
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DB 333 TGGGCGGCAAG--TACGCGAAGATTTCTGAGCCCAAGGAGTCTTACCTATCCCTGA 389
QY 662 CTTCCTAGAGCGCGCTGTGCGCAAGTCCCAAGAGCAACTGAGAGAGAGAGAGT 721
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QY 842 ACCAGTGTACAGCAAGTACTTCACTGAGTTCAGAGTGTGAGGAAAGTGTGTTGGGGA 901
DB 567 GCCAGTACCAAAAACACCTTCAAGCAATACAGAGTCTGAGTAAAGTGTGTTGGGGA 626
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DB 867 CCAAGCTGAGCTTCCCGAAGCGCGCGCTCTTCTTACGCGCGAGATCTGTGAGGCT 926
QY 1202 GCTGACCTTCATGAACTCCGAGATGCTATGAGAGAGATGAGAGATGAGATGCTTCT 1261
DB 927 GAGAGAGCTGACCGGAGCGCATGTGTGACAGGAGACCTGAAACCCGAGAAATCTTGCT 986
QY 1262 GATGACCTGCGCACTGAGAGTATCTGAGCTGAGGCTGAGGCTGAGAGAGAGAGAG 1321
DB 987 GATGACAGAGCGACATCCGACATCTTACCTGAGAGTACTGCTGATGATGCTGCGAGG 1046
QY 1322 CAAGCCATACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1381
DB 1047 CCAAGCCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1103
QY 1382 AAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1441
DB 1104 GAATGAAAGCTGTACAGTTCAGCCCTGAGCTGAGGCGCTGCGCTCTGTACAGAT 1163
QY 1442 GATTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1501
DB 1164 GATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1223
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DB 1224 GCGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1283
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DB 1524 CTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1583
QY 1862 GAGAGCTGTTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1886
DB 1584 CGAGTGTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1608

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RESULT 10
 US-08-454-439-12
 Sequence 12, Application US/08454439
 Patent No. 5591618
 GENERAL INFORMATION:
 APPLICANT: Chantry, David
 APPLICANT: Gray, Patrick W.
 APPLICANT: Hoeckstra, Merle F.
 TITLE OF INVENTION: A No. 5591618el G Protein-Coupled Receptor
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ADDRESSEE: Bortun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/454,439
 FILING DATE: 30-MAY-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/221,817
 FILING DATE: 31-MAR-1994
 APPLICATION NUMBER: 08/123,932
 FILING DATE: 17 SEP 1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5591618and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 31981
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2204 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 31..1758
 US-08-454-439-12

Query Match 19.0%; Score 418.2; DB 1; Length 2204;
 Best Local Similarity 56.2%; Pred. No. 2.5e-93;
 Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;
 QY 305 GGCCCTGACAACTGATGCGCAACGCGCTGACCTGCGCGCGGAAAGCCCTCGGACCTG 364
 DB 33 GAGGCTCGAAGACATGTCAGCAACGAGTCTGCTGCAAGGCGCGGAAAGGTGGCGGTGG 92
 QY 365 CGACAGCAAAAG--AGCTGACGCGCGCGCGCTGAGCTGCGCTGCGCGGCTGCGAGG 421
 DB 93 AATTCGAAAGGCAAAAGCAAGAAATGCGCGCGAGATGCTCGAGTTCCTCATCATGAGCA 152
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 DB 153 GTGCGAAGGCTGCGGCTGAGCTGAGCTGATCATCAAGCTGTGTGAGAGGAGCCG 212
 QY 482 CATCGGTGCGCGCTCTTCTGAGACTTCTGACCAAGTGCACAGTTCGCGCAAGGCGAG 541
 DB 213 CATGGGCGCTGCTGCTTCCGAGATTCGTGCGACAGGCGGAGCTGAGCCGCTGGCT 272
 QY 542 AACCTTCTGAGGACGTGCAAACTGGGAGCTGGCGAGAGGAGCCCAACCAAGACAG 601
 DB 273 CGCTTCTCGATGGGAGTGGCGAGATGAGTGAACCCGAGATGACAGCGGAAAGGCAAG 332
 QY 602 CGGCTGCAAGGAGCTGTGGCACTTGTGCGAGTGGCCCTGCGCGGAAACCCGAGAC 661
 DB 333 TGGGCGGCGACG--TAAAGCAAGATTTCTAGGCAACGAGGCTCTGATCTCATCTGA 389
 QY 662 CTTCCTCAAGCGCGGTGGCGACCAAGTGCACAGGAGCCCACTGAGAGAGAGAGT 721
 DB 390 GGTGCGCGCGAGCTGTGTGAGAC--TGCACCGACCGGCTGAGAGAGGAGTCCCTGCAAG 448
 QY 722 GAGTGAAGTACGCTGCGCAAGGCTGAGGCAATGCTTTTTCAGAGAGAGCCCTTTAA 781
 DB 449 ACCTTTTCAAGGAATTAACCGGCTGA--CCACAGAGTACTGAGGCTGAGCCCTTTTTC 506
 QY 782 GAGATTGTGACCAAGGCTTTTACAGCAAGTTCTGCAAGTGAAGAACTTTCAAGATGA 841
 DB 507 CGACTACTGCAAGCAATCTTCAACCGTTCCTGCAAGTGAAGTGGCTGAGAAAGCA 566
 QY 842 ACAGGTGACAGCAAGTACTTCACTGATTAAGATGCTGGGAGAAAGTGGTTTGGGGA 901

DB 567 GCCAGTGAACAAAACACCTTCAGGCAATACGAGTCTCGGCTAAAGGTGGCTTTGGGGA 626
 QY 902 GGTATGTGCTCCTCAAGTAAAAAATCTGGGAGATGTATGCTGTAAAGAACTGAGCA 961
 DB 627 GGTGTGCGCTGCGAGGTGGGCGCAAGTAAATGTATGTCTGCAAGAGCTTAAAGAA 686
 QY 962 GAGCGGCTGAAGAAAGTGTGGAGAGATGTGCTCTTGTGAAAGAAATCTTGA 1021
 DB 687 AAGCGGATCAAGAGCGGAAAGGAGGAGCCATGGCGCTGAACGAGAGCATCTCGGA 746
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 QY 1082 CTGCGCTGCAAGGCTGATGAATGGGAGAGCTCAAGTTCACATCTCAACAGTGG 1141
 DB 807 GTGCTGT 866
 QY 1142 CAGCGTGTGCTGACATGAGCCGAGTATCTTTTACTGTGCGCCAGATAGCTGTGGAT 1201
 DB 867 CAGGCTGTGCTTCCCGAAGCGCGCGCTCTTCTAGCGCGCGAGATCTGTGTGCT 926
 QY 1202 GCTGCACTTCAATGAACTGGGATGTGTCTATCTGGGACATGAAGCTTGAGATGTCT 1261
 DB 927 GAGAGACTGTGACCGGAGGCGCATGTGTGAAGGACCTGAAGCCGAGAACTTGTCT 986
 QY 1262 GAGTGAACCTGTGCAACCTGAGTATCTGACCTGTGGGCTGCGCGTGAAGAGAGTGG 1321
 DB 987 GAGTGAACCGGCGCATCTGTGATCTGTGACCTGTGAGCTGTGTGATGTGCGGAGG 1046
 QY 1322 CAAGCCATCAACCAAGGAGGCTGAACCAATGTGTATAGTCTCTGAGATCTTAATGA 1381
 DB 1047 CAGAGCATCAAGAGGAGGTGTGGGACGCTGGGTTAATGCTCCGAG--GTGGTGA 1103
 QY 1382 AAGGTATGTATTTCTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1441
 DB 1104 GAATGAACGCTACAGTTCAGCTGAGCTGTGGGCTGTGGCTGTCTGTGTGTGTGTGT 1163
 QY 1442 GTTGTGTGACCAACCATTTCAAGATTTACAGAGAAAGTGTGTGTGTGTGTGTGTGT 1501
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 DB 1404 TGGCATCTGAGCGCGCTTCAAGCTGTACCCCGAGCCATTTACTGAGAGATGTCT 1463
 QY 1742 TGAATTTGATTTCTGTGAGTGTGGGAGTGTGAATTTGATGAACAAGATTAAGCT 1801
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 QY 1802 CTTCAAAACCTTTGCAAGAGTGTCTTCTATATGATGAGAGAGAAATTAAGAAAC 1861
 DB 1524 CTACCAAGATTTGCAAGAGAGATGTGCGCATCCCTGTGAGAGAGATGTGAGAC 1583
 QY 1862 GGAAGCTTTGAGAACTGAATGAC 1886
 DB 1584 CGAGTCTTCAAGAGCTGAATGTC 1608

PCT-US94-10487-12
; Sequence 12, Application PC/TUS9410487
; GENERAL INFORMATION:
; APPLICANT: ICOS Corporation
; TITLE OF INVENTION: A Novel G Protein-Coupled Receptor
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10487
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/221,817
; FILING DATE: 31 MAR 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,932
; FILING DATE: 17 SEP 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/31981
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELETYPE: 25-3856
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2204 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..1758
; PCT-US94-10487-12

Query Match 19.0%; Score 418.2; DB 5; Length 2204;
Best Local Similarity 56.2%; Pred. No. 2.5e-93;
Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;

QY 305 GGCCTTGACAACTGATCGCAACACCGCTTACTGAGAGCCCGGAGACCTCTGAGCTG 364
DB 33 GGAAGCTGAGAAATCGTAGGACACGGGTCTACTCAAGGCCCGGAGAGGTGGGGTGG 92
QY 365 CGACAGCAAG--AGCTGAGCGGGGGGGGGGTAGCTTGGCCCTTCCGGGCTGCAAGG 421
DB 93 AATTCGAAAGCAAAAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 152
QY 422 CTGCGGAGAGCTTCGCGAAGAGCTGCTCCGTAATTCACAGAGCTGTGTGAGCAGAGCC 481
DB 153 GTGCGAAGAGCTGCGGCTCAAGCTTCGAGAGTATATACAGAGCTGTGTGAGCAGAGCC 212
QY 482 CATGCTGCGCGCTCTTCTTCTGATCTTCTAAGCAAGAGTCCAGAGTCCAGAGAGAGG 541
DB 213 CATGCGCGCTGCTGCTTCTGAGAGTCTGTGCTCAGAGAGCTCGAAGCTGAGAGCCCTG 272
QY 542 AACCTTCTAGAGAGAGTGAAGAACTGGAGAGTGGCGAGAGAGAGAGAGAGAGAGAGAG 601

DB 273 CGCCTTCTGAGTGGGGGTGGCCGATGATGAGTACCCTGGATGACAGAGAGAGAGATG 332
QY 602 CGGCTGAG 661
DB 333 TGGGCGGAG--TAAAGCAATTTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 389
QY 662 CTTCCTGAG 721
DB 390 GGTCCCGGAG 448
QY 722 GGTGAG 781
DB 449 ACCCTTTCAG 506
QY 782 GGAATTCGAG 841
DB 507 GCACTTCTGAG 566
QY 842 ACCAGTGTGAG 901
DB 567 GCGAGTGTGAG 626
QY 902 GGTATGTGCGCTGAG 961
DB 627 GGTGTGCGCTGAG 686
QY 962 GAAAGCTGAG 1021
DB 687 AAGCGAGTGTGAG 746
QY 1022 GAAAGTGTGAG 1081
DB 747 GAAAGTGTGAG 806
QY 1082 CTGCTTGTGATGAG 1141
DB 807 GTGCTGTGCTGAG 866
QY 1142 CAGCGGTGCTGAG 1201
DB 867 CAGCGGTGCTGAG 926
QY 1202 GCTGACCTGATGAG 1261
DB 927 GAG 986
QY 1262 GATGAG 1321
DB 987 GATGAG 1046
QY 1322 GAG 1381
DB 1047 CAG 1103
QY 1382 AAG 1441
DB 1104 GATGAG 1163
QY 1442 GGTGCTGAG 1501
DB 1164 GATGAG 1223
QY 1502 GGAAG 1561
DB 1224 GGGGCTGAG 1283
QY 1562 AGATATTTGAG 1621
DB 1284 ACTTTGCTGAG 1343
QY 1622 GTCTGATGATGAG 1681

Db 1344 TGCCCCGAGAGTAAAGAGACACCCCTCTTTAAGAGCTGAATCTTCAAGGGCTGGAGGC 1403
Qy 1682 TGGCTAATTGAACCCCAATTTGGCAAGCCCTTCACTGTTTATGCAAGACATGCC 1741
Db 1404 TGGCATCTGGAGCCCGCTTCAAGCTGACCCCAAGGCCATTTTACATGCAAGAGATGTTCT 1463
Qy 1742 TGAATTGATGATTTCTCTGAGGTGGGGGGGGTGAATTTGATGACAAAGATGACAGTT 1801
Db 1464 GAGACATGAAACAGTTCTCTAAGCTCAAGGCGTGGAGCTTGAAGCTTCCAGACGAGACTT 1523
Qy 1802 CTTCAAAAACCTTGGCAAGAGTGTCTTCTTATAGCATGCGAGGAAATTAATGAAGC 1861
Db 1524 CTACCAAGAGTTTCCACAGAGAGTGTGCCCATCCCTCGGAGAAAGAGATGTTGAGAC 1583
Qy 1862 GGGACTGTTTGAAGAACTGATGAC 1886
Db 1584 CGAGTGTCTCCAGAGCTGATGTC 1608

RESULT 12
US-08-221-817-21
; Sequence 21, Application US/08221817
; Patent No. 5532151
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
APPLICANT: Hoeckstra, Merle P.
TITLE OF INVENTION: A No. 5532151e1 G Protein-Coupled Receptor
TITLE OF INVENTION: Kinase GRK6
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,817
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5532151and, Grete E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 13..1740
US-08-221-817-21

Query Match 18.0%; Score 395.8; DB 1; Length 1983;
Best Local Similarity 55.3%; Pred. No. 7.9e-88;
Matches 876; Conservative 0; Mismatches 697; Indels 12; Gaps 5;

Qy 305 GGCCCTGAGACAACCTGATGCGCAACCGCCTTACTGAGGCCCGGAAAGCCTTGAGATG 364
Db 15 GAGAGCTGAGAACTGCTAGCGAACAAGGGGCTTACTGAAGGCCCGGAAAGGTGTGGCG 74
Qy 365 GAGACAGAAAG--AGTGGAGGCGGCGGCGTGAAGCTGCGCCCTGCGGGCTGAGAGG 421
Db 75 GAATCGTAAAGGCAAGAGCAAGAAATGGCGCGCAAGATGCTGCAAGTTCCCAATCGCA 134
Qy 422 CTGCGGAGAGCTCGGCGAGAGCTGCTTGAATCTTCAAGCTGTGTGAGCAAGCGC 481
Db 135 GTGTGAAGAGCTCGGCTCACTTGAAGCTGACTTACCAAGCTGTGTGAGCTGAGTC 194
Qy 482 CATGCTGCGCGCTCTTCCGTACTCTTACCAAGTGGCCCAAGTTCGCAAGCGCGC 541
Db 195 CATGGGCGGCGCTTATTAATGATGTTGCGGTACAGAGGCTGAGCTGAGCCCGCTGAC 254
Qy 542 AACCTTCTAAGAGAGCTGCAAGCTGGAGCTGGCGGAGAGAGAGCCACCAAGACAG 601
Db 255 TGCTTCTGATGAGGAGTGGCTGAGTATGAGGTGACCCCTGATGAGAAACGAAAGGATG 314
Qy 602 CGGCGTGAAGGCGCTGGTGGCACTTGTGCAAGTGCCTGCGCGGAGAAACCCGCAAGC 661
Db 315 TGGGCGTC--GGCTAATGCAAAATTTCTAGCGCAACAGGCTCTGACCTCATCCCTGA 371
Qy 662 CTCTCTCAAGCAGGCGCTGGCCACCAAGTGCAGAGCCCACTGAGAAAGCGAGT 721
Db 372 AGTTCCCGGAGAGCTGAGTGAAC-TGAGCCAGCGCTAGAGAGGAGGAGCCCTGCAAA 430
Qy 722 GGTGCAAGTGAAGCTGCGGCAAGCTGAGGCTGAGCTTGTGCAAGAGAGCCCTTGA 781
Db 431 ACCTCTTCCAGAGAGTGAACCGGCTACCAATGATGATCAAAACAGAGGAC--CTTTTGG 488
Qy 782 GGAATTCGACCAAGCGCTTCTACAGCAAGTTCTGAGTGAAGTCTTGGAGATGA 841
Db 489 GCACTACTGACAGCATCTTCAACCGTTCTGAGATGGAAGTGGCTGAGAAAGCA 548
Qy 842 ACCAGTGTGAGCAAGATCTTCACTAGATTGAGTGTGGGAGAAAGTGTGTTGGGGA 901
Db 549 GCGAGTGAACAAACACCTTAGGAGATGACGAGTCTGGGAGAAAGGTGGCTTGGGGA 608
Qy 902 GGTATGTGCGCTGCGAGTGAAGAAACCTGGGAGATGATGCTGTAAGAAATGCGCA 961
Db 609 GGTGTGTGCTGCGAGGTGCGAGCAACAGGCAAGTGTATGCTGTAACAAACTGGAAAA 668
Qy 962 GAAGCGCTGAAGAAAGGTGGCGAGAAAGTGTCTCTTGGAAAGAAATCTTGA 1021
Db 669 GAAAGCAATGAAGAGCGAGAGGAGGCGCATGTCTTCAAGAGAAAGCATCTGGA 728
Qy 729 GAAAGTGAACAGATGATTTGATGATCTTACCTACCATATGAGACCAAGATGAC 788
Db 1022 GAAAGTGAAGAGCTTCACTTGTCTCTGCTGAGCTGATGCTTGAAGCAAGACCATCT 1081
Qy 1082 CTGCTGTGTATGAGCTGAGTGAAGTGGGAGAGCTGAAGTGCATGATCAAGTGGG 1141
Db 789 GTGCTGTGTCTGATGATGATGATGAGGAGCACTCAAGTTCATCTTACCAATGAG 848
Qy 1142 CAAGCGTGTGCTGAGCATGAGCCGAGTGAATCTTACTGCGCCCAATGACCTGTGGAT 1201
Db 849 CAGAGCTGGCTTCCGAGAGACGTGTGTGTTCTATGCTGCGAGATCTGTGTGGTCT 908
Qy 1202 GCTGACCTTCATGAATCTGAGATGCTGATGAGGAGTGGCGCTGAGAGTGAAGTGG 1261
Db 909 GAGAGACTTACCGGAGAACCATGATGATGAGGAGACTTAAAGCAGAAATATCTTCT 968
Qy 1262 GATGACCTTCGAGATGAGTGAATGATGATGATGATGATGATGATGATGATGATG 1321
Db 969 GATGACCTTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1028
Qy 1322 CAAGCCATCAACCAAGAGGCTGAGAACCAATGATGATGATGATGATGATGATGATG 1381
Db 1029 CAGACATCAAGAGGCGGTGTGGGAGCTGTGGCTAATGCTCAAG--GTGGTGA 1085

QY 1382 AAAGTAAGTATTCCTATCTGAGCTGTTGGCCATGGAGATTTATGAAT 1441
 Db 1086 GAATGAGGCGTACACATTCAGTCTGAGTGGGCGCTGCTCTGTAAGAGAT 1145
 QY 1442 GGTGCTGAGCAACACATTCAGAGATTAAGAGAAAGGTCAGTAAAGAGATCTGAA 1501
 Db 1146 GATTGGGAGACGTGCGCTTCCAGCAGAGAAAGAGATTAAGAGAGAGAGATGGA 1205
 QY 1502 GCAAGAACTCTGAGAAAGAGAGTCAATTCAGCATGATTAATTCAAGAGAGAGAGAA 1561
 Db 1206 GCGGCTGCTCAAGAGAGGTGCTGAGAGATCAACCGACCCCTTCTCCCAAGGCAAGCTC 1265
 QY 1562 AGATATTGACAGCTCTTCTGCTGAGTAAAGAACAGAGCAACCTTAAAGAGAGAGAA 1621
 Db 1266 ACTGCTCTCTAGCTTCTCAACAGAGACCTGCTGAGCGCTGAGGCTGTGTGAGAGTGG 1325
 QY 1622 GTCTGATGATCCAGAAACATCTTCTTAAAGAGATCACTTCTGCTGAGAGAGC 1681
 Db 1326 TGCCGCTGAGGTAAAGAGAGACCCCTTTCAGAAAGATTAAGAGAGAGAGAGAGC 1385
 QY 1682 TGCCCTATTAAGACCCCATTTGTCAGAGACCTTCAAGTGTATGCAAGAGAGAGAGC 1741
 Db 1386 TGGAATGCTAGAACACCTTTAACTGACCCCAAGGCACTTAAGAGAGAGAGTGTCT 1445
 QY 1742 TGAATTTGATATTCCTGAGGTCGAGGAGGAGATTTGATGACAAATAGAGATT 1801
 Db 1446 GAGCATTAACAGATTCCTCAAGATTAAGGAGTGTGAGTGTGAGAGAGAGAGAGAGCTT 1505
 QY 1802 CTTCAAAACCTTGGACAGAGTGTCTCTATAGATGAGAGAGAAATTAATAGAAAC 1861
 Db 1506 CTACCAAGAGATTGCCAGCGGTAGTGTCTCATCCCTGAGAGAGAGAGATGTGAGAGC 1565
 QY 1862 GGGAGCTTTTGAAGAACTGAATGAC 1886
 Db 1566 TGAGTGCTCCAGAGAACTAAATGTC 1590

RESULT 13

US-08-454-439-21

Sequence 21, Application US/08454439

Patent No. 5591618

GENERAL INFORMATION:

APPLICANT: Chantry, David

APPLICANT: Gray, Patrick W.

APPLICANT: Hoekstra, Merle P.

TITLE OF INVENTION: A No. 5591618el G Protein-Coupled Receptor

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/454,439

FILING DATE: 30-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/221,817

FILING DATE: 31-MAR-1994

APPLICATION NUMBER: 08/123,932

FILING DATE: 17 SEP 1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: No. 5591618and, Greta E.

REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 31981
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1983 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 13..1740
 US-08-454-439-21

Query Match 18.0%; Score 395.8; DB 1; Length 1983;
 Best Local Similarity 55.3%; Pred. No. 7,9e-88;
 Matches 876; Conservative 0; Mismatches 697; Indels 12; Gaps 5;

QY 305 GGCCTGAGCAACCTGATGCGCAACACCGCCTTACCTGACAGCCCGAAGACCTGAGACTG 364
 Db 15 GAGGCTCGAAGACATCGTAGGAGAACCGGAGGCTACTCAAGCCCGGAGAGGTGGTGGCGG 74
 QY 365 CGACAGCAAG--AGCTGACAGCGCGGCGGCTAGCTTGGCCCTGCGGAGCTGACAGG 421
 Db 75 GAATCTTAAGGCAAGAGCAAGAAATGAGGCGCAGATCTGCAATTCCTCCCAATCAACCA 134
 QY 422 CTGCGGAGAGCTCCGCAAGAGCTGCTGCACTTGCACAGCTGTGTGAGAGAGAGC 481
 Db 135 GTGTGAGAGAGCTCCGAGCTGACCTTGAACGTGACACAGCTGTGTGAGAGAGCTGATC 194
 QY 482 CATGCGTCCGCTCTTCCGTGACTTCTTACGCAAGTCCAGCTTCCGCAAGGCGGC 541
 Db 195 CATTGGGCGCTGTTATTTATGATGATGAGTGTGAGGAGTGAACCTGATGAGAAACGGAAGCATG 254
 QY 542 AACCTTCTTAAGAGAGCTGCAAGACTGAGAGAGTGGCCGAGAGAGAGAGAGAGAG 601
 Db 255 TGCTTCTGAGAGAGAGTGTGAGATGAGAGTGAACCTGATGAGAAACGGAAGCATG 314
 QY 602 CCGGCTGAGAGAGAGTGTGAGCACTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 661
 Db 315 TGAGGAGTCC--GGCTATGAGAAATTTCTGAGCAACAGGATCTTGAATCTTGA 371
 QY 662 CTTCTGAGCAAGCGCGTGTGCAACAGTGTGCAAGAGAGAGAGAGAGAGAGAGT 721
 Db 372 AGTTCCCGGAGAGCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 430
 QY 722 GGTGAGTGAAGCTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGA 781
 Db 431 ACCTTCTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGA 488
 QY 782 GATTTCTGAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGA 841
 Db 489 GAGTACCTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 548
 QY 842 ACCAGTGTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 901
 Db 549 GCGAGTGTGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 608
 QY 902 GGTATGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGA 961
 Db 609 GGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGA 668
 QY 962 GAGGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGA 1021
 Db 669 GAAAGATTAAG 728
 QY 1022 GAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGA 1081
 Db 729 GAAAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGA 788

QY	1082	CTGCCTTATGATAGCGCTGATGATATGAGGAGAGACCTTCAGTTCCATCTCAACAAGTGGG	1141
Db	789	GTGCTGTGCTGACATTTGATGATATGAGAGGAGACCTCAAGTTCCATCTCAACAATGGG	848
QY	1142	CAGCGTGTGCGTGGACATGAGACCGGGGTATCTTTTAACTGCGGCCAGATACCTGTGGGAT	1201
Db	849	CCAGGCTGTGGCTTTCCGAGAGCAGTGTGTGTGTTCTTAAGCTGCGGAGATCTGTGTGGTCT	908
QY	1202	GCTGGACCTCCATGAAACTGCGATCGCTATGCGGAGACATGAAGCCTGGAATGTGCTTC	1261
Db	909	GAGAGACTTAAACCGGAGAAACGATTCGTGTACAGGAGACCTTAAGCCAGAGATATCTCTTC	968
QY	1262	GGATGACCTCGGCAACTGCAAGGTATCTGACTGTGGGCTGGCCGTGGAGATGAGGGTGG	1321
Db	969	GGAATACCAATGGCCACATTCGATCTCCGACTGTGGGCTGTGCTGTGATGTTCTGAGGG	1028
QY	1322	CAGGCCATCAACCCAGAGGGCTGGAACCAATGTGTAACATGGCTCCTGATGATCTTAATGGA	1381
Db	1029	CCAGACCAATCAAGGCGCGTGTGGGCACTGTGGGCTAATGAGCTCCAGAG---GTGTGAA	1085
QY	1382	AAAGGTAAGTATTCCTATCTGCTGTGACTGTGTTCCATGGGATGCAAGCATTTATGAAT	1441
Db	1086	GAAATGAGGCTTACATTAATGATCTGTACTGTGTGGCCGTGAGTGCTCTGTATCAGAT	1145
QY	1442	GATTGTGAGCAACACATTTCAAGATTAACAAGAAAGGTGATGAAGAATCTGA	1501
Db	1146	GATTGTGCGGAGACGTGCGCCTTCACAGCAGAGAAAGAGATCAGCGGAGAGGTGGA	1205
QY	1502	GCAAAAGACTCTGAAAGAGAGGTCAATTTCCAGCATATTAATTCAAGAGAGCAAA	1561
Db	1206	GCGGCTGTCAAGAGAGGTGTGGTGAAGAGTACACGACCGCTTCTCCCAAGGCAACGCTC	1265
QY	1562	AGATATTTCACAGGCTCTTCTGGCTAAGAAACCAAGACCAAGCTTAAGAGCAGAGAAAA	1621
Db	1266	ACTGTGTTCAAGCTTCTGAAACAGAACCGCTGTAGGCGCTGGGGTGTGTGTGAGATGG	1325
QY	1622	GTCGTGATGCCAGAGAAACATCATTTCTTTAAACGATCAACTTTCTCGCCCTGGAAGC	1681
Db	1326	TGCCGTGTGAGTAAAGAGAGACCCCTTTTCAAGAACTGAATTTTCAAGCGGCTGGAGGC	1385
QY	1682	TGGCGTAAATGAAACCCCAATTTGAGCCAGACCCCTTCACTGGTATTATGCCAAGACATCGC	1741
Db	1386	TGGAATGTGAAACCACTTTTAACTGACCCCAAGGCCATTTATCTGAGAGACGTGT	1445
QY	1742	TGAATTTGATGATTTCTCTGAGGTTCTGGGGGTGGAATTTGATGACAAAGTAATGACGTT	1801
Db	1446	GGAATTTGAAAGCTTCTCCACAGTTTAAAGGTGTGATCTGGAGGCCACAGACCAAGCTT	1505
QY	1802	CTTCAAAAACTTTGGCAGAGTGTCTCTTAATGATGTGGAGAGAAATTAATATGAAC	1861
Db	1506	CTTACAAAGATTTCACAGGGTATGTGTTCATCTCCCTGGCAGAACGATGTGTGAGAC	1565
QY	1862	GGAGCTGTGAGAACTGATGAC	1886
Db	1566	TGAATGCTTCCAGAGACTTAATGTC	1590

RESULT 14
PCT-US94-10487-21
: Sequence 21, Application PC/TUS9410487

APPLICANT: ICOS Corporation
 TITLE OF INVENTION: A Novel G Protein-Coupled Receptor
 TITLE OF INVENTION: Klnase GRK6
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ADDRESSEE: Borum
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA

ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10487
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/221,817
FILING DATE: 31 MAR 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 13..1740
PCT-US94-10487-21

Query Match	18.0%	Score 395.8	DB 5	Length 1983
Best Local Similarity	55.3%	Pred. No. 7.9e-88		
Matches 876	Conservative	0	Mismatches 697	Indels 12
				Gaps 5
QY	305	GGCCCTGGACACACTGATGCGCAACCCGCTACTCTGCAAGCCCGAGACCCCTTGACCTG	364	
Db	15	GGAGCTCGAGACACTGCTGAGCGAACACGGGGGCTACTCAAGGCCCGGGAAAGGTGGTGGCG	74	
QY	365	CGACAGCAAAAG--AGCTCAGCGCGCGCGGTGAGCTTGCCCTTCCCGGGCTGACGGG	421	
Db	75	GAATCGTAAAGCAAGCAAGCAAAATGCGCCCGCAGATGCTGAGTTCCTCCCACTACGCCA	134	
QY	422	CTGCGCGGAGCTCGCCGCAAGACTGTCTCCGAACTTCCACAGCCTGTGTGAGCAGCAGCC	481	
Db	135	GTGTGAAAGAGCTCTCGAGTCACTTGAAACGTGACTACAGACTGTGTGAGACGTCAAGTC	194	
QY	482	CATCGGTGCGCGCCTCTCCGTGACTTCTTAGCCACAGTGGCCACGTTCCGCAAGCGCGC	541	
Db	195	CATTGGGCGCCTGTATTATGTGAGATTCTGCGTGAAGGCGTGAAGCTGACCCGCTGTAC	254	
QY	542	AACTTCTCTAGAGACGTGCAGACTGCGAGCTGCGACGAGAGGCCACCAACAAAGACAG	601	
Db	255	TGCTCTTCGTGATGAGGATGAGATGAGAGTGACCCCTGATGAGAAACGMAAGGATG	314	
QY	602	CGGCGTGCAGGGGCTGTGTGCCACTTGTGGGAATGCGCCCTGCCCCCGGGGMAACCGCAAC	661	
Db	315	TGGGCGTCT---GGCTAATGAGATATTTCTGACGCCACAGGGTCTTGACCTATCTCTGA	371	
QY	662	CTTCTCTCACCAGCGCGGTGGCCACCAAGTGGCAAGCAGGCCACCACTAGAGAAAGACGAGT	721	
Db	372	AGTTTCCCGGACGCTGTGTGAGTAC-TGTGGCCAGCGGCTGAGCAGGACCCCTTGAAAG	430	
QY	722	GGCTGCAGTGAAGCTGTGGCAAGGCTTGAAGCCATGCGCTTTCTTTCGAAGAGCAGCCCTTTAA	781	
Db	431	ACCTCTTCCAGAGAGTACCCCGGCTGACCCATGAGTACTCTTAAGATGGGC--CCTTTTGG	488	

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QY 782 GGAATTGCGACGAGCGCTTACGACAAAGTTCTGACAGTGAACCTTTGACATGCA 841
DB 489 CGACTACCTCGACGACATCTACTTACACCGTTTCTGACAGTGAAGGCTGGAAGGCA 548
QY 842 ACCAGTGTGACAAAGTACTTCTGAGTTCAGAGTGTGGGAAAGGTGTTTGGGGA 901
DB 549 GCCAGTGAACCAAAACCTTTTGGGACATCCGAGTCTGGGCAAAAGGTGCTTTGGGGA 608
QY 902 GGTATGTGCGCTGACAGGTGAAAAACACTGGGAGATGTATGCTGTAAAGAACTGACAA 961
DB 609 GGTGTGTGCTGCGCAGGTGGGCAACAAGGGAATGTATGCTGAAAAAACTGGAAAAA 668
QY 962 GAAGCGGCTGAAGAAAGAGTGGGAGAAAGATGCTCTCTTGGAAAAAGAAATCTTGA 1021
DB 669 GAACGCAATAAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 728
QY 1022 GAAGTCAAGCAGCGCTTCACTTGTCTCTGCGGCTATGCTTGGAGCAAGACCAATCT 1081
DB 729 GAAAGTGAACAGTATGATTTGTATGATCTTATGCTTACGATATGAGACCAAGATGCACT 788
QY 1082 CTGCGCTGTCACTGACCTGATGATGATGAGGAGAGCTCAAGTTCACATCTACACGTTGG 1141
DB 789 GTGCTGTGCTGACATTTATGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 848
QY 1142 CAGCGTGGCTTGAACATGAGCGGCTGATCTTTTCTGCGCCCAATAGCTGTGGGAT 1201
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QY 1202 GCTGACCTTCATGATCTGCGGATGCTGCTATCGGGAATGAAGCCTGAGAAATGCTTCT 1261
DB 909 GAGAGATTTACACCGGGAAGCATGCTGTACAGGAGCTTAAGCCAGAGAAATCTTCTCT 968
QY 1262 GATATACCTCGGCACTGACAGGTATCTGACCTGCGGCTGCGCTGAGATGAGAGGTTG 1321
DB 969 GATATACCTCGGCACTGACAGGTATCTGACCTGCGGCTGCGCTGAGATGAGAGGTTG 1028
QY 1322 CAGGCTGCTTGAACCAAGGCTGGAACCAATGTTATCATGCTCTGAGATCTTATGGA 1381
DB 1029 CAGGCTGCTTGAACCAAGGCTGGAACCAATGTTATCATGCTCTGAGATCTTATGGA 1085
QY 1382 AAGAGTATGATTTCTATCTGAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCTG 1441
DB 1086 GATATACCTCGGCACTGACAGGTATCTGACCTGCGGCTGCGCTGAGATGAGAGGTTG 1145
QY 1442 GATATACCTCGGCACTGACAGGTATCTGACCTGCGGCTGCGCTGAGATGAGAGGTTG 1501
DB 1146 GATATACCTCGGCACTGACAGGTATCTGACCTGCGGCTGCGCTGAGATGAGAGGTTG 1205
QY 1502 GGAAGAACTGTGCAAGAGAGAGTCAATTCAGCATGATTAATTCAGAGAGGAGCAAA 1561
DB 1206 GCGGCTGTGCAAGAGAGTGTGCAAGAGTCAATTCAGCATGATTAATTCAGAGAGG 1265
QY 1562 AAGATATGAGGCTCTTCTGCGGCTGAGGAAACAGGCAAGCTTAAAGAGGAGGAGG 1621
DB 1266 ACTCTGTTCTGACCTTCTGACAGAGACCTGCTGAGGCTGCGGCTGCGGCTGAGG 1325
QY 1622 GTCTGATGATCCAGAGAAACATCTTCTTAAAGCAATCTTCTGCTGCTGAGAGC 1681
DB 1326 TGCCTGAGTAAAGAGCAACCCCTTTTCAAGAAACGAAATTTCAAGGAGCTGGAGC 1385
QY 1682 TGGCTGATTTGAACCCCTTCTTGGGAGCCTTCAAGTGTGTTATGCTGCAAGAGATGC 1741
DB 1386 TGGATGTGAAACCACTTTTAAACCTGAGCCCAAGGCAATTTTACGCAAGAGTGTCT 1445
QY 1742 TGAATGATGATTTCTGAGGTTGCGGAGGTGGAATTTATGATGCAAAAGATTAACAGTT 1801
DB 1446 GGAATTTGAACATTTCTCAAGATTTAAAGGTGTGATCTGAGGCTGCAAGCAAGACTT 1505
QY 1802 CTTCAAAACCTTTGCAAGAGTGTCTTCTATGATGAGAGAGAAATTTATGAAC 1861
DB 1506 CTTACCAAGATTTGCAAGAGTGTGTCTCAATCCCTGCGAGAGAGATGTGTGAAC 1565
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QY 1862 GGAAGCTTTGAGGAAGTGAATGAC 1886
DB 1566 TGAGTGTCTTCAGGAATAATGTC 1590

RESULT 15
US-08-221-817-10
; Sequence 10, Application US/08221817
; Patent No. 5532151
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Gray, Patrick W.
; APPLICANT: Hoekstra, Merle F.
; TITLE OF INVENTION: A No. 5532151e1 G Protein-Coupled Receptor
; TITLE OF INVENTION: Kinase GRK6
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,817
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,932
; FILING DATE: 17 SEP 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5532151and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31981
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2206 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..1926
; US-08-221-817-10

Query Match 17.7%; Score 389.4; DB 1; Length 2206;
Best Local Similarity 55.3%; Pred. No. 3.1e-86;
Matches 866; Conservative 0; Mismatches 681; Indels 18; Gaps 5;
```

Db 213 CATTGGGCGCTGTGTCTCCGAGATTCTGTGCGCCAGAGCGCGAGCTGAGCGCGTGGT 272
Qy 542 AACCTTCTAGAGAGCGTGCAGAACTGAGAGCTGGCCGAGGAGGAGCCCAACAAAGACAG 601
Db 273 CGGCTTCTGAGATGGGGTGGCGAGATGTAAGATGACCCCGAGTACAAAGCGGAAGCANG 332
Qy 602 CGGCTGAGAGGGCTGTGTGCGCACTTGTGCGAGTGCCTGCGCCCGGGGAAACCCGAAAC 661
Db 333 TGGGCGGACG--TAAAGAGATTTTCTGAGCACAAGGATCTTACCTCATCTCTGA 389
Qy 662 CTTCCTCAGCAGGCGCTGGCCACCAAGTGCAGAGCACAACCTGAGAGAGAGAGT 721
Db 390 GGTCCCCGGGAGCTGTGTGACGGACTGCAACCCAGC-----GCTGAGAGAGGCTCTGC 443
Qy 722 GGGTGAATGACGCTGCGCAAGCTGAGGCCATGGCTTTCTTGCAAGACAGCCCTTAA 781
Db 444 AAGACCTTTTCCAGGAACTACCCGCTGAGCCACGAGTACCTGAGCGTGGCCCTTTGC 503
Qy 782 GGAATTCGTGACAGCGCCCTTACAGCAATTTCTGAGTGGAAACTCTTGAGATGCA 841
Db 504 CGATACCTGCAAGCATCTTACACCTTTCTGAGTGAAGTGGCTGGAAGGCA 563
Qy 842 ACCAGTGCAGACAACTGACTTCACTGAGTTCAGAGTGTGGGAAAGGAGTGTGGGA 901
Db 564 GCCAGTACCAAAACACTTCAAGCATACCGATCTGGGTAAAGGTGGCTTTGGGA 623
Qy 902 GGTATGTGCGCTCAGAGTGAACCACTGAGAGATGATGCTGTAAAGAACTGAGCA 961
Db 624 GGTGTGCGCTGCGAGGTGCGGCGCAAGGTAAATGATGCTGCAAGAGCTAGAGAA 683
Qy 962 GAAGGCGCTGAAGAAAGTGGGAGAGATGGCTCTTGAAGAAAGAAATCTTGA 1021
Db 684 AAGCGGATCAAGAAAGCGAAAGGAGGAGCCATGGCTGAACGAGAGCATCTTGA 743
Qy 1022 GAAGTCAAGACCCCTTTCACTGTCTCTGAGCTTATGCTTGAAGACCAAGCCATCT 1081
Db 744 GAATGGAACAGTAGTTGTGTAGTAGCTTGGCTACGCTATGAGAACAAAGGACGCGCT 803
Qy 1082 CTGCTTGTGATGAGCTTGAATGAATGGGAGACCTTGAATTCACATTCACAGTGG 1141
Db 804 GTGCTGTGCTGACACTGATGAAAGGAGGAGCACTTCAAGTTCCACATTCACATGG 863
Qy 1142 CAGCGTGGCTGAGACATGAGCGGAGTATCTTTTACTGAGCCAGATAGCTGTGGAT 1201
Db 864 CAGGCTGGCTTCCCGAAGCGGAGCGCTTCTTACGCGCGAGATCTGCTGTGGCT 923
Qy 1202 GCTGACCTCCTGAGACTCGGCACTGCTATCGGAGCATGAAAGCTGAGAAATGCTTCT 1261
Db 924 GAGAGACCTGACCGGAGGCGATGTGTACAGGGAACCTGAAGCCGAGAACATCTTGT 983
Qy 1262 GAATGACTGGCAACTGCAAGTATCTGACCTGGGAGTGGCGGTGAGATGAAGGTGG 1321
Db 984 GGATGACACAGGCCACATCCGATCTCTGACCTGGGACTAGCTGTGCATGTGCCAGG 1043
Qy 1322 CAGGCCATCAACCAAGAGGCTGAACCAATGTTATCATGGCTCTGAGATCTTAATGA 1381
Db 1044 CAGACCATCAAGAGGCGTGTGGACCGTGGGTTATATGCTCCGAG--GTGTGA 1100
Qy 1382 AAGGTAAATTAATCTATCTGTGAGCTGTGGTGGATGGAGTGCAGATTTAATAAT 1441
Db 1101 GAATGAACGTTACAGTTCAGCCCTGACTGTGGGCGCTCGGCTGCTCTGTACAGAT 1160
Qy 1442 GGTGTGAGAGACACATTCAAAGATTAACAAGAAAGTCAAGTAAAGAGATCTGAA 1501
Db 1161 GATCGAGGCGAGTGGCTTCCAGCAGAGAAAGAAAGATCAAGCGGAGAGGTGA 1220
Qy 1502 GCAAGAGACTGCAAGAGAGGTGAATTCAGATGATTAATTCACAGAGAGCAAA 1561
Db 1221 GCGGCTGTGAAGAGGTCCCGAGAGATTCAGAGCGTTTCCCGCAGGCGGCTC 1280
Qy 1562 AGATATTTCAGGCTCTTCTGTGAAGAACAGAGCAACGCTTAGAGACAGAGAAA 1621

Db 1281 ACTTGTCAAGACTCTCTGCAAGGACCTGCGAAACGACCCGTGGGTGTGTGGGG 1340
Qy 1622 GTCTG--ATGATCCAGGAAACATCATTTCTTAAAGATCAATTTCTCGCTGA 1678
Db 1341 CAGTCCCGAGGAGGAGCACTCCCTTTTAAAGCTGAATTCAGCGGCTGG 1400
Qy 1679 AGTGGCTAATTAAGACCCCATTTGTGCAAGCTTTCAGTGTGTTATGCAAGAT 1738
Db 1401 AGCTGGATGTGAGCGCGCGCTTCAAGCTGACCCCGACATTTACTGCAAGAT 1460
Qy 1739 CGTGAATTAATGATTTCTGTAGGTTGCGGAGGTGAAATTTGATCAAGATTAAGCA 1798
Db 1461 TCTGACATTTGAACGTTCTTACGCTCAAGGCGTGGAGCTGAGCTTACCGAG 1520
Qy 1799 GTCTTCAAACTTTGCAAGAGTGTCTTATGATGCAAGCAAGAAATTAATGA 1858
Db 1521 CTCTTACAGAAATTTGCAAGGCAAGTGTGCTTCCCTGCAAGAGATGTGA 1580
Qy 1859 AACGG 1863
Db 1581 GACCG 1585

Search completed: August 13, 2004, 18:45:32
Job time : 121.544 secs

XX

The present invention relates to the isolation of a novel human G protein-coupled receptor (GPCR) kinase (GPCRK) designated 69087, a novel human nuclear signalling protein designated 15821, and a novel human mitogen-activated protein kinase (MAPK) phosphatase MAPKP designated 15418, and the polynucleotide sequences encoding them. The sequences of the invention are useful for treating and diagnosing disorders such as cellular proliferative and differentiative disorders (e.g. haematopoietic neoplastic disorders, leukaemia, carcinoma, sarcoma or metastatic disorders). They are also useful in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics), and in methods of treatment (e.g. therapeutic and prophylactic). The sequences may also be used to screen public databases to identify other family members or related sequences. The polypeptide sequences are useful as immunogens to generate antibodies that bind the polypeptides. The polynucleotide sequences are useful for mapping their respective genes on a chromosome, identifying gene regions associated with cellular proliferative or differentiative disorders, and in gene therapy. The present sequence encodes human GPCRK 69087

Query Match	100.0%	Score 2198;	DB 7;	Length 2198;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2198; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

OY	1	GACCCTTAAGATGAAGGGAACCTCACTATATAGGGCTCCAGAGCGGCGCCGCGGCAAGTGTCTTTC	60
Db	1	GACCCTTAAGATGAAGGGAACCTCACTATATAGGGCTCCAGAGCGGCGCCGCGGCAAGTGTCTTTC	60
OY	61	GCCTTGGCAGGTGGGAGCATGACCTATGTGTGTGCACTTCTCGGCGGCTATATCATACCA	120
Db	61	GCCTTGGCAGGTGGGAGCATGACCTATGTGTGTGCACTTCTCGGCGGCTATATCATACCA	120
OY	121	GTCAAAGCTCTTACAAAAGAAACCTCTTTTACACCTTCCAGGAGTCCACCCAGAGCC	180
Db	121	GTCAAAGCTCTTACAAAAGAAACCTCTTTTACACCTTCCAGGAGTCCACCCAGAGCC	180
OY	181	ACAGAGCTCACTGTAATTCCTTGGACGTTGTCTCACCCGGGAAAGGAAAGCAGCAGCA	240
Db	181	ACAGAGCTCACTGTAATTCCTTGGACGTTGTCTCACCCGGGAAAGGAAAGCAGCAGCA	240
OY	241	GCCTTCACGCTCTTGTGTCTTCCCTGGGAGTGTGCGCCCGTGTCAAGGCAAGTGTGACA	300
Db	241	GCCTTCACGCTCTTGTGTCTTCCCTGGGAGTGTGCGCCCGTGTCAAGGCAAGTGTGACA	300
OY	301	TGGGGGCGCTGGACACACTGATGCGCAACACGCTTACCTGAGGCGCGGAAAGCCCTCG	360
Db	301	TGGGGGCGCTGGACACACTGATGCGCAACACGCTTACCTGAGGCGCGGAAAGCCCTCG	360
OY	361	ACTGCGACGACAAAGAGTGTGACGCGCGCGCGGTGACTGTGGCCCTTCCCGGGCTGTAGG	420
Db	361	ACTGCGACGACAAAGAGTGTGACGCGCGCGCGGTGACTGTGGCCCTTCCCGGGCTGTAGG	420
OY	421	GCTGCGGGAGGCTCCGCGACAGAGCTGTGCTCGGAACCTTCCACAGCCTGTGTGAGCAGAC	480
Db	421	GCTGCGGGAGGCTCCGCGACAGAGCTGTGCTCGGAACCTTCCACAGCCTGTGTGAGCAGAC	480
OY	481	CCATCGGTGCGGCTCTTCCGTGACTTCCTAGCACAAGTGCACAGTTCGCAAGGCGG	540
Db	481	CCATCGGTGCGGCTCTTCCGTGACTTCCTAGCACAAGTGCACAGTTCGCAAGGCGG	540
OY	541	CACACTTCTTAAGGAGCGTGCAGAACTGGAGGCTGGCGGAGGAGGACCCACAAAGACA	600
Db	541	CACACTTCTTAAGGAGCGTGCAGAACTGGAGGCTGGCGGAGGAGGACCCACAAAGACA	600
OY	601	CGCGGCTGACGGGCGTGTGGCCACTTGTGTGAGTGCCTTGTCCCGGGAAACCTCGCAC	660
Db	601	CGCGGCTGACGGGCGTGTGGCCACTTGTGTGAGTGCCTTGTCCCGGGAAACCTCGCAC	660
OY	661	CGTTCCTCAGCCGCGTGGCCGACCAAGTCCAGAGCACCACACTGAGGAAAGGCGAG	720

Db	661	CTTTCCTGAGCCGAGCCGTGGCCAGACCAAGTGCAGAGCCACACTAGAGAAAGAGGAG	720
Qy	721	TGCGCTGAGTGAAGCTGGCGAAGCTGAGGCGATGGCTTTCTTGCAAGCAAGCCCTTTA	780
Db	721	TGCGCTGAGTGAAGCTGGCGAAGCTGAGGCGATGGCTTTCTTGCAAGCAAGCCCTTTA	780
Qy	781	AGGATTTGGTACAGAGGCGCTTACAGACAAAGTTTCGCAATGGAAAACCTTCCAGATGCG	840
Db	781	AGGATTTGGTACAGAGGCGCTTCTACAGAAAGTTTCGCAATGGAAAACCTTCCAGATGCG	840
Qy	841	AACCAATGTGACAGACAAATCACTAGTTCAAGTCTGGGGGAAAAGGTGGTTTGGGG	900
Db	841	AACCAATGTGACAGACAAATCACTAGTTCAAGTCTGGGGGAAAAGGTGGTTTGGGG	900
Qy	901	AGGATTTGGTACAGAGGCGCTTACAGACAAAGTTTCGCAATGGAAAACCTTCCAGATGCG	960
Db	901	AGGATTTGGTACAGAGGCGCTTACAGACAAAGTTTCGCAATGGAAAACCTTCCAGATGCG	960
Qy	961	AGGAGGCGTGAAGAAAGGTGGCGAGAAATGGCTCTTTGGAAAAGAAACTTTGG	1020
Db	961	AGGAGGCGTGAAGAAAGGTGGCGAGAAATGGCTCTTTGGAAAAGAAACTTTGG	1020
Qy	1021	AGGAGTGAAGAGCCCTTTCATTTGCTCTCTGGCGCTTAAGCTTTGAGACCAAGCCATC	1080
Db	1021	AGGAGTGAAGAGCCCTTTCATTTGCTCTCTGGCGCTTAAGCTTTGAGACCAAGCCATC	1080
Qy	1081	TCGGCCCTGTCAATGAGCGTGAATGAATGGGGGGAACCTCAATTTCAACTTCAACCTGG	1140
Db	1081	TCGGCCCTGTCAATGAGCGTGAATGAATGGGGGGAACCTCAATTTCAACTTCAACCTGG	1140
Qy	1141	GCAAGGTGGCGTGAATGAATGAATGGGGGGAACCTCAATTTCAACTTCAACCTGG	1200
Db	1141	GCAAGGTGGCGTGAATGAATGAATGGGGGGAACCTCAATTTCAACTTCAACCTGG	1200
Qy	1201	TGCGCAAGCTCCAGAAAGCTGGCAATCGCTATCGGGAATGAAGCTGAGATGCTTGG	1260
Db	1201	TGCGCAAGCTCCAGAAAGCTGGCAATCGCTATCGGGAATGAAGCTGAGATGCTTGG	1260
Qy	1261	TGATGACCTCGGCAACTGAGAGTTATGTAACCTGGGGCTGGCGGTGAGATGAAGGTTG	1320
Db	1261	TGATGACCTCGGCAACTGAGAGTTATGTAACCTGGGGCTGGCGGTGAGATGAAGGTTG	1320
Qy	1321	GCAAGCCCTATCCCAAGAGGCTGGAACCAATGGTTTCAATGGCTCCGAGATCCATATG	1380
Db	1321	GCAAGCCCTATCCCAAGAGGCTGGAACCAATGGTTTCAATGGCTCCGAGATCCATATG	1380
Qy	1381	AAAAGGTGAATTTCTTACCTGTGACATGGTTTGCATGGGATGAGCATTTATGAAA	1440
Db	1381	AAAAGGTGAATTTCTTACCTGTGACATGGTTTGCATGGGATGAGCATTTATGAAA	1440
Qy	1441	TGGTTGTGAGAGCAACCACTTAAAGTTTCAAGAAAAGGTGATGAAGAAGATCTGA	1500
Db	1441	TGGTTGTGAGAGCAACCACTTAAAGTTTCAAGAAAAGGTGATGAAGAAGATCTGA	1500
Qy	1501	AGCAAAAGACTGTGAGAGAGAGTCAATTTCCAGAGATGATATCTTCAAGAGAGAGCA	1560
Db	1501	AGCAAAAGACTGTGAGAGAGAGTCAATTTCCAGAGATGATATCTTCAAGAGAGAGCA	1560
Qy	1561	AAGATATTTGCAAGGCTTTCTTGGCTTAAGAAACCAAGCAAGCTTTAGAACAGAGAAA	1620
Db	1561	AAGATATTTGCAAGGCTTTCTTGGCTTAAGAAACCAAGCAAGCTTTAGAACAGAGAAA	1620
Qy	1621	AGTCTGATATCCCAAGAAACATCACTTTCTTAAACATCACTTCTCCGCTGAGAG	1680
Db	1621	AGTCTGATATCCCAAGAAACATCACTTTCTTAAACATCACTTCTCCGCTGAGAG	1680
Qy	1681	CTGCGCTTAATGAACCCCATTTGGCCAGACCTTCACTGGTTTATGCCAAAGCAATCG	1740
Db	1681	CTGCGCTTAATGAACCCCATTTGGCCAGACCTTCACTGGTTTATGCCAAAGCAATCG	1740
Qy	1741	CTGAAATGATGATTTCTTGAAGTTTGGGGGGTGAATTTGATGAAGAAATGACAGT	1800

	XX	New NOVX polypeptides and polynucleotides, useful in gene therapy,
	PT	particularly for treating or preventing a syndrome associated with a
	PT	human disease e.g. diabetes, obesity, cancer, Alzheimer's disease,
	PT	hypertension or hemophilia.
	XX	
	PS	Claim 20; SEQ ID NO 165; 748bp; English.
	XX	
	CC	The invention relates to new isolated NOVX polypeptides, the genes
	CC	encoding them or sequences having at least 95% identity to the amino acid
	CC	or nucleotide sequences. The NOVX polypeptide is useful as a therapeutic,
	CC	particularly in the manufacture of a medicament for treating a syndrome
	CC	associated with a human disease, which includes a pathology associated
	CC	with NOVX polypeptide. The NOVX polypeptide is particularly useful for
	CC	treating, preventing or alleviating pathology associated with NOVX
	CC	polypeptide in a mammal, e.g. a human. The NOVX nucleic acid and
	CC	polypeptide are especially useful for treating or preventing e.g.
	CC	diabetes, obesity, cancers (e.g. lymphoma, uterus cancer or prostate
	CC	cancer), dyslipidemias, anorexia, wasting disorders, Alzheimer's disease,
	CC	Parkinson's disorder, cachexia, cardiomyopathy, AIDS, asthma, Crohn's
	CC	disease, multiple sclerosis, hypertension, atherosclerosis, hemophilia,
	CC	graft-versus-host disease or Abiright hereditary osteodystrophy. The DNA
	CC	encoding the protein is useful in gene therapy for treating the above
	CC	conditions. These are also useful in developing powerful assay system for
	CC	functional analysis of various human disorders, as well as in diagnostic
	CC	applications. This sequence represents one of the NOVX genes of the
	CC	invention.
	CC	
	XX	
	SQ	Sequence 1821 BP; 453 A; 459 C; 524 G; 385 T; 0 U; 0 Other;
	Query Match	82.7%; Score 1817.8; DB 9; Length 1821;
	Best Local Similarity	99.9%; Pred. No. of
	Matches 1819, Conservative	0; Mismatches 2; Indels 0; Gaps 0
OY	CGGAGAGGGAAAGACAGCAGACCCTTCATGCCCTTGTGCTTTCCCTGGAGTGCGGC	278
DB	1 CGGAAAGGGAAGACAGCACAGCCCTCATAGCCCTTGTGCTTTCCCTGGAGTGCGGC	60
OY	279 CCGTGCTCAAGCCATGTGTGACATGTGGGGCCCTGTGAACAATTGATGCAACAACGGCCATAC	338
DB	61 CCGTGCTCAAGCCATGTGTGACATGTGGGGCCCTGTGAACAATTGATGCAACAACGGCCATAC	120
OY	339 CTGAGAGGCCCGGAGAACCCCTCGACTGTGCACAGCAAAGAAGCTGCAGCGCGCGGCGGTAGC	398
DB	121 CTGAGAGGCCCGGAGAACCCCTCGACTGTGCACAGCAAAGAAGCTGCAGCGCGCGGCGGTAGC	180
OY	399 CTGAGCCCTGCGCGGCTGTGCAGGGCTGTGGCGGAGTCCGCGAAGCTGTCTTGAATTC	458
DB	181 CTGAGCCCTGCGCGGCTGTGCAGGGCTGTGGCGGAGTCCGCGAAGCTGTCTTGAATTC	240
OY	459 CACAGCCCTGTGTGAGCAGCAGCCANCGGTGTGCGGCTTTCCTGTGACTCTTAGCCACA	518
DB	241 CACAGCCCTGTGTGAGCAGCAGCCATCGGTGTGCGGCTTTCCTGTGACTCTTAGCCACA	300
OY	519 GTGCGCCACGTTCCGAGAGCGGCAACCTTCTCTAGAGGACGTGTGCAAACTGGGAGCTGGCC	578
DB	301 GTGCGCCACGTTCCGAGAGCGGCAACCTTCTCTAGAGGACGTGTGCAAACTGGGAGCTGGCC	360
OY	579 GAGAGAGGACCCACCAANAAGACGCGGTGTGAGGGGCTGTGTGCACTGTGTGAGTGGC	638
DB	361 GAGAGAGGACCCACCAANAAGACGCGGTGTGAGGGGCTGTGTGCACTGTGTGAGTGGC	420
OY	639 CCTGCCCCCGGGAGAACCGGCAACCTTCTCTCAAGCAGGCGGTGTGACACGATGCCAAGCA	698
DB	421 CCTGCCCCCGGGAGAACCGGCAACCTTCTCTCAAGCAGGCGGTGTGACACGATGCCAAGCA	480
OY	699 GCACCACTGAGAGGAAGACGAGTGTGTGACATGACCTTGTGAAAGCTTAGAGCTCATGGCT	758
DB	481 GCACCACTGAGAGGAAGACGAGTGTGTGACATGACCTTGTGAAAGCTTAGAGCTCATGGCT	540
OY	759 TTCTTGAAGAGACACCCCTTAAGATTTCTGTACACAGGCGCTTCTATGACAAGTTTCTG	818
DB	541 TTCTTGAAGAGACACCCCTTAAGATTTCTGTACACAGGCGCTTCTATGACAAGTTTCTG	600

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QY 819 CAGTGAAGAACTCTTGCAGATGACACCACTGTCAACAAGTACTTCACTGAGTTCAAGTGTG 878
| | | | |
Db 601 CAGTGAAGAACTCTTGCAGATGACACCACTGTCAACAAGTACTTCACTGAGTTCAAGTGTG 660
QY 879 CTGGGAGAAAGGTGGTGGTGGGAGGATGTCGCTCCAGGTGAAAAACCTGGAGAAAGT 938
| | | | |
Db 661 CTGGGAGAAAGGTGGTGGGAGGATGTCGCTCCAGGTGAAAAACCTGGAGAAAGT 720
QY 939 TATGCTGTGAAGAACTGACCAAGAGCGCTGAAGAGAAAGAGTGGCGAGAAAGTGGCT 998
| | | | |
Db 721 TATGCTGTGAAGAACTGACCAAGAGCGCTGAAGAGAAAGAGTGGCGAGAAAGTGGCT 780
QY 999 CTCTTGGAAAAAGAAATCTTGGAGAAAGTGCAGAGCCCTTTCATTTGCTCTCTGGCCTAT 1058
| | | | |
Db 781 CTCTTGGAAAAAGAAATCTTGGAGAAAGTGCAGAGCCCTTTCATTTGCTCTCTGGCCTAT 840
QY 1059 GCGTTGAGACAGAACCCATCTCGCTGTGTCAAGAGCTGTAAGATGGGGAGAGCTTC 1118
| | | | |
Db 841 GCGTTGAGACAGAACCCATCTCTGCTGTGTCAAGAGCTGTAAGATGGGGAGAGCTTC 900
QY 1119 AAGTTCACATCTTCAACAGTGGGACAGCGTGGCTGGAATAGAGCGGGTGTATCTTTTAC 1178
| | | | |
Db 901 AAGTTCACATCTTCAACAGTGGGACAGCGTGGCTGGAATAGAGCGGGTGTATCTTTTAC 960
QY 1179 TCGGCCAGATAGCTGTGGGATGCTGCACTCTCATGAACTCGGATCTGTATTCGGGAC 1238
| | | | |
Db 961 TCGGCCAGATAGCTGTGGGATGCTGCACTCTCATGAACTCGGATCTGTATTCGGGAC 1020
QY 1239 ATGAAGCTGAGAAATGTCCTCTGATGACCTCGGAGACCTGAGAGTTATCTGACCTGGAG 1298
| | | | |
Db 1021 ATGAAGCTGAGAAATGTCCTCTGATGACCTCGGAGACCTGAGAGTTATCTGACCTGGAG 1080
QY 1299 CTGGCCCTGAGATGAAGAGGTGGCAAGCCCATCAGACAGAGGCTGGAAACCAATGGTTAC 1358
| | | | |
Db 1081 CTGGCCCTGAGATGAAGAGGTGGCAAGCCCATCAGACAGAGGCTGGAAACCAATGGTTAC 1140
QY 1359 ATGGCTCTGAGATCTTAATGAGAAAGGTAAAGTTATTCCTATCTGAGACTGGTTTGC 1418
| | | | |
Db 1141 ATGGCTCTGAGATCTTAATGAGAAAGGTAAAGTTATTCCTATCTGAGACTGGTTTGC 1200
QY 1419 ATGGAGTGCAGCAATTTATGAATGTGTCTGAGCAACCACTTCAAAAGTTTCAAGGAA 1478
| | | | |
Db 1201 ATGGAGTGCAGCAATTTATGAATGTGTCTGAGCAACCACTTCAAAAGTTTCAAGGAA 1260
QY 1479 AAGTCACTAAGAGATCTGAAGCAAGAACTCTGCAAGAGAGTCAATTTCCAGCAT 1538
| | | | |
Db 1261 AAGTCACTAAGAGATCTGAAGCAAGAACTCTGCAAGAGAGTCAATTTCCAGCAT 1320
QY 1539 GATTACTTCAAGAGAGCAAGAAAGATATTGAGAGGCTCTTCTTGGCTAAGAAACAGAG 1598
| | | | |
Db 1321 GATTACTTCAAGAGAGCAAGAAAGATATTGAGAGGCTCTTCTTGGCTAAGAAACAGAG 1380
QY 1599 CAAGCTTAGAGAGAGAGAGAAAGTCTGATGATCCCAAGAAACATCTTTCTTTAAACG 1658
| | | | |
Db 1381 CAAGCTTAGAGAGAGAGAGAAAGTCTGATGATCCCAAGAAACATCTTTCTTTAAACG 1440
QY 1659 ATCAACTTCTCGCTGAGAGCTGCTAATTTGAACCCCATTTGGCCAGAACCTTCA 1718
| | | | |
Db 1441 ATCAACTTCTCGCTGAGAGCTGCTAATTTGAACCCCATTTGGCCAGAACCTTCA 1500
QY 1719 GTGGTTTATGCAAAAGACATGCTGAAATTTGATTTCTGAGGTTGGGGGGGTGAAA 1778
| | | | |
Db 1501 GTGGTTTATGCAAAAGACATGCTGAAATTTGATTTCTGAGGTTGGGGGGGTGAAA 1560
QY 1779 TTTGATGACAAAGATAGAGTCTTCAAAAATCTTGGAGAGAGTGTCTTCTTATACA 1838
| | | | |
Db 1561 TTTGATGACAAAGATAGAGTCTTCAAAAATCTTGGAGAGAGTGTCTTCTTATWACA 1620
QY 1839 TGGCAGAGAGAAATTTATGAAACGGGACTGTTTGAAGAACTGATAGCCCAAGAGACT 1898
| | | | |
Db 1621 TGGCAGAGAGAAATTTATGAAACGGGACTGTTTGAAGAACTGATAGCCCAAGAGACT 1680

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QY 1899 ACGGTTTGAAGAGAGGTAATTATCAAGTCTGCGTGTGTTTGTATTGTAATTTGCT 1958
| | | | |
Db 1681 ACGGTTTGAAGAGAGGTAATTATCAAGTCTGCGTGTGTTTGTATTGTAATTTGCT 1740
QY 1959 CTCTTTACAGACAGGACAGAGAGTCTGGGTGACATTAATCTCGAATGTTCCAGAGT 2018
| | | | |
Db 1741 CTCTTTACAGACAGGACAGAGAGTCTGGGTGACATTAATCTCGAATGTTCCAGAGT 1800
QY 2019 GGAATCTGTGGAATGAGGGC 2039
| | | | |
Db 1801 GGAATCTGTGGAATGAGGGC 1821

RESULT 5
ABZ56943
ID ABZ56943 standard; DNA; 1761 BP.
AC ABZ56943;
XX
XX 04-APR-2003 (first entry)
XX
XX Human gene sequence relative to the invention # SEQ ID 11.
XX
XX Human; heart disease; cancer; omentopathy; gene; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 26..1687
XX FT /tag= a
XX
XX MO2002103020-A1.
XX
XX PD 27-DEC-2002.
XX
XX PF 14-JUN-2002; 2002MO-JP005942.
XX
XX PR 15-JUN-2001; 2001JP-00182654.
XX
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Koyama N, Tanida S, Yamamoto K;
XX
XX MPI; 2003-157045/15.
XX
XX P-PSDB; ABP60079.
XX
XX PT Novel disease-associated gene of the RGS gene family and its product,
XX applicable in diagnosis of and screening for drugs for heart diseases,
XX cancers and omentopathy.
XX
XX Example 3; Page 85-86; 96pp; Japanese.
XX
XX CC The invention relates to a novel disease associated gene and its uses.
XX CC The gene and its encoded protein are useful for diagnosis of and
XX CC screening for drugs for heart diseases, cancers and omentopathy. The
XX CC current sequence represents a human gene sequence relative to the
XX CC invention
XX
XX SQ Sequence 1761 BP; 441 A; 441 C; 504 G; 375 T; 0 U; 0 Other;

Query Match 80.0%; Score 1757.8; DB 7; Length 1761;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1759; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 266 CTGGAGTGTGCGCCCGTGTCTGACCTCATGTGGAATGAGGAGCCCTGGAGCAACTGATCGC 325
| | | | |
Db 1 CTGGAGTGTGCGCCCGTGTCTGACCTCATGTGGAATGAGGAGCCCTGGAGCAACTGATCGC 60
QY 326 CAACACCGGCTTACCTGCAAGGCGCCGAGAGCCCTGGAAGTGGAGAGAGCTGACAGG 385
| | | | |
Db 61 CAACACCGGCTTACCTGCAAGGCGCCGAGAGCCCTGGAAGTGGAGAGAGCTGACAGG 120
QY 386 GCGGCGGCGTACCTGAGCTGCGCCGAGGCTGCAAGGCTGCGGAGAGCTCGGCAAGAGCT 445
| | | | |

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Db		1201	AGATTCAAGGAAAGAGTCAATTAAGAGACTCGAAGCAAAGAATCTTGCAAGACGAGGT	1260
Oy		1526	CAATTTCCAGATATATTAATCTTCAGCAGGAGAGCAAAAATAATTTGGAGGCTCTCTTGCG	1589
Db		1261	CAAAATTCAGAGTGAATTAATCTTCCAAGGAGAAAGAAAAATATTTGGAGGCTCTCTTGCG	1320
Oy		1586	TAAAGAACCCAGAGCAACGCTTTAGAGACAGCAAGAAAAGCTGATGATCCCGAGAAACATCA	1645
Db		1331	TAGAAACCCAGAGCAACGCTTTAGAGACAGCAAGAAAAGCTGATGATCCCGAGAAACATCA	1380
Oy		1646	TTTTCTTAAANAGATCAACTTTCCTGCCTGAGAGCTGACCCTAATTGAAACCCCATTTGT	1705
Db		1381	TTTCTTAAANAGATCAACTTTCCTGCCTGAGAGCTGACCCTAATTGAAACCCCATTTGT	1440
Oy		1706	GCCAGACCCCTCAGTGGTTATGCCAAGACATCCGTGAATTGATGATTTCTCGAGGT	1765
Db		1441	GCCAGACCCCTCAGTGGTTATGCCAAGACATCCGTGAATTGATGATTTCTCGAGGT	1500
Oy		1766	TCCGGGGGGGTGAATTTTGATGACAAGAGTAAGCAGTTCTTCAAAACTTTGCGACAGGTGC	1821
Db		1501	TCCGGGGGGGTGAATTTTGATGACAAGAGTAAGCAGTTCTTCAAAACTTTGCGACAGGTGC	1560
Oy		1826	TGTTCTATAGCATATGACAGAGAAATTAATAGAAAACGGACTGTTTGAAGAACTGAATGA	1885
Db		1561	TGTTCTATAGCATATGACAGAGAAATTAATAGAAAACGGACTGTTTGAAGAACTGAATGA	1620
Oy		1886	CCCCAACAACCTTCGSGGTTGTGAGAGAGGTTATTCATCCAAAGCTGAGGCTGTGTTGTT	1945
Db		1621	CCCCAACAACCTTCGSGGTTGTGAGAGAGGTTATTCATCCAAAGCTGAGGCTGTGTTGTT	1680
Oy		1946	ATTGTAATATGCTCTCTTTACACAGACAGGAGCAGGAGTCTCGGCTGACATATATCTCCA	2005
Db		1681	ATTGTAATATGCTCTCTTTACACAGACAGGAGCAGGAGTCTCGGCTGACATATATCTCCA	1740
Oy		2006	ATGTTCCACACGTGGAAATCT 2026	
Db		1741	ATGTTCCACACGTGGAAATCT 1761	
RESULT 6				
ABQ86178				
ID		ABQ86178	standard; DNA; 1662 bp.	
XX		ABQ86178;		
AC		10-SEP-2002	(first entry)	
XX				
DT				
DE			Novel human gene. SEQ ID 49.	
XX				
KM			Human; cytostratic; vulnery; antilarteriosclerotic; antiparkinsonian;	
KM			nootropic; neuroprotective; immunosuppressive; haemostatic;	
KM			antiinflammatory; cardiant; antidiucic; vituicide; antithyroid;	
KM			cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;	
KM			wound healing disorders; athrosclerosis; Parkinson's disease;	
KM			Alzheimer's disease; autoimmune disorder; haematopoietic disorder;	
KM			inflammation; neoplastic disease; nervous system disorder;	
KM			cardiovascular disorders; pancreatitis; respiratory disorder;	
KM			hyperproliferation; systemic autoimmune disease; hyper-immunity;	
KM			developmental abnormality; gastrointestinal ulceration; neuropathy;	
KM			haematological disease; metabolic diseases; sperm dysfunction;	
KM			thyroid disorder; hypochyroidism; brain damage; colitis;	
KM			cone photo-transduction deficiency; neurological disease; stroke;	
KM			angioneuensis; ovulation disorder; spinal cord; thyroid gland; heart;	
KM			trachea; thymus; lymph node; muscular system; obesity; anorexia;	
KM			growth abnormality; precocious puberty; gene; ss.	
OS			Homo sapiens.	
PN			WO200250105-A1.	
PD			27-JUN-2002.	
XX				
PF			17-DEC-2001; 2001MO-US049232.	

	RESULT 6
ABQ86178	
ID	ABQ86178 standard; DNA; 1662 BP.
XX	
AC	ABQ86178;
XX	
DT	10-SEP-2002 (first entry)
XX	
DE	Novel human gene. SEQ ID 49.
XX	
KW	Human; cytosstatic; vulnerey; antitartreiosclerotic; antiparkinsonian;
KW	neotrophic; neuroprotective; immunosuppressive; haemostatic;
KW	antihypertory; cardiac; antilucifer; vitucide; antithyroid;
KW	cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
KW	wound healing disorders; atherosclerosis; Parkinson's disease;
KW	Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
KW	inflammation; neoplastic disease; nervous system disorder;
KW	cardiovascular disorders; pancreatitis; respiratory disorder;
KW	hyperproliferation; systemic autoimmune disease; hyper-immunity;
KW	developmental abnormality; gastrointestinal ulceration; neuropathy;
KW	haematological disease; metabolic disease; sperm dysfunction;
KW	thyroid disorder; hypothyroidism; brain damage; colitis;
KW	cone photo-transduction deficiency; neurological disease; stroke;
KW	angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;
KW	trachea; thymus; lymph node; muscular system; obesity; anorexia;
XX	growth abnormality; precocious puberty; gene; ss.
XX	
OS	Homo sapiens.
PN	WO200250105-A1.
XX	
PD	27-JUN-2002.
XX	
PF	17-DEC-2001; 2001WO-US049232.

XX 19-DEC-2000; 2000US-0256710P.
PR 20-DEC-2000; 2000US-0257048P.
PR 09-JAN-2001; 2001US-0260482P.
PR 30-JAN-2001; 2001US-0264922P.
PR 06-FEB-2001; 2001US-0266797P.
PR 19-MAR-2001; 2001US-0276988P.
PR 04-APR-2001; 2001US-0281535P.
PR 08-MAY-2001; 2001US-0289622P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Agarwal P, Birkeland M, Cogswell JP, Kadnick KF, Lai Y;
PI Martensen SA, Rikvi SK, Smith RF, Strum JC, Xie Q;
XX
XX MPI: 2002-508784/54.
DR P-8EDB; ABP61013.
XX
XX Secreted proteins and polynucleotides useful as vaccines for preventing
PT or treating various diseases e.g. cancer, wounds, atherosclerosis,
PT Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.
XX
PS Claim 2(a); Page 255-256; 335pp; English.
XX
XX The invention relates to an isolated polypeptide with signal sequences
CC which allow it to be secreted extracellularly or membrane associated. The
CC activity of polypeptides of the invention may be described as,
CC cytosolic, vunerary, antiarteriosclerotic, antiparkinsonian, nootropic,
CC neuroprotective, immunosuppressive, haemostatic, antiinflammatory,
CC cardiant, antitumor, virucide, antihypertensive, cerebroprotective, anorectic,
CC and metabolic. Polypeptides and polynucleotides of the invention are
CC useful in the treatment, or as a vaccine in the prevention of, cancer,
CC wound healing disorders, infection, atherosclerosis, Parkinson's disease
CC and Alzheimer's disease, autoimmune disorder, hematopoietic disorder,
CC inflammation, neoplastic diseases, nervous system related disorders and
CC cardiovascular disorders, pancreatitis, respiratory disorder,
CC hyperproliferation, systemic autoimmune disease, hyper-immunity,
CC developmental abnormality, gastrointestinal ulceration, neuropathy,
CC haematological diseases, metabolic diseases, sperm dysfunction, thyroid
CC disorders e.g. hypothyroidism, brain damages, colitis, cone photo-
CC transduction deficiency, neurological diseases, stroke, angiodogenesis,
CC ovulation disorders, diseases in the spinal cord, thyroid gland, heart,
CC trachea, thymus, lymph node and muscular system, obesity, anorexia,
CC growth abnormalities, and alleviation of precocious puberty. The
CC sequences given in records ABQ66130-ABQ66184 represent novel human cDNA's
CC of the invention
XX
SQ Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;
Query Match 75.5%; Score 1658.8; DB 6; Length 1662;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 241 CGCAAGGCGCAACCTTCCTAGAGACGTGCAAGACTGGAGCTGCGAGAGGAGACC 300
QY ACCAAGAAGAGCGCGCTGAGAGGAGCTGATGGCCACTGTGTGAGAGTCCCTGCCCCGAGG 650
QY 591 ACCAAGAAGAGCGCGCTGAGAGGAGCTGATGGCCACTGTGTGAGAGTCCCTGCCCCGAGG 650
Db 301 ACCAAGAAGAGCGCGCTGAGAGGAGCTGATGGCCACTGTGTGAGAGTCCCTGCCCCGAGG 360
QY 651 AACCCGCAACCTTCCTGAGCGAGGCGTGGCCAGCAAGTCCAGACAGCAGCAGTGG 710
Db 361 AACCCGCAACCTTCCTGAGCGAGGCGTGGCCAGCAAGTCCAGACAGCAGCAGTGG 420
QY 711 GAAAGAGAGTGGCTGAGTACGCTGCGAAGAGCTGAGGCTATGCTTTCTTGAAGAG 770
Db 421 GAAAGAGAGTGGCTGAGTACGCTGCGAAGAGCTGAGGCTATGCTTTCTTGAAGAG 480
QY 771 CAGCCCTTTAAGATTTGTGTACCAAGGCGCTTCTGAGCAAGTTCTGAGAGGAAATC 830
Db 481 CAGCCCTTTAAGATTTGTGTACCAAGGCGCTTCTGAGCAAGTTCTGAGAGGAAATC 540
QY 831 TTGAGATGCAACAGTGTGAGCAAGTACTTCACTGAGTTCAAGTGTGCGGAAAGT 890
Db 541 TTGAGATGCAACAGTGTGAGCAAGTACTTCACTGAGTTCAAGTGTGCGGAAAGT 600
QY 891 GGTTTGGGAGGATGTGCTGCTGAGTGAAGAAACACTGGAAAGATGTATGCTGTAG 950
Db 601 GGTTTGGGAGGATGTGCTGCTGAGTGAAGAAACACTGGAAAGATGTATGCTGTAG 660
QY 951 AACCTGACAGAGAGCGGCTGAAGAGAAAGTGGCGAGAAAGTGGCTCTTGGAAAG 1010
Db 661 AACCTGACAGAGAGCGGCTGAAGAGAAAGTGGCGAGAAAGTGGCTCTTGGAAAG 720
QY 1011 GAAATCTTGGAGAGGTGAGAGGCTTTCAATGTCTCTGAGCTATGCTTTGAGAGC 1070
Db 721 GAAATCTTGGAGAGGTGAGAGGCTTTCAATGTCTCTGAGCTATGCTTTGAGAGC 780
QY 1071 AAGAGCCATTTGCTGCTTGTATGAGCTGATGAATGGGAGAGACTCAATGTTCAATC 1130
Db 781 AAGAGCCATTTGCTGCTTGTATGAGCTGATGAATGGGAGAGACTCAATGTTCAATC 840
QY 1131 TACAAGTGGGACGCGGTGAGCATGAGAGCGGGATGATCTTTAATCGGCGCAGATA 1190
Db 841 TACAAGTGGGACGCGGTGAGCATGAGAGCGGGATGATCTTTAATCGGCGCAGATA 900
QY 1191 GCTGTGGAGATGCTGACCTTCATGAACTCGGATGCTGATCGGAGCATGAGAGCTGAG 1250
Db 901 GCTGTGGAGATGCTGACCTTCATGAACTCGGATGCTGATCGGAGCATGAGAGCTGAG 960
QY 1251 AATGTGCTTGTGAGATGCTGAGCACTGAGATGCTGATGACTGCGGAGCTGAGAG 1310
Db 961 AATGTGCTTGTGAGATGCTGAGCACTGAGATGCTGATGACTGCGGAGCTGAGAG 1020
QY 1311 ATGAAGGATGGAGAGCCATACCCAGAGGAGCTGGAAACAAATGTTACATGGCTCGAG 1370
Db 1021 ATGAAGGATGGAGAGCCATACCCAGAGGAGCTGGAAACAAATGTTACATGGCTCGAG 1080
QY 1371 ATCTTAATGAGAAAGTAAATTTCTTATCTCTGAGATGCTGTTTCCATGAGATGAGC 1430
Db 1081 ATCTTAATGAGAAAGTAAATTTCTTATCTCTGAGATGCTGTTTCCATGAGATGAGC 1140
QY 1431 ATTATTAATGAGTGTGCTGAGCAAGCAACATTCATTAAGAAAGTCAATGAA 1490
Db 1141 ATTATTAATGAGTGTGCTGAGCAAGCAACATTCATTAAGAAAGTCAATGAA 1200
QY 1491 GAGGATGAGCAAGAACTGTGCAAGAGAGGCAAAATTCAGAGATATATCATGACA 1550
Db 1201 GAGGATGAGCAAGAACTGTGCAAGAGAGGCAAAATTCAGAGATATATCATGACA 1260
QY 1551 GAGGAGCAAAAGATATTTGAGGCTCTTCTGCTAAGAAACAGAGCAAGCTTGAAG 1610
Db 1261 GAGGAGCAAAAGATATTTGAGGCTCTTCTGCTAAGAAACAGAGCAAGCTTGAAG 1320
QY 1611 AGCAGAGAAAGTCTGATGATCCCAAGAAACATATTTCTTTAAACAGTAACTTTCT 1670
Db 1321 AGCAGAGAAAGTCTGATGATCCCAAGAAACATATTTCTTTAAACAGTAACTTTCT 1380

QY 1671 CGCTGGAGAGCTGGCTTAATTGACCCCATTTGTCAGACCCCTTGAGTGTATGCG 1730
 DB 1381 CGCTGGAGAGCTGGCTTAATTGACCCCATTTGTCAGACCCCTTGAGTGTATGCG 1440
 QY 1731 AAGACATCGCTGAATTAATGATTTCTCTGAGGGTTCGAGGAGTTGATGACAA 1790
 DB 1441 AAGACATCGCTGAATTAATGATTTCTCTGAGGGTTCGAGGAGTTGATGACAA 1500
 QY 1791 GATAGCAGTCTTCAAAAACCTTGGCAGAGTCTCTTCTATAGCATGGCAGAA 1850
 DB 1501 GATAGCAGTCTTCAAAAACCTTGGCAGAGTCTCTTCTATAGCATGGCAGAA 1560
 QY 1851 ATTAATGAGAGGGAGCTGTTTGGAGACCTGAATACCCCAAGACCTAGGGTGTGAG 1910
 DB 1561 ATTAATGAGAGGGAGCTGTTTGGAGAGCTGAATACCCCAAGACCTAGGGTGTGAG 1620
 QY 1911 GAGGTTAATTCATCCAGTCTGCGTGTGTTTATTTGTA 1952
 DB 1621 GAGGTTAATTCATCCAGTCTGCGTGTGTTTATTTGTA 1662

RESULT 7
 AAD26466 standard; cDNA; 1662 BP.
 ID AAD26466;
 AC AAD26466;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human kinase PKIN-19 cDNA.
 XX

Human; kinase; PKIN-19; cancer; leukaemia; adenocarcinoma; osteoporosis;
 immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;
 Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;
 allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;
 autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;
 Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;
 rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;
 hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;
 cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;
 congestive heart failure; ischaemic heart disease; lung tumour; gout;
 fatty liver; Niemann-Pick's disease; gene therapy; ss.

OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1662
 FT /*tag= a
 FT /product= "Human PKIN-19 protein"
 XX
 XX
 PN W0200196547-A2
 XX
 PD 20-DEC-2001.
 XX
 XX
 PF 14-JUN-2001; 2001MO-US019444.
 XX
 PR 15-JUN-2000; 2000US-0212073P.
 PR 23-JUN-2000; 2000US-0213467P.
 PR 30-JUN-2000; 2000US-021651P.
 PR 07-JUL-2000; 2000US-021650P.
 PR 13-JUL-2000; 2000US-0218372P.
 PR 25-AUG-2000; 2000US-0228056P.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 XX
 PI Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;
 PI Gandhi AR, Tribouley CW, Walla NK, Yao MG, Lu DM, Greenwald SR,
 PI Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT,
 PI Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gurunajan R,
 PI Lo TP, Khan F, Reclison SA, Azimtai Y, Policky DJ, Ding L,
 PI Grether W, Elliott VS, Thangavelu K, Bacra S, Ison CH;
 XX

DR WP1; 2002-090207/12.
 DR P-PSDB; AAE16273.
 XX
 FT New polypeptides, useful for diagnosing, treating or preventing disorders
 FT of growth and development, cardiovascular and lipid, and diseases such as
 FT cancer, comprise human kinase polypeptides.
 PS
 XX
 Claim 5, Page 190; 197pp; English.

The invention relates to human kinase PKIN proteins and their
 corresponding cDNAs. A composition containing PKIN agonist is useful for
 treating a disease or condition associated with decreased expression of
 PKIN and a composition comprising PKIN antagonist is useful for treating
 a disease or condition associated with overexpression of PKIN. The
 disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,
 myeloma, sarcoma, teratocarcinoma, Hodgkin's disease), immune disorder
 (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,
 atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,
 autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes
 mellitus, multiple sclerosis, Good pasture's syndrome, Reiter's disease,
 osteoarthritis, osteoporosis, pancreatitis, psoriasis, ulcerative colitis,
 rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,
 bacterial, parasitic, fungal, viral, protozoal and helminthic infections)
 growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,
 Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts), cardio
 vascular disease (arteriovenous fistula, hypertension, vasculitis,
 aneurysms, congestive heart failure, angina pectoris, myocarditis,
 ischaemic heart disease, chronic bronchitis, lung tumours), lipid
 disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,
 hypcholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity
 of a test compound and in gene therapy. The present sequence is human
 PKIN-19 cDNA

Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;
 50

Query Match 75.5%; Score 1658.8; DB 6; Length 1662;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1660; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

291 ATGGTGAACATGGGGGCGCTGACCACTGATGGCAACCGCTACCTGAGGCGG 350
 1 ATGGTGAACATGGGGGCGCTGACCACTGATGGCAACCGCTACCTGAGGCGG 60
 351 AAGCCTCGGACTGCGACAGCAAGAGCTGACGCGCGCGCTGAGCCTGCGCC 410
 61 AAGCCTCGGACTGCGACAGCAAGAGCTGACGCGCGCGCTGAGCCTGCGCC 120
 411 GGGCTGACGAGGCTGCGGAGCTCGCAGAGCTGCTCTGAACTTCCACAGCTGTGT 470
 121 GGGCTGACGAGGCTGCGGAGCTCGCAGAGCTGCTCTGAACTTCCACAGCTGTGT 180
 471 GAGCAGAGGCGCATGCGGTGCGCGCTTTCCTGAGCTTCCAGGCAAGTGCACGTTT 530
 181 GAGCAGAGGCGCATGCGGTGCGCGCTTTCCTGAGCTTCCAGGCAAGTGCACGTTT 240
 531 CGCAGAGGCGCAACTTCTCTAGAGAGCTGACGAACCTGAGCTGAGGAGGAGCC 590
 241 CGCAGAGGCGCAACTTCTCTAGAGAGCTGACGAACCTGAGCTGAGGAGGAGCC 300
 591 ACCAAAGACGCGGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGGAGG 650
 301 ACCAAAGACGCGGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGGAGG 360
 651 AACCGGCAACCTTCTCTAGAGAGCTGAGGAGCTGAGGAGCTGAGGAGGAGG 710
 361 AACCGGCAACCTTCTCTAGAGAGCTGAGGAGCTGAGGAGCTGAGGAGGAGG 420
 711 GAAAGCAGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGG 770
 421 GAAAGCAGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGCTGAGGAGG 480
 771 GAGCCTTTAAGATTTTGTATCCAGGCGCTTCTAGCAAGTTTTCAGAGTGAATC 830

Db 481 CAGCCCTTAAGGATTTGTCAGACAGCGCTTACAGACAAAGTTCTGACAGTAACTC 540
 QY 831 TTGAGATGCAACCAAGTGTGAGCAAGATCTTCACTGAGTTCAGAGTGTGGGAAAGT 890
 Db 541 TTGAGATGCAACCAAGTGTGAGCAAGATCTTCACTGAGTTCAGAGTGTGGGAAAGT 600
 QY 891 GGTTTGGGAGGATATGCGCTCCAGGTTGAAAAAAGCTGGGAAATATGCTGTANG 950
 Db 601 GGTTTGGGAGGATATGCGCTCCAGGTTGAAAAAAGCTGGGAAATATGCTGTANG 660
 QY 951 AAAGTGAAGCAAGAGCGGCTGAAAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1010
 Db 661 AAAGTGAAGCAAGAGCGGCTGAAAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 QY 1011 GAATCTTGGAGAAAGTCAAGAGCGCTTCACTGAGTTCAGAGTGTGGGAAAGT 1070
 Db 721 GAATCTTGGAGAAAGTCAAGAGCGCTTCACTGAGTTCAGAGTGTGGGAAAGT 780
 QY 1071 AAGACCCATCTCTGCTTGTGATGAGCTGATGAAATGGGAGAGAGAGAGAGAGAGAG 1130
 Db 781 AAGACCCATCTCTGCTTGTGATGAGCTGATGAAATGGGAGAGAGAGAGAGAGAGAG 840
 QY 1131 TACAAGTGGGAG 1190
 Db 841 TACAAGTGGGAG 900
 QY 1191 GCTGTGGAGATGTCAGACCTTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1250
 Db 901 GCTGTGGAGATGTCAGACCTTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
 QY 1251 AATGTGCTTGGAGATGTCAGACCTTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1310
 Db 961 AATGTGCTTGGAGATGTCAGACCTTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
 QY 1311 ATGAAGGTTGGCAAGCCCATCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1370
 Db 1021 ATGAAGGTTGGCAAGCCCATCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
 QY 1371 ATCTTAATGAAAAAGTAAATCTTCTATCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1430
 Db 1081 ATCTTAATGAAAAAGTAAATCTTCTATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
 QY 1431 ATTTATGAAATGTTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1490
 Db 1141 ATTTATGAAATGTTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
 QY 1491 GAGGATCTGAAGCAAGAACTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1550
 Db 1201 GAGGATCTGAAGCAAGAACTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
 QY 1551 GAGGAGCAAGAAATATTTGAGAGCTCTTCTGCTTGAAGAAACAGAGAGAGAGAGAG 1610
 Db 1261 GAGGAGCAAGAAATATTTGAGAGCTCTTCTGCTTGAAGAAACAGAGAGAGAGAGAG 1320
 QY 1611 AAGCAAGAAAAAGTGTGATGATCCAGGAAACATCATTTCTTAAACAGATCAACTTCT 1670
 Db 1321 AAGCAAGAAAAAGTGTGATGATCCAGGAAACATCATTTCTTAAACAGATCAACTTCT 1380
 QY 1671 CCGCTGAAGCTGGCCCTAATGAAACCCCATTTTGGCCAGAGAGAGAGAGAGAGAGAGAG 1730
 Db 1381 CCGCTGAAGCTGGCCCTAATGAAACCCCATTTTGGCCAGAGAGAGAGAGAGAGAGAGAG 1440
 QY 1731 AAAGATCATGCTGAAATGATGATTTCTGAGAGTTCGAGAGAGAGAGAGAGAGAGAGAG 1790
 Db 1441 AAAGATCATGCTGAAATGATGATTTCTGAGAGTTCGAGAGAGAGAGAGAGAGAGAGAG 1500
 QY 1791 GATAGCAAGTTCTTCAAAAACCTTTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1850
 Db 1501 GATAGCAAGTTCTTCAAAAACCTTTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1560
 QY 1851 ATTATGAAAG 1910
 Db 1561 ATTATGAAAG 1620

QY 1911 GAGGATATTCATCCAGTCTGAGTGTGTTGTTATTTGTA 1952
 Db 1621 GAGGATATTCATCCAGTCTGAGTGTGTTGTTATTTGTA 1662

RESULT 8
 AAD46350
 ID AAD46350 standard; cDNA; 1662 BP.
 XX
 AC AAD46350;
 XX
 DT 27-JAN-2003 (first entry)
 XX
 DE Human cone opsin kinase (GRK7) cDNA.
 XX
 KW Human; enzyme; cone opsin kinase; G-protein coupled receptor kinase 7;
 KW GRK7; cone visual signalling; visual sensitivity; visual resolution;
 KW night blindness; colour blindness; Oguchi disease; pineal gland activity;
 KW chromobiological desynchrony; depression; anxiety; memory loss; headache;
 KW mental foginess; fatigue; jet lag; circadian rhythm; ophthalmological;
 KW gene therapy; antidepressant; analgesic; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 1..1662
 FT CDS /tag= a
 FT /product= "Human GRK7 protein"
 FT
 PN WC0200272541-A2.
 XX
 PD 19-SEP-2002.
 XX
 EF 07-MAR-2002; 2002M0-US007025.
 XX
 PR 07-MAR-2001; 2001US-0274006P.
 XX
 PA (IMMW) IMMUNEX CORP.
 XX
 PI Bird TR, Spencer M, Mosley BA;
 XX
 DR WPI; 2002-723307/78.
 DR P-PSDB; AAE28952.
 XX
 PT Identifying compounds that alter inhibition of cone opsin kinase
 PT polypeptide activity for creating a conditions related to cone visual
 PT signalling, comprises mixing a compound with a cone opsin kinase and with
 PT an inhibitory polypeptide.
 XX
 PS Example 4; Page 45-46; 61pp; English.
 XX
 CC The present invention relates to novel human cone opsin kinase (G-protein
 CC coupled receptor kinase 7; GRK7) and their corresponding polynucleotides.
 CC The invention further relates to a method of identifying compounds that
 CC alter the inhibition of GRK7 polypeptide activity which involves mixing a
 CC test compound with GRK7 protein and an inhibitory polypeptide and
 CC determining if the test compound alters the inhibition of GRK7 protein
 CC activity by the inhibitory polypeptide. GRK7 sequences are useful for
 CC treating conditions related to cone visual signalling (e.g., night
 CC blindness, colour blindness, difficulty with colour vision, visual
 CC sensitivity, visual resolution or in adapting to changes in light
 CC intensity, Oguchi disease or dominant congenital stationary night
 CC blindness), pineal gland activity (e.g., chromobiological desynchrony,
 CC depression, anxiety, mental foginess, memory loss, headaches, fatigue,
 CC or jet lag). Agonists of GRK7 polypeptide activity may be used to treat
 CC or ameliorate symptoms of a disease for which increased GRK7 polypeptide
 CC activity is beneficial, e.g., decreased colour sensitivity or other cone
 CC photoreceptor-mediated diseases. The GRK7 proteins are also useful in the
 CC preparation of a medicament for treating a condition or disease related
 CC to cone photoreceptor visual signalling or circadian rhythm, as molecular
 CC probes to screen for inherited defects in colour vision, circadian rhythm
 CC and vision resolution. They are also used as gene therapy tools for

CC individuals with such disorders. The present sequence is human GRK7 cDNA
XX
SQ Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;

Query Match	75.5%	Score 1658.8	DB 6	Length 1662
Best Local Similarity	99.9%	Pred. No. 0		
Matches 1660; Conservative	0	Mismatches 2	Indels 0	Gaps 0

Qy	291	ATGAGTGAATATGAGGAGGAGCCCTGGACAACCTGATATGCAACACGACCTACCTGACAGGAGCCG	350
Db	1	ATGGTGAACATATGAGGAGGAGCCCTGGACAACCTGATATGCAACACGACCTACCTGACAGGAGCCG	60
Qy	351	AAAGCCTTGGACTGCGACAGCAAGAAAGAGCTGACAGCGAGCGAGCGATAGCTGAGCCTTGCC	410
Db	61	AAAGCCTTGGACTGCGACAGCAAGAAAGAGCTGACAGCGAGCGAGCGATAGCTGAGCCTTGCC	120
Qy	411	GAGCTGCAAGGCTGCGGAGAGCTCCGCAAGAGCTGTCCCTGAACCTTCCACAGAGCTGT	470
Db	121	GAGCTGCAAGGAGCTCGGAGAGCTCCGCAAGAGCTGTCCCTGAACCTTCCACAGAGCTGT	180
Qy	471	GAGAGCACACCCCATCGAGTGCAGCGACCTCTTCCGTGACCTTCCAGACCTTCCAGAGTGCACAGTTC	530
Db	181	GAGAGCACACCCCATCGAGTGCAGCGACCTCTTCCGTGACCTTCCAGAGTGCACAGTTC	240
Qy	531	CGCAAGCGCGCAACTTCTCTAGAGGAGCGTGCAGAACTGAGACTGAGCGAGCGAGAGGAGCC	590
Db	241	CGCAAGCGCGCAACTTCTCTAGAGGAGCGTGCAGAACTGAGAGCTGAGCGAGCGAGAGGAGCC	300
Qy	591	ACCAAGAGACAGCGGCTGCGAGGAGCTGATGAGCACTTGTGTGAGATGCCCGCGCGAGG	650
Db	301	ACCAAGAGACAGCGGCTGCGAGGAGCTGATGAGCACTTGTGTGAGATGCCCGCGCGAGG	360
Qy	651	AAACCCGAACCCCTTCTCAGACAGGAGCGTGGCCACCAAGTGCACAGACAGCACCACTGAG	710
Db	361	AAACCCGAACCCCTTCTCAGACAGGAGCGTGGCCACCAAGTGCACAGACAGCACCACTGAG	420
Qy	711	GAAAGCGAGTGGCTGCAAGTGAAGCTGTGGCGAAGGCTGAGGACACTGCTTTCTTGCAGAGG	770
Db	421	GAAAGCGAGTGGCTGCAAGTGAAGCTGTGGCGAAGGCTGAGGACACTGCTTTCTTGCAGAGG	480
Qy	771	CAGCCTTTAAGATTTCCGTGACACAGGCGCTTCTACAGCAAGTTCTGAGATGGAGAACTC	830
Db	481	CAGCCTTTAAGAGATTTCCGTGACACAGGCGCTTCTACAGCAAGTTCTGAGATGGAGAACTC	540
Qy	831	TTCCAGATGCACACAGTGTGACAGCAAGTCTTCACTGATTCAGATGTCGAGGAGAAAGT	890
Db	541	TTCCAGATGCACACAGTGTGACAGCAAGTCTTCACTGATTCAGATGTCGAGGAGAAAGT	600
Qy	891	GATTTTGGAGAGTATATGTCCTGTCCAGTGTAAAAAACCTGGAGAAATGTATGCTGTAGG	950
Db	601	GATTTTGGAGAGTATATGTCCTGTCCAGTGTAAAAAACCTGGAGAAATGTATGCTGTAGG	660
Qy	951	AAATCGGACAAAGACGAGCTGAAAGAAAGAGTGGCGAAGATGAGCTCTTGTGAAAGAG	1010
Db	661	AAATCGGACAAAGACGAGCTGAAAGAAAGAGTGGCGAAGATGAGCTCTTGTGAAAGAG	720
Qy	1011	GAATCTCTGAGAGAGTCAAGACCCCTTCAATTGTCTCTGAGCTATGACCTTTGAGAGC	1070
Db	721	GAATCTCTGAGAGAGTCAAGACCCCTTCAATTGTCTCTGAGCTATGACCTTTGAGAGC	780
Qy	1071	AAAGACCATCTGCTCTTGTGATGAGCTTGATGATGGGAGAGACTTCAAGTGCACATTC	1130
Db	781	AAAGACCATCTGCTCTTGTGATGAGCTTGATGATGGGAGAGACTTCAAGTGCACATTC	840
Qy	1131	TACAAAGTGGAGAGCGGCTGGAGCTGAGACATGAGCGGAGTATCTTTATCTGGAGCCAGATA	1190
Db	841	TACAAAGTGGAGAGCGGCTGGAGCTGAGACATGAGCGGAGTATCTTTATCTGGAGCCAGATA	900
Qy	1191	GCTGTGAGATCTGCACTTCATGAACTTCGAGATGCTTATTCGAGACATGAAAGCTGAG	1250
Db	901	GCTGTGAGATCTGCACTTCATGAACTTCGAGATGCTTATTCGAGACATGAAAGCTGAG	960
Qy	1251	AATGTGCTTGTGATGACTCGGCAACTGCAAGTATCTGACTGTGGGCTGGCGGTGGAG	1310

Db		961	AATGTGCTTCTGGATTGAACCTCGGCAACTGAGATTATGTGACTCTGGGGTGCGCGTAGAG	1020
Oy		1311	ATGAAAGGTGGCAAGCCCATCACCAGAAGGCTGSAACCAATGGTTAATCATGGCTCTGAG	1370
Db		1021	ATGAAAGGTGGCAAGCCCATCACCAAGAGGGCTGSAACAATGGTTAATCATGGCTCTGAG	1080
Oy		1371	ATCTTAATGAAAAAGGTAAATTAATTCATACCTGGTGAACGTGGTTTGCATGGATGGAC	1430
Db		1081	ATCTTAATGAAAAAGGTAAATTAATTCATACCTGGTGAACGTGGTTTGCATGGATGGAC	1140
Oy		1431	ATTATGAAATGTTGCTGSAAGAACCATTTCAAAGATTCAAGSAAAAGGTCAATMA	1490
Db		1141	ATTATGAAATGTTGCTGSAAGAACCATTTCAAAGATTCAAGSAAAAGGTCAATMA	1200
Oy		1491	GAGGATCTGAAGCAAAAGACTCTGCAAGAGGGTCAATTTCAAGATGATTAATCTTACA	1550
Db		1201	GAGGATCTGAAGCAAAAGACTCTGCAAGAGGGTCAATTTCAAGATGATTAATCTTACA	1260
Oy		1551	GAGGAGCAAAAGATTATTGACAGCTCTTCTTGCTTAAGAAACAGAGCAACGCTTAGA	1610
Db		1261	GAGGAGCAAAAGATTATTGACAGCTCTTCTTGCTTAAGAAACAGAGCAACGCTTAGA	1320
Oy		1611	AGCAGAGAAAAGCTGTGATGATCCCAAGAAACATCATTTCTTTAAACGATCACTTCCCT	1670
Db		1321	AGCAGAGAAAAGCTGTGATGATCCCAAGAAACATCATTTCTTTAAACGATCACTTCCCT	1380
Oy		1671	CAGCTGAAGAGCGCCATAATGAACCCCATTTGTGCCAGACCCCTCAGTGGTTTATGCC	1730
Db		1381	CAGCTGAAGAGCGCCATAATGAACCCCATTTGTGCCAGACCCCTCAGTGGTTTATGCC	1440
Oy		1731	AAAGACATGCGCTGAATATGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGACAAA	1790
Db		1441	AAAGACATGCGCTGAATATGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGACAAA	1500
Oy		1791	GATPACCAATCTTCCA AAAA AACTTCCGACAGGCTGTTCTCTATACATGCGACAGAGAA	1850
Db		1501	GATPACCAATCTTCCA AAAA AACTTCCGACAGGCTGTTCTCTATACATGCGACAGAGAA	1560
Oy		1851	ATTATGAAAACGGAGACTGTTTGAGGAACGTAATGACCCCAACAGACTTACGGGTTGTGAG	1910
Db		1561	ATTATGAAAACGGAGACTGTTTGAGGAACGTAATGACCCCAACAGACTTACGGGTTGTGAG	1620
Oy		1911	GAGGTTAATTCATCCAAAGTGTGGCGTGTGTTTGTAATGTAA	1952
Db		1621	GAGGTTAATTCATCCAAAGTGTGGCGTGTGTTTGTAATGTAA	1662
RESULT 9				
AAH78797				
ID	AAH78797	standard,	cDNA, 1662 BP.	
XX	AAH78797;			
AC				
DT	08-MAR-2002	(first entry)		
DE				
XX				
XX				
KM				
KW				
XX				
OS	Homo sapiens.			
XX				
FH	Key	Location/Qualifiers		
FT	CDS	1..1662		
FT	/tag= a			
FT	/product= "G-protein coupled receptor kinase 1"			
PN	MO200168869-A2.			
PD	20-SEP-2001.			

Claim 1; Page 30; 34pp; English.

The present cDNA sequence encodes a human G-protein coupled receptor kinase (GRK), also designated NRP (novel human protein) in the specification, which is claimed in the invention. The invention comprises novel human nucleotide and protein sequences which have similarity to G-protein coupled receptor kinases. Oligonucleotides derived from the nucleotides of the invention are useful as hybridization probes for screening libraries and assessing gene expression patterns. The nucleotides of the invention are also useful in drug screening and gene therapy for the modulation of GRK expression. The nucleotides of the invention can be used to genetically engineer host cells to express GRK products *in vivo*. The nucleotide sequences of the invention are also useful in addressable arrays for identifying and characterising the temporal and tissue specific expression of a gene and in microarrays to screen collections of genetic material from patients who have a particular medical condition. The proteins of the invention are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to GRK, and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders/diseases

Sequence 1662 BP; 420 A; 410 C; 479 G; 352 T; 0 U; 1 Other;

Query Match	75.5%	Score 1658.4;	DB 4;	Length 1662;
-------------	-------	---------------	-------	--------------

Matches 1659; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 1 ATGTGGATATGGGGGCCCTGGATYAACTGATGCCAATCCGCTTACTTGCAGGCCG 60

QY 351 AAGCCCTCGAATTGCGACAGCAAAAGAGTGAAGCGCGCGCGCTAGCTGTGGCCCTGGCC 410

Db 61 AAGCCCTCGAATTGCGACAAAGAGTGAAGCGCGCGCGCTAGCTGTGGCCCTGGCC 120

QY 411 GGGCTCGAGGCTGTGGCGGAGGCTCCGCGAAGCTGTCCTGAATTTCACAGCTGTGT 470

Db 121 GGGCTCGAGGCTGTGGCGGAGGCTCCGCGAAGCTGTTCCTGAATTTCACAGCTGTGT 180

QY 471 GAGCAACAGCCATTCGGTGGCGGCTCTTCCGTGAATTCTTACCAAGTCCACGTTTC 530

Db 181 GAGCAACAGCCCATTCGGTGGCGGCTCTTCCGTGAATTCTTACCAAGTCCACGTTTC 240

QY 531 CGCAAGCGGGCAACTCTTCAGAGGAGCTGTGAAATCTGGAGACTGCGCGAGAGGAGACC 590

Db 241 CGCAAGCGGGCAACTCTTCAGAGGAGCTGTGAAATCTGGAGACTGCGCGAGAGGAGACC 300

QY 591 ACCAAGACAGCGCGCTGCAAGGGGCTGGTGGCCACTTGTGCGAGTGCCTGTGCCCGGGG 650

Db 301 ACCAAGACAGCGCGCTGCAAGGGGCTGGTGGCCACTTGTGCGAGTGCCTGTGCCCGGGG 360

QY 651 AACCGCAACCTTCTCAAGCCAGGCTGTGCAACCAATGCGCAAGACCAACTAG 710

Db 361 AACCGCAACCTTCTCAAGCCAGGCTGTGCAACCAATGCGCAAGACCAACTAG 420

QY 711 GAAGAGCGATGGCTGCAATGAAGCTGCGCGCAAGGCTGAAGCCATGGCTTTCTTGCAGAG 770

Db	421	GAAAGAGAGTGGCTGCAAGTACGCTGGCCMAAGCTGAGGCAATGGCTTTCTTCAGAGG	480
QY	771	CAGCCCTTTAAGATATTCGTGACAGGGCTTTTCACAGCAAGTTTCTGAGTGGAACTC	830
Db	481	CAGCCCTTTAAGATATTCGTGACAGGGCTTTCTTCAGCAAAAGTTTCTGAGTGGAACTC	540
QY	831	TTGAGATGCACAACAGATGCACAGAAATTCACACGATTCAGACATGCTGTGGGAAAAGCT	890
Db	541	TTGAGATGCACAAGTGTACAGAAATTCACACGATTCAGACATGCTGTGGGAAAAGCT	600
QY	891	GGTTTTGGGGAAGTATGTGCGTCCAGGTGAAAAACACTGGGAAATGATATGCTGTGAAG	950
Db	601	GGTTTTGGGGAAGTATGTGCGTCCAGGTGAAAAACACTGGGAAATGATATGCTGTGAAG	660
QY	951	AAACTGGACAAAGAACCGGCTGAAGAAAGAGTGGCGAGAAATGAGCTCTTTGAAAAAG	1010
Db	661	AAACTGGACAAAGAACCGGCTGAAGAAAGAGTGGCGAGAAATGAGCTCTTTGAAAAAG	720
QY	1011	GAAATCTTGAGAAAGTGCAGAGCCCTTTCAATGTCTCTGCGCTATAGCCTTTGAGAGC	1070
Db	721	GAAATCTTGAGAAAGTGCAGAGCCCTTTCAATGTCTCTGCGCTATAGCCTTTGAGAGC	780
QY	1071	AAAGCCATCTCTGCTTCTCATAGAGCTGATGAAATGGGGAGACCTCCAGTTCACATC	1130
Db	781	AAAGCCATCTCTGCTTCTCATAGAGCTGATGAAATGGGGAGACCTCCAGTTCACATC	840
QY	1131	TACACATGAGGACAGGTGGCGCTGGACATAGACCGGGATGATCTTTTACTGGGCCAGATA	1190
Db	841	TACACATGAGGACAGGTGGCGCTGGACATAGACCGGGATGATCTTTTACTGGGCCAGATA	900
QY	1191	GCGTGGGATGCTGCACCTCCATGAACCTCGCATCGTATCGGAGACATGAAGCTGAG	1250
Db	901	GCGTGGGATGCTGCACCTCCATGAACCTCGCATCGTATCGGAGACATGAAGCTGAG	960
QY	1251	AAATGCTCTTCGTGATGACTCGGCAATCGAGGTTATCTAATCTGAGGCTGAGCGTGAG	1310
Db	961	AAATGCTCTTCGTGATGACTCGGCAATCGAGGTTATCTAATCTGAGGCTGAGCGTGAG	1020
QY	1311	ATGAGAGGTGGCAAGCCCATACCCACAGGGGCTGGAAACAAATGGTTATATGAGCTCTGAG	1370
Db	1021	ATGAGAGGTGGCAAGCCCATACCCACAGGGGCTGGAAACAAATGGTTATATGAGCTCTGAG	1080
QY	1371	ATCCCTAATGAAAAAGGAAATTAATTCATTCCTGTGCACTGGTTGCCATGGANTCAGC	1430
Db	1081	ATCCCTAATGAAAAAGGAAATTAATTCATTCCTGTGCACTGGTTGCCATGGANTCAGC	1140
QY	1431	ATTATGAAATGAGTGTGTGTGGAGCAACCACTTCMAAGTTATCAGAGAAAGGTCAATAA	1490
Db	1141	ATTATGAAATGAGTGTGTGTGGAGCAACCACTTCMAAGTTATCAGAGAAAGGTCAATAA	1200
QY	1491	GAGATCTGAAGCAAAAGACTCTGTCAAGACGAGGTCAAAATCCAGCATGAAATCTTACA	1550
Db	1201	GAGATCTGAAGCAAAAGACTCTGTCAAGACGAGGTCAAAATCCAGCATGAAATCTTACA	1260
QY	1551	GAGAGCAAAAGATATTTTGAGGGCTTTCTTGGCTAAGAAACAGAGCAACGCTTAGGA	1610
Db	1261	GAGAGCAAAAGATATTTTGAGGGCTTTCTTGGCTAAGAAACAGAGCAACGCTTAGGA	1320
QY	1611	AGCAGAGAAAGTGTATATCCACAGAAACATATTTCTTTAAAGCATCAATCTTCT	1670
Db	1321	AGCAGAGAAAGTGTATATCCACAGAAACATCAITTTCTTTAAAGCATCAATCTTCT	1380
QY	1671	CGCTGAGAGCTGACCTAATGAAACCCCAATTTGTGCAGACCCCTTCAGTGGTTATGCG	1730
Db	1381	CGCTGAGAGCTGACCTAATGAAACCCCAATTTGTGCAGACCCCTTCAGTGGTTATGCG	1440
QY	1731	AAAGACATCGTGAAATGATGATTTCTCTGAGGTGTGGGGGTGTGAATTTGATGCAAA	1790
Db	1441	AAAGACATCGTGAAATGATGATTTCTCTGAGGTGTGGGGGTGTGAATTTGATGCAAA	1500
QY	1791	GATTAAGCATTTCTTCAAAAATTGTGACAGGTGTGCTTTCTATATGATGGCAGAGAA	1850

acid expression. The present sequence is human kinase C α expressed in

Db 901 GCCTGTGGATGCTGCACCTCCATGAACTCGGCATCGCTTATCGGGACATGAAGCCTGAG 96

Dy 1251 AATGTGCTTCTGATGACCTCGCAACTGACAGTTATCTGACCTGGGGCTGGCCGTGGAG 13

Db 961 ATATGCTTCTGATGACCTCGGCAACTGACGATTATCTGACCTGGGCTGGCCGTGAG 1020
 QY 1311 ATGAAGGTGGCAAGCCCATCCAGAGGCTGGAAACCAATGTTATCATGCTCTGAG 1370
 Db 1021 ATGAAGGTGGCAAGCCCATCCAGAGGCTGGAAACCAATGTTATCATGCTCTGAG 1080
 QY 1371 ATCTTAATGAAAGTAACTTATCTCATCTGCTGATCTGCTTGGCATGGATGACGAC 1430
 Db 1081 ATCTTAATGAAAGTAACTTATCTCATCTGCTGATCTGCTTGGCATGGATGACGAC 1140
 QY 1431 ATTTATGAATGTTGCTGGAGCAACACATTCMAAGATTACAGAGAAAGTCACTAA 1490
 Db 1141 ATTTATGAATGTTGCTGGAGCAACACATTCMAAGATTACAGAGAAAGTCACTAA 1200
 QY 1491 GAGGATCTGAAGCAAGAACTCTGACAGAGAGTCAAAATTCACAGATTAATCTTACA 1550
 Db 1201 GAGGATCTGAAGCAAGAACTCTGACAGAGAGTCAAAATTCACAGATTAATCTTACA 1260
 QY 1551 GAGGAGCAAGAAAGTAACTTATGAGGCTCTCTTGGCTAAGAAACCAAGCAAGCTTAA 1610
 Db 1261 GAGGAGCAAGAAAGTAACTTATGAGGCTCTCTTGGCTAAGAAACCAAGCAAGCTTAA 1320
 QY 1611 AGCAGAGAAAGTCTGATGATCCAGAGAAACATCTTCTTAAACGATCAACTTCT 1670
 Db 1321 AGCAGAGAAAGTCTGATGATCCAGAGAAACATCTTCTTAAACGATCAACTTCT 1380
 QY 1671 GCGCTGGAAGTGGCTCTTAATGAAACCCCATTTTGGCCAGACCTTCAGTGGTTATGCC 1730
 Db 1381 GCGCTGGAAGTGGCTCTTAATGAAACCCCATTTTGGCCAGACCTTCAGTGGTTATGCC 1440
 QY 1731 AAGACATCGCTGAAATGATGATTTCTGAGGTTCCGGGGGTGGAAATTTGATACAA 1790
 Db 1441 AAGACATCGCTGAAATGATGATTTCTGAGGTTCCGGGGGTGGAAATTTGATACAA 1500
 QY 1791 GATTAAGCAAGTCTTCAAAAACCTTGGCAGAGTGTCTTCTATAGCATGGCAGAGAA 1850
 Db 1501 GATTAAGCAAGTCTTCAAAAACCTTGGCAGAGTGTCTTCTATAGCATGGCAGAGAA 1560
 QY 1851 ATTATGAAGACGGGACTGTTTGAAGAACTGATGACCCCAAGACCTTACGGGTTGTAG 1910
 Db 1561 ATTATGAAGACGGGACTGTTTGAAGAACTGATGACCCCAAGACCTTACGGGTTGTAG 1620
 QY 1911 GAGGGTAATTCATCCAAAGTCGAGTGTGTGTGTATGTGTA 1952
 Db 1621 GAGGGTAATTCATCCAAAGTCGAGTGTGTGTGTATGTGTA 1662
 RESULT 11
 ID AAS06702 standard; cDNA, 1662 BP.
 XX AAS06702;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Polynucleotide sequence encoding human protein kinase #2.
 XX
 KW human; protein kinase; PTK; STK; cancer; cardiovascular disease;
 KW metabolic disorder; immune related disease; neurological disorder;
 KW neurodegenerative disorder; inflammatory disorder; infectious disease;
 KW reproductive disorder; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200138503-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 22-NOV-2000; 2000MO-US032085.
 XX
 PR 24-NOV-1999; 99US-0167482P.
 XX
 PA (SUGEN -) SUGEN INC.

XX Plozman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
 PI Flanagan P, Clary D;
 XX
 DR WPI, 2001-343960/36.
 DR P-PSDB; AAU03502.
 XX
 PT Nucleic acids encoding human kinase polypeptides, useful for preventing
 PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
 PT neuronal-associated diseases, and microbial infections.
 XX
 ES Example 1; Fig 1; 433bp; English.
 XX
 CC AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel
 CC protein kinases have been identified as members of the tyrosine or
 CC serine/threonine kinase (PTK and STK) families. The polynucleotides
 CC encoding protein kinases and the polypeptides may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate kinase expression. For example, they may be used to treat
 CC cancers (especially cancers of haematopoietic origin), cardiovascular
 CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
 CC immune related diseases (e.g. rheumatoid arthritis), neurological
 CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
 CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
 CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
 CC Additionally, polynucleotides encoding protein kinases may be used for
 CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
 CC polypeptides may be used as antigens in the production of antibodies
 CC against the protein kinases and in assays to identify modulators of
 CC protein kinase expression and activity.
 XX
 SQ Sequence 1662 BP; 421 A; 411 C; 479 G; 351 T; 0 U; 0 Other;
 Query Match 75.3%; Score 1655.6; DB 4; Length 1662;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1658; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 291 ATGTGACATGAGGGGCGCTGGACAACTGAGCCCAACCGCTACCTGAGGCGCGG 350
 Db 1 ATGTGACATGAGGGGCGCTGGACAACTGAGCCCAACCGCTACCTGAGGCGCGG 60
 QY 351 AAGCCCTGGAAGTCTGAGCAAGCAAGAGCTGAGCGGCGGCTGAGGCGCGGCGG 410
 Db 61 AAGCCCTGGAAGTCTGAGCAAGCAAGAGCTGAGCGGCGGCGGCTGAGGCGGCGG 120
 QY 411 GGGCTGAGGGCTGCGGAGGCTCCGCAAGCTGTCTTGAACCTTCAACAGCTGTGT 470
 Db 121 GGGCTGAGGGCTGCGGAGGCTCCGCAAGCTGTCTTGAACCTTCAACAGCTGTGT 180
 QY 471 GAGCAGAGCCCATCGGTGCGCGGCTCTTCCGTGACTTCTTACGCAAGTCCCAAGTTC 530
 Db 181 GAGCAGAGCCCATCGGTGCGCGGCTCTTCCGTGACTTCTTACGCAAGTCCCAAGTTC 240
 QY 531 CGCAAGCGGCAACCTTCTTGAAGAGCGTGAAGAGCTGAGCGGCGGCGGAGGAGCC 590
 Db 241 CGCAAGCGGCAACCTTCTTGAAGAGCGTGAAGAGCTGAGCGGCGGCGGAGGAGCC 300
 QY 591 ACCAAGCAACCGGCTGAGAGGGGTGTGTGCACTTGTGAGAGTGCCTTGCCTGGGG 650
 Db 301 ACCAAGCAACCGGCTGAGAGGGGTGTGTGCACTTGTGAGAGTGCCTTGCCTGGGG 360
 QY 651 AACCGCAACCTTCTTCTGAGCGAGGCGGTGGCCACCAAGTGCAGAGAGCAACTAG 710
 Db 361 AACCGCAACCTTCTTCTGAGCGAGGCGGTGGCCACCAAGTGCAGAGAGCAACTAG 420
 QY 711 GAAAGCGAGTGTCTCAAGTGAAGTGTGCAAGGCTGAGGCGCATGTCTTCTTGAAGAG 770
 Db 421 GAAAGCGAGTGTCTCAAGTGAAGTGTGCAAGGCTGAGGCGCATGTCTTCTTGAAGAG 480
 QY 771 CAGCCCTTAAGGATTTGTGACAGAGGCGCTTCTACGACAGTTCTGACAGGAAATTC 830
 Db 481 CAGCCCTTAAGGATTTGTGACAGAGGCGCTTCTACGACAGTTCTGACAGGAAATTC 540

QY 831 TTGAGATGCAACGAGTGTGAGAAAGTACTTCACTGATGAGAGTGTGAGGAAAGGT 890
 DB 541 TTGAGATGCAACGAGTGTGAGAAAGTACTTCACTGATGAGAGTGTGAGGAAAGGT 600
 QY 891 GGTGTTGGGAGGATGATGAGCCGTCCAGTGTGAGAAACACTGAGAAAGTATGCTGTAG 950
 DB 601 GGTGTTGGGAGGATGATGAGCCGTCCAGTGTGAGAAACACTGAGAAAGTATGCTGTAG 660
 QY 951 AAATCTGAGCAAGAGGAGGCTGAGAGAAAGGTGCGAGAAAGTGTCTCTTTGAGAAAG 1010
 DB 661 AAATCTGAGCAAGAGGAGGCTGAGAGAAAGGTGCGAGAAAGTGTCTCTTTGAGAAAG 720
 QY 1011 GAAATCTTGGAGAGAGGTGAGAGCCCTTATTTGCTCTGAGCTTATGCTTTGAGAGC 1070
 DB 721 GAAATCTTGGAGAGAGGTGAGAGCCCTTATTTGCTCTGAGCTTATGCTTTGAGAGC 780
 QY 1071 AAGACCCATCTGCTTGTGATGAGCTGATGAAATGAGGAGAGACTGAAAGTTCCACATC 1130
 DB 781 AAGACCCATCTGCTTGTGATGAGCTGATGAAATGAGGAGAGACTGAAAGTTCCACATC 840
 QY 1131 TACAAAGTGGGACGCGGTGCTGAGATGAGCCGAGTATCTTTTACTGCGCCAGATA 1190
 DB 841 TACAAAGTGGGACGCGGTGCTGAGATGAGCCGAGTATCTTTTACTGCGCCAGATA 900
 QY 1191 GCGTGTGGAGATGCTGAGACTCCATGAACTGAGCATGCTTATGCGGACATGAAAGCTGAG 1250
 DB 901 GCGTGTGGAGATGCTGAGACTCCATGAACTGAGCATGCTTATGCGGACATGAAAGCTGAG 960
 QY 1251 AATGTGCTTGTGATGAGCTGCGGCACTGAGAGGTTATGCACTGAGGAGTGTGCGGTGAG 1310
 DB 961 AATGTGCTTGTGATGAGCTGCGGCACTGAGAGGTTATGCACTGAGGAGTGTGCGGTGAG 1020
 QY 1311 ATGAAAGGTGGCAAGCCCATCACTGAGAGGCTGAGAACTGATGTTATGAGTCTCTAG 1370
 DB 1021 ATGAAAGGTGGCAAGCCCATCACTGAGAGGCTGAGAACTGATGTTATGAGTCTCTAG 1080
 QY 1371 ATCCATATGCAAAAGGTATGATTCCTATCTGAGTGTGAGTGTGAGTGTGAGTGTGAGC 1430
 DB 1081 ATCCATATGCAAAAGGTATGATTCCTATCTGAGTGTGAGTGTGAGTGTGAGTGTGAGC 1140
 QY 1431 ATTATGAAATGCTGTGAGAGCAACACATCAAAAGTTATCAAGAAAGGTCACTAAA 1490
 DB 1141 ATTATGAAATGCTGTGAGAGCAACACATCAAAAGTTATCAAGAAAGGTCACTAAA 1200
 QY 1491 GAGATCTGAAAGCAAGAACTGTGAGAGCAAGGTCAAAATTCAGCATGATTAATCTTACA 1550
 DB 1201 GAGATCTGAAAGCAAGAACTGTGAGAGCAAGGTCAAAATTCAGCATGATTAATCTTACA 1260
 QY 1551 GAGAGAGCAAAAGATTTTGGAGGCTCTTGTGCTTAAAGCAAGAGCAAGCTTAAAG 1610
 DB 1261 GAGAGAGCAAAAGATTTTGGAGGCTCTTGTGCTTAAAGCAAGAGCAAGCTTAAAG 1320
 QY 1611 AGCAGAGAAAGTGTGATGATCCAGAAACATCATTTCTTAAAGCATCACTTCTCT 1670
 DB 1321 AGCAGAGAAAGTGTGATGATCCAGAAACATCATTTCTTAAAGCATCACTTCTCT 1380
 QY 1671 CGCTGGAAGTGTGCTTAAATGAAACCCCATTTTGTGCAAGACCTTCAAGTGTGAGC 1730
 DB 1381 CGCTGGAAGTGTGCTTAAATGAAACCCCATTTTGTGCAAGACCTTCAAGTGTGAGC 1440
 QY 1731 AAAGCATGCGTAAATTTGATGATTTCTCTGAGGTTGCGGAGGTGAGATTTGATGACAA 1790
 DB 1441 AAAGCATGCGTAAATTTGATGATTTCTCTGAGGTTGCGGAGGTGAGATTTGATGACAA 1500
 QY 1791 GATAGCAGTCTTCTCAAAAACCTTGGAGAGGCTGTCTTATGATGAGCAAGAA 1850
 DB 1501 GATAGCAGTCTTCTCAAAAACCTTGGAGAGGCTGTCTTATGATGAGCAAGAA 1560
 QY 1851 ATTATGAAACGAGAGCTGTTGAGAGCACTGATACCCCAAGAGCAAGCTTAAAGGAG 1910
 DB 1561 ATTATGAAACGAGAGCTGTTGAGAGCACTGATACCCCAAGAGCAAGCTTAAAGGAG 1620
 QY 1911 GAGGTAAATTATCAAGTGTGCGAGTGTGTTGATTTGAA 1952

DB 1621 GAGGTAAATTATCAAGTGTGCGAGTGTGTTGATTTGAA 1662
 RESULT 12
 ACC44826
 ID ACC44826 standard; cDNA; 1662 BP.
 XX
 AC ACC44826;
 XX
 DT 04-JUN-2003 (first entry)
 DE Human G protein-coupled receptor kinase encoding cDNA SEQ ID NO:1.
 XX
 KW Human; G protein coupled receptor kinase; GRK; cytosolic; antidiabetic;
 KW neuroprotective; nontoxic; cardiovascular; anti-Parkinsonian; cardiant;
 KW vasotrophic; antidiabetic; gene therapy; cancer; diabetes; CNS disorder;
 KW central nervous system disorder; cardiovascular disorder; asthma; COPD;
 KW chronic obstructive pulmonary disorder; anxiety; mood disorder; enzyme;
 KW Alzheimer's disease; Parkinson's disease; congestive heart failure;
 KW myocardial infarction; ischaemic disease; hypertensive vascular disease;
 KW gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FH CDS 1..1662
 FT /tag= a
 FT /product= "G protein-coupled receptor kinase (GRK)"
 XX
 PN WO2003018815-A2.
 XX
 PD 06-MAR-2003.
 XX
 PF 19-AUG-2002; 2002WO-BP009235.
 XX
 PR 21-AUG-2001; 2001US-0313464P.
 XX
 PA (PARB) BAYER AG.
 XX
 FI Xiao Y;
 XX
 XX MPI; 2003-278669/27.
 DR P-PSDB; ABP96707.
 PT New G-protein coupled receptor kinase polypeptides and polynucleotides,
 PT useful in identifying modulators of the enzyme for treating cancer,
 PT diabetes, a central nervous system disorder, a cardiovascular disorder or
 PT asthma.
 PS Claim 1; Fig 1; 129pp; English.
 XX
 CC The present sequence encodes a human G protein-coupled receptor kinase
 CC (GRK) protein (1). (1) has cytosolic, antidiabetic, neuroprotective,
 CC nontoxic, cardiovascular, anti-Parkinsonian, cardiant, vasotropic and
 CC antisthmatic activities, and can be used in gene therapy. (1) can be
 CC regulated to treat cancer, diabetes, a central nervous system (CNS)
 CC disorder (e.g. anxiety or mood disorders), Alzheimer's disease and
 CC Parkinson's disease), cardiovascular disorders (e.g. congestive heart
 CC failure, myocardial infarction, ischaemic diseases of the heart or
 CC hypertensive vascular disease), asthma and chronic obstructive pulmonary
 CC disorder (COPD). GRK molecules are useful in screening for agents that
 CC regulate or decrease the activity of a GRK. GRK sequences may also be used
 CC for detecting diseases and abnormalities or susceptibility to diseases
 CC and abnormalities related to the presence of mutations in the nucleic
 CC acid sequences that encode the GRK enzyme
 CC
 SQ Sequence 1662 BP; 421 A; 411 C; 479 G; 351 T; 0 U; 0 Other;

Query Match 75.3%; Score 1655.6; DB 7; Length 1662;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1658; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX Novel disease-associated gene of the RGS gene family and its product.
 PT applicable in diagnosis of and screening for drugs for heart diseases,
 PT cancers and omentopathy.
 XX
 PS Claim 6; Page 81-82; 96pp; Japanese.
 XX
 CC The invention relates to a novel disease associated gene and its uses.
 CC The gene and its encoded protein are useful for diagnosis of and
 CC screening for drugs for heart diseases, cancers and omentopathy. The
 CC current sequence represents the human RGS9 encoding DNA sequence
 XX
 SQ Sequence 1191 BP; 274 A; 320 C; 363 G; 234 T; 0 U; 0 Other;
 Query Match 54.0%; Score 1187.8; DB 7; Length 1191;
 Best Local Similarity 99.8%; Pred. No. 6,3e-297;
 Matches 1189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 291 ATGGTGAACATGGGGGCTGGGACCAACCTGATCCCAACACGCTTACCTGACAGCCCG 350
 Db 1 ATGGTGAACATGGGGGCTGGGACCAACCTGATCCCAACACGCTTACCTGACAGCCCG 60

QY 351 AAGCCTTGAGTGGAGCAGCAAGAGCTGAGCGCGCGGCTGAGCTGGCTGGCC 410
 Db 61 AAGCCTTGAGTGGAGCAGCAAGAGCTGAGCGCGCGGCTGAGCTGGCTGGCC 120

QY 411 GGGCTGAGGGGCTGGGAGCTCGCGCAAGAGCTGCTGACTGCTGACAGCTGTGT 470
 Db 121 GGGCTGAGGGGCTGGGAGCTCGCGCAAGAGCTGCTGACTGCTGACAGCTGTGT 180

QY 471 GAGCAGACGCCATCGTCCGCGCTCTTCCGTGACTTCTTACGACAGTCCGACGTT 530
 Db 181 GAGCAGACGCCATCGTCCGCGCTCTTCCGTGACTTCTTACGACAGTCCGACGTT 240

QY 531 CGCAAGCGCGCACTCTCTAGAGAGCTGAGAGCTGAGAGCTGAGAGAGAGAG 590
 Db 241 CGCAAGCGCGCACTCTCTAGAGAGCTGAGAGCTGAGAGCTGAGAGAGAGAG 300

QY 591 ACCAAGAGAGGCGCTGAGAGGCGCTGAGAGCTGAGAGGCGCTGAGAGGCG 650
 Db 301 ACCAAGAGAGGCGCTGAGAGGCGCTGAGAGCTGAGAGGCGCTGAGAGGCG 360

QY 651 AACCGCAACCTCTCTAGAGAGCTGAGAGGCGCTGAGAGCTGAGAGGCG 710
 Db 361 AACCGCAACCTCTCTAGAGAGCTGAGAGGCGCTGAGAGCTGAGAGGCG 420

QY 711 GAAGAGCGAGTGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 770
 Db 421 GAAGAGCGAGTGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 480

QY 771 CAGCCTTTAAGAGATTGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 830
 Db 481 CAGCCTTTAAGAGATTGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 540

QY 831 TTGAGATGCAACAGTGTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 890
 Db 541 TTGAGATGCAACAGTGTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 600

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 Db 841 TACAAAGTGGGCAAGGCTGAGAGGCTGAGAGGCTGAGAGGCTTCTTACTGGCCCAATA 900

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 Db 1021 ATGAAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAG 1080

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 Db 1081 ATCTAATGAGAGAGTAAAGTATCTTCTGAGAGGCTGAGAGGCTGAGAGGCT 1140

QY 1431 ATTATGAAATGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGG 1491
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RESULT 14
 AAD46351
 ID AAD46351 standard; cDNA, 1486 BP.
 XX
 AC AAD46351;
 XX
 DT 27-JAN-2003 (first entry)
 XX
 DE Human cone opsin kinase (GRK7) OK6 splice variant cDNA.
 XX
 KW Human; enzyme; cone opsin kinase; G-protein coupled receptor kinase 7;
 KW night blindness; colour blindness; visual sensitivity; visual resolution;
 KW chromoblastic dysynchrony; depression; anxiety; memory loss; headache;
 KW mental foginess; fatigue; jet lag; circadian rhythm; ophthalmological;
 KW gene therapy; antidepressant; analgesic; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key location/Qualifiers
 FT CDS 1..1062
 FT /*tag= a
 FT /product= "Human GRK7 OK6 splice variant protein"
 XX
 PN W0200272541-A2.
 XX
 PD 19-SEP-2002.
 XX
 PF 07-MAR-2002; 2002MO-US007025.
 XX
 PR 07-MAR-2001; 2001US-0274006P.
 XX
 PA (IMMUNEX CORP.
 XX
 PI Bird TA, Spencer M, Mosley BA;
 XX
 DR WPI: 2002-723307/78.
 DR P-PSDB; AAE28953.
 XX
 PT Identifying compounds that alter inhibition of cone opsin kinase
 PT polypeptide activity for treating a conditions related to cone visual
 PT signaling, comprises mixing a compound with a cone opsin kinase and with
 PT an inhibitory polypeptide.
 XX
 PS Example 4; Page 48-49; 61pp; English.
 XX
 CC The present invention relates to novel human cone opsin kinase (G-protein

XX	RESULT 15
XX	AAH78798
ID	AAH78798 standard; cDNA; 1062 BP.
AC	AAH78798;
DT	08-MAR-2002 (first entry)
XX	
DE	Human G-protein coupled receptor kinase 2 cDNA sequence.
XX	
KW	G-protein coupled receptor kinase; GRK; human; ss; gene therapy;
KM	drug screening; gene expression characterisation; NHP;
XX	novel human protein.
XX	
OS	Homo sapiens.
FH	
FT	Key Location/Qualifiers
FT	CDS 1..1062
FT	/tag= a
FT	/product= "G-protein coupled receptor kinase 2"
PN	MO200168689-A2.
PD	20-SEP-2001.
XX	
PF	08-MAR-2001; 2001WO-US007500.
PR	10-MAR-2000; 2000US-0188449P.
XX	
PA	(LEXI-) LEXICON GENETICS INC.
PI	Walke DM, Wilganowski NL, Turner CA;
DR	NPI; 2001-570872/64.
XX	P-PADB; AAG77816.
PT	New polynucleotides encoding human proteins that share sequence
PT	similarity with animal kinases e.g. G-protein coupled receptor kinases,
PT	useful for drug screening, diagnosis and in gene therapy of biological
PT	disorders.
PS	
PS	Claim 4; Page 32; 34pp; English.
XX	
CC	The present cDNA sequence encodes a human G-protein coupled receptor
CC	kinase (GRK), also designated NRP (novel human protein) in the
CC	specification, which is claimed in the invention. The invention comprises
CC	novel human nucleotide and protein sequences which have similarity to G-
CC	protein coupled receptor kinases. Oligonucleotides derived from the
CC	nucleotides of the invention are useful as hybridisation probes for
CC	screening libraries and assessing gene expression patterns. The
CC	nucleotides of the invention are also useful in drug screening and gene
CC	therapy for the modulation of GRK expression. The nucleotides of the
CC	invention can be used to genetically engineer host cells to express GRK
CC	products in vivo. The nucleotide sequences of the invention are also
CC	useful in addressable arrays for identifying and characterising the
CC	temporal and tissue specific expression of a gene and in microarrays to
CC	screen collections of genetic material from patients who have a
CC	particular medical condition. The proteins of the invention are useful
CC	for generating antibodies, as reagents in diagnostic assays, for
CC	identifying other cellular gene products related to GRK, and as reagents
CC	in assays for screening for compounds that are useful in the treatment of
CC	mental, biological or medical disorders/diseases
XX	
SQ	Sequence 1062 BP; 237 A; 296 C; 330 G; 199 T; 0 U; 0 Other:
Query Match	47.6%; Score 1046.8; DB 4; Length 1062;
Best Local Similarity	99.8%; Pred. No. 1.9e-260;
Matches 1048; Conservative	0; Mismatches 2; Indels 0; Gaps 0
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1	ATTGTGGACATGGGGGCCCTCGACAACTGAATGCCAACAACCGCTTACTCGAGGCCTCGG 60

Qy	351	AAACCTCTGGACTGCAAGCAAGAAAGACTGACAGCGCGCGCGCTGAGCTCTGACCTCTCC	410
Db	61	AAACCTCTGGACTGCAAGCAAGAAAGACTGACAGCGCGCGCGCTGAGCTCTGACCTCTCC	120
Qy	411	GGGCTGCAAGGCTTCCGCGAGCTTCGCTCAAAAGTCTCTCCGAACTTCCAGAGCTCTGAT	470
Db	121	GGGCTGCAAGGCTTCCGCGAGCTTCGCTCAAAAGTCTCTCCGAACTTCCAGAGCTCTGAT	180
Qy	471	GAGCAGACAGCCATCGATGCGCGCCTCTTCCTCGTGACTTCCCTAGCACAAGTGCACAGTTC	530
Db	181	GAGCAGACAGCCATCGATGCGCGCCTCTTCCTCGTGACTTCCCTAGCACAAGTGCACAGTTC	240
Qy	531	CGCAAGGCGGCACACTTCTCTAGAGAGCTGTCCAGAACTGGAGACTGGCGCGAGAGAGACCC	590
Db	241	CGCAAGGCGGCACACTTCTCTAGAGAGCTGTCCAGAACTGGAGACTGGCGCGAGAGAGACCC	300
Qy	591	ACCAAGACACGCGCTGAGAGGGGCTGATGGCCACTTGTGAGATGACCCCTGACCCCGAGG	650
Db	301	ACCAAGACACGCGCTGAGAGGGGCTGATGGCCACTTGTGAGATGACCCCTGACCCCGAGG	360
Qy	651	AAACCGCAACCTTCTCTCAAGCCAGGCGCTGTGACCAAGATGCGCAAGACCAACCACTGAG	710
Db	361	AAACCGCAACCTTCTCTCAAGCCAGGCGCTGTGACCAAGATGCGCAAGACCAACCACTGAG	420
Qy	711	GAAGACCGAGTGTGCTGAGTGAAGCTGTGCGAAGAGCTGAAGCACTGAGCTTCTTGCAAGAG	770
Db	421	GAAGACCGAGTGTGCTGAGTGAAGCTGTGCGAAGAGCTGAAGCACTGAGCTTCTTGCAAGAG	480
Qy	771	CAGCCTTTAAGATTTCTGTACCAAGGCTTCTACAGCAAGTTTCTGCAGTGGAACTG	830
Db	481	CAGCCTTTAAGATTTCTGTACCAAGGCTTCTACAGCAAGTTTCTGCAGTGGAACTG	540
Qy	831	TTGAGATGCAACAGATGTCAGACAAGATCTTCACTGAGTTCAAGATGCTGGAGAAAGGT	890
Db	541	TTGAGATGCAACAGATGTCAGACAAGATCTTCACTGAGTTCAAGATGCTGGAGAAAGGT	600
Qy	891	GGTTTTGGAGAGTATGTGCGCTGCAGGTGAAGAAACACTGGAAAGATGATGTCTCTGTAAAG	950
Db	601	GGTTTTGGAGAGTATGTGCGCTGCAGGTGAAGAAACACTGGAAAGATGATGTCTCTGTAAAG	660
Qy	951	AAACTGCAAGAAAGGCGGCTGAAGAAAGAGTGGCGAAGATGGCTCTTGAGAAAG	1011
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Qy	1011	GAATCTTGGAGAAAGTGCAGAGGCTTTCATTGTCTCTGTGCGCTATGCTCTTGAAGAGC	1071
Db	721	GAATCTTGGAGAAAGTGCAGAGGCTTTCATTGTCTCTGTGCGCTATGCTCTTGAAGAGC	780
Qy	1071	AAAGCCCAATCTGCTGCTGTCATGAGCTGATGCAATGAGGAGGAGACCTCAAGTCCACATC	1131
Db	781	AAAGCCCAATCTGCTGCTGTCATGAGCTGATGCAATGAGGAGGAGACCTCAAGTCCACATC	840
Qy	1131	TACACAGTGGGACGCGCTGAGCTTGAAGTGAAGCGAGGTGATCTTTATCTGCGCCCAATA	1191
Db	841	TACACAGTGGGACGCGCTGAGCTTGAAGTGAAGCGAGGTGATCTTTATCTGCGCCCAATA	900
Qy	1191	GCGCTGGGAGATGTCGACCTCCATGAAGACTGGGATGTGCTATGCGGACATGAAGCTGAG	1251
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Qy	1251	AATGTCTTCTGATGAAGCTTGCGCAACTGCAAGGTTATCTGAAGCTGGCGGCTGGCGTGAAG	1311
Db	961	AATGTCTTCTGATGAAGCTTGCGCAACTGCAAGGTTATCTGAAGCTGGCGGCTGGCGTGAAG	1020
Qy	1311	ATGAAGGTCGAGACCCCAATCAACCAAGG	1340
Db	1021	ATGAAGGTCGAGACCCCAATCAACCAAGG	1050

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Job time : 598.249 secs

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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 10:30:45 ; Search time 5722.66 Seconds

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Title: US-10-044-205A-1

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

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7: gb_ph: *
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
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5	1988.8	90.5	3186	6	AF282269
6	1795.8	81.7	1799	9	AF439409
7	1757.8	80.0	1761	6	BD186115
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17	1640.8	74.6	1701	6	AX921933
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19	1404	63.9	2420	4	AY049726
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ALIGNMENTS

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DEFINITION Sequence 1 from Patent WO02095032.
ACCESSION AX797552
VERSION AX797552.1 GI:37518055
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Kapeller-Libermann, R. and Bandaru, R.
TITLE Method and compositions of human proteins and uses thereof
JOURNAL Patent: WO 02095032-A 1 28-NOV-2002;

QY 1495 ATCTGAAGCAAGAACTCTGCAAGACGAGCTCAAAATTCGACATGATTAATCTTCAAGAG 1554
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 DB 2218 TTTTCACTGAGGGAGGAGAAAGAACACTCA 2249

RESULT 4
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 LOCUS AX710216
 DEFINITION Sequence 4 from Patent WO03018815.
 ACCESSION AX710216
 VERSION AX710216.1 GI:29786804
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 Xiao, Y.
 TITLE Regulation of human g protein-couple receptor kinase
 JOURNAL Patent: WO 03018815-A 4 06-MAR-2003;
 Bayer Aktiengesellschaft (DE)
 FEATURES
 source Location/Qualifiers
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ORIGIN

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 DB 61 TGGAGTGCAGCCCGCTGCTCAGCCATGTTGACATGAGGAGCCCTGACCAACTGATGCC 120
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 QY 387 GGGGAGGCTAGCTGAGCCCTGCTCCGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 446
 DB 181 GGGGAGGCTAGCTGAGCCCTGCTCCGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 240
 QY 447 TCCCTGAATTCACAGCCTGTGTGACAGACCCATTCGCTGCGCCTTCCGTGAC 506
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RESULT 5
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LOCUS AF282269
DEFINITION Homo sapiens G protein-coupled receptor kinase 7 mRNA, complete cds.

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ACCESSION AF282269
VERSION AF282269.1 GI:17026317
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Osawa, S., Ducceschi, M.H., Horner, T.J., Li, A., Craft, C.M. and Weiss, E.R., 1 (bases 1 to 3186)
TITLE Species-specific differences in expression of G-protein-coupled receptor kinase (GRK) 7 and GRK1 in mammalian cone photoreceptor cells: implications for cone cell phototransduction
JOURNAL J. Neurosci. 21 (23), 9175-9184 (2001)
MEDLINE 21574315
PubMed 11717351
REFERENCE
AUTHORS Osawa, S. and Weiss, E.R.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-2000) Cell Biology and Anatomy, University of North Carolina, CB#7090, 108 Taylor Hall, Chapel Hill, NC 27599-7090, USA
FEATURES
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 ACCESSION BD186115.1 GI:31878315
 VERSION WO 02103020-A/10.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1761)
 AUTHORS Koyama, N., Tanida, S. and Yamamoto, K.
 TITLE A novel gene relating to disease and use thereof
 JOURNAL Patent: WO 02103020-A 10 27-DEC-2002;
 TAKEDA CHEMICAL INDUSTRIES LTD, NOBUYUKI KOYAMA, SEIICHI TANIDA, KOJI
 YAMAMOTO
 COMMENT OS Homo sapiens (human)
 EN WO 02103020-A/10
 PD 27-DEC-2002
 PR 14-JUN-2002 WO 2002JP005942
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 PI NOBUYUKI KOYAMA, SEIICHI TANIDA, KOJI YAMAMOTO
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DEFINITION Sequence 3 from Patent WO2095032.
ACCESSION AX797554
VERSION AX797554.1 GI:37518056

KEYWORDS
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Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
1 Kapeller-Libermann, R. and Bandaru, R.
AUTHORS Method and compositions of human proteins and uses thereof
TITLE Patent: WO 02095032-A 3 28-NOV-2002;
JOURNAL MILLENIUM PHARMACEUTICALS, INC. (US)
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ACCESSION AX642968
VERSION AX642968.1 GI:28550117
KEYWORDS
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ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS Yee, H., Lal, P., Bandman, O., Borowsky, M., Au-Young, J., Lu, Y.,
Gandhi, A.R., Tribouley, C.M., Walla, N., Yao, M.G., Lu, D.A.,
Greenwald, S.R., Runkumar, J., Griffin, J.A., Kearney, L., Burford, N.,
Nguyen, D.B., Tang, T.T., Baughn, M.R., He, A., Thornton, K.,
Hafalla, A., Patterson, C., Gururajan, R., Lo, T.P., Khan, F.,
Recipon, S.A., Azimzal, Y., Policky, J.L., Ding, L., Grether, M.,
Elliot, V.S., Thangavelu, K., Batra, S. and Ison, C.H.
HUMAN KINASES
TITLE Patent: WO 01096547-A 45 20-DEC-2001;
JOURNAL Inocyte Genomics, Inc. (US)
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Best Local Similarity 99.9%; Pred. No. 0;
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Qy 1191 GCTGTGGAGTGTGACACTTCAATGAACTCGGACATCTGTATGGGAGATGAAGCTGAG 1250
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DB 1621 GAGGTAATTCAATCCAAAGCTGCGGTGTGTTTATTGTA 1662

RESULT 10
AR225817 1662 bp DNA linear PAT 20-DEC-2002
LOCUS AR225817
DEFINITION Sequence 1 from patent US 644456.
ACCESSION AR225817
VERSION AR225817.1 GI:27263947
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1662)
AUTHORS Walke,D.W., Wilganowski,N.L. and Turner,C.A. Jr.
TITLE Human G-coupled protein receptor kinases and polynucleotides
JOURNAL Patent: US 644456-A 1 03-SEP-2002;
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source 1..1662
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ORIGIN
Query Match 75.5%; Score 1658.4; DB 6; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1659; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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LOCUS Sequence 1 from Patent WO0168869.
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VERSION AX252439.1 GI:15985733
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Walke, D.W., Wilganski, N.L. and Turner, C.A.
AUTHORS Human g-coupled protein receptor kinases and polymucleotides
TITLE encoding the same
JOURNAL Patent: WO 0168869-A 1 20-SEP-2001;
Lexicon Genetics Incorporated (US)
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 1659; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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LOCUS Sequence 1 from patent US 6331423.
DEFINITION

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ACCESSION AR263766
 VERSION AR263766.1 GI:28075747
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1662)
 AUTHORS Guegler, K., Beasley, E.M. and Di Francesco, V.
 TITLE Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof
 JOURNAL Patent: US 631423-A 18-DEC-2001;
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 DEFINITION Sequence 1 from patent US 6579709.
 ACCESSION AR343544
 VERSION AR343544.1 GI:3739257
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 ORGANISM Unknown.
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 Guegler, K., Beasley, E.M. and Di Francesco, V.

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Db	421	GAAAGACAGTGGCTGTGAGTGAAGCTGTGGCAAGAGCTGAGAGCCACTTCTTGTGAAGAG	480
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Oy	1011	GAATCTTGTGAGAAAGTCAAGACCCCTTTCAATGTCTCTCTGTGCTCATGTGCTTGTGAGAC	1070
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Db	781	AAAGCCCATCTTGTGCTTGTATGAGCTGTGAATGTGGGAGAGACCTTAAGTTTCAATC	840
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AUTHORS	Guegler, K., di Francesco, V. and Beasley, E.M.			
TITLE	Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof			
JOURNAL	Patent: WO 0192496-A, 1 06-DEC-2001.			
	Coporation Robert A. Willman Assistant Secretary (US)			
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VERSION AX166511.1 GI:14546856
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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1 Plozman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,
Flanagan,P. and Clary,D.S.
TITLE Novel human protein kinases and protein kinase-like enzymes
JOURNAL Patent: WO 0138503-A 2 31-May-2001;
Sugen, Inc. (US)
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GenCore version 5.1.6
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4	1655.8	99.8	1662	US-10-451-168-49	Sequence 49, Appl1
5	1655.4	99.8	2249	US-10-217-745-5	Sequence 5, Appl1
6	1654.2	99.7	1662	US-10-217-745-1	Sequence 1, Appl1
7	1654.2	99.7	1662	US-09-964-469-1	Sequence 1, Appl1
8	1654.2	99.7	1662	US-10-425-962-1	Sequence 1, Appl1
9	1589.8	95.8	1701	US-10-072-012-273	Sequence 273, Appl1
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33	151	9.1	2070	US-10-038-010-47	Sequence 47, Appl1
34	151	9.1	3073	US-10-029-020-11	Sequence 11, Appl1
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44	127.6	7.7	2362	US-10-117-722-273	Sequence 273, Appl1
45	112.4	6.8	1661	US-10-087-192-989	Sequence 989, Appl1

ALIGNMENTS

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US-10-044-205a-3
Sequence 3, Application US/10044205A
Publication No. US00020123464A1
GENERAL INFORMATION:
APPLICANT: BANDARU, RAJASEKHAR
TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Protein
FILE REFERENCE: 10147-5201
CURRENT APPLICATION NUMBER: US/10/044, 205A
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/242, 428
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: US 60/241, 884
PRIOR FILING DATE: 2000-10-20
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US-10-044-205a-3
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCTGACATGGGAGCCCTGACACCTGATCGCCAAACGCGCTTACCTGAGAGCCCGG 60
DB 1 ATGCTGACATGGGAGCCCTGACACCTGATCGCCAAACGCGCTTACCTGAGAGCCCGG 60
QY 61 AAGCCTCGAGACTCGACACCAAGAGCTGAGAGGCGGCGCGCTGAGCTGCGCCCTGCGCC 120
DB 61 AAGCCTCGAGACTCGACACCAAGAGCTGAGAGGCGGCGCGCTGAGCTGCGCCCTGCGCC 120

QY 121 GGGCTGACGAGGCTGCGGAGCTCCGACAGACTGTCCCTGAACTTCCACAGCTGTGT 180
DB 121 GGGCTGACGAGGCTGCGGAGCTCCGACAGACTGTCCCTGAACTTCCACAGCTGTGT 180
QY 181 GAGCAGAGCCCATCGGTGGCGGCTCTTCCGTGACCTTCCAGCCACAGGCGCCAGTTC 240
DB 181 GAGCAGAGCCCATCGGTGGCGGCTCTTCCGTGACCTTCCAGCCACAGGCGCCAGTTC 240
QY 241 CGCAGAGGCGCACTTCTTAGAGAGAGCTGAGAACTGGGAGCTTGGCGAGAGGAGCC 300
DB 241 CGCAGAGGCGCACTTCTTAGAGAGAGCTGAGAACTGGGAGCTTGGCGAGAGGAGCC 300
QY 301 ACCAAGAGAGCGCGCTGACAGGAGGCTGTGCGCACTTGTGCGAGAGCTTGGCGAG 360
DB 301 ACCAAGAGAGCGCGCTGACAGGAGGCTGTGCGCACTTGTGCGAGAGCTTGGCGAG 360
QY 361 AACCGCAAGCCCTTCTCAGCCAGAGCGTGGCGCACTTGTGCGAGAGCTTGGCGAG 420
DB 361 AACCGCAAGCCCTTCTCAGCCAGAGCGTGGCGCACTTGTGCGAGAGCTTGGCGAG 420
QY 421 GAAGAGCGAGTGTGCGAGTGAAGCTGCGCAAGGCTGAGGCGCTTCTTCTTCAAGAG 480
DB 421 GAAGAGCGAGTGTGCGAGTGAAGCTGCGCAAGGCTGAGGCGCTTCTTCTTCAAGAG 480
QY 481 CAGCCCTTAAAGATTCTGTGACAGAGCGCTTCTTCAAGCAAGTCTTCTGAGAGAACTTC 540
DB 481 CAGCCCTTAAAGATTCTGTGACAGAGCGCTTCTTCAAGCAAGTCTTCTGAGAGAACTTC 540
QY 541 TTGAGAGAGCAAGAGTGTGAGCAAGAGTCTTCAAGTGTGAGAGTCTTGGGAGAAAGT 600
DB 541 TTGAGAGAGCAAGAGTGTGAGCAAGAGTCTTCAAGTGTGAGAGTCTTGGGAGAAAGT 600
QY 601 GGTCTTGGGAGAGTGTGCGCTCAGGTGAGAAACATGAGAGAGTATGCTGTAG 660
DB 601 GGTCTTGGGAGAGTGTGCGCTCAGGTGAGAAACATGAGAGAGTATGCTGTAG 660
QY 661 AAATGAGACAGAGAGCGCTGAGAGAGAGTGTGCGAGAGAGTGTGCGAGAGAG 720
DB 661 AAATGAGACAGAGAGCGCTGAGAGAGAGTGTGCGAGAGAGTGTGCGAGAGAG 720
QY 721 GAAATCTGAGAGAGTGTGAGAGAGAGTGTGCGAGAGAGTGTGCGAGAGAG 780
DB 721 GAAATCTGAGAGAGTGTGAGAGAGAGTGTGCGAGAGAGTGTGCGAGAGAG 780
QY 781 AAGAGCCATCTCTGCTTGTGATGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 840
DB 781 AAGAGCCATCTCTGCTTGTGATGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 840
QY 841 TACAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 900
DB 841 TACAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 900
QY 901 GCCGTGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 960
DB 901 GCCGTGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 960
QY 961 AATGTGCTTGTGATGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1020
DB 961 AATGTGCTTGTGATGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1020
QY 1021 ATGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1080
DB 1021 ATGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1080
QY 1081 ATCTTAATGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1140
DB 1081 ATCTTAATGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1140
QY 1141 ATTTATGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1200
DB 1141 ATTTATGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1200

QY 1201 GAGGATCTGAGCAAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1260
DB 1201 GAGGATCTGAGCAAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1260
QY 1261 GAGGAGCAAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1320
DB 1261 GAGGAGCAAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1320
QY 1321 AGCAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1380
DB 1321 AGCAGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1380
QY 1381 CGCTGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1440
DB 1381 CGCTGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1440
QY 1441 AAAGACATGCTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1500
DB 1441 AAAGACATGCTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1500
QY 1501 GATAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1560
DB 1501 GATAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1560
QY 1561 ATTTAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1620
DB 1561 ATTTAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1620
QY 1621 GAGGATCTGAGCAAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1680
DB 1621 GAGGATCTGAGCAAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 1680

RESULT 2
US-10-044-205A-1
; Sequence 1, Application US/10044205A
; Publication No. US20020123464A1
; GENERAL INFORMATION:
; APPLICANT: KAPILLER, LIBERMAN, Rosana
; APPLICANT: BANDARU, Rajasekhari
; TITLE OF INVENTION: Uses thereof
; FILE REFERENCE: 10147-52U1
; CURRENT APPLICATION NUMBER: US/10/044, 205A
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/242,428
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: US 60/241,884
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 60/241,877
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2198
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-044-205A-1

Query Match 100.0%; Score 1659; DB 14; Length 2198;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARGGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 60
DB 291 ARGGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 350
QY 61 AAGCCCTGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 120
DB 351 AAGCCCTGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAGAGTGTGAGAG 410
QY 121 GGGCTGACGAGGCTGCGGAGGCTCCGACAGAGTGTCCCTGAACTTCCACAGCTGTGT 180

Qy	1261	GAGGAGACAAAAGAAATTTGGACAGGCTCTCTGTGGCTAAGAAACAGACGACGCTTNGA	1320
Db	1551	GAGGAGACAAAAGAAATTTGGACAGGCTCTCTGTGGCTAAGAAACAGACGACGCTTNGA	1610
Qy	1321	AGCAGAGAAAAGTCTGATGATCCAGAGAAACATCTTTCTTTAAACGATCACTTCCCT	1380
Db	1611	AGCAGAGAAAAGTCTGATGATCCAGAGAAACATCTTTCTTTAAACGATCACTTCCCT	1670
Qy	1381	CGCTTGAAAGCTGGCTTAATTGAACCCCAATTTGGCCAGACCCCTTCACTGATTAATGCC	1440
Db	1671	CGCTTGAAAGCTGGCTTAATTGAACCCCAATTTGGCCAGACCCCTTCACTGATTAATGCC	1730
Qy	1441	AAAGACATCGCTGAAATTTGATGATTTCTGACAGGTTCCGGGGGGTGGAAATTTGACAAA	1500
Db	1731	AAAGACATCGCTGAAATTTGATGATTTCTGACAGGTTCCGGGGGGTGGAAATTTGACAAA	1790
Qy	1501	GATAGCAGTCTTTCAAAAACCTTTGGCAGCAGGTGCTTCTTCAATGACAGCAGAGAA	1560
Db	1791	GATAGCAGTCTTTCAAAAACCTTTGGCAGCAGGTGCTTCTTCAATGACAGCAGAGAA	1850
Qy	1561	ATTATGAGAAACGGGACGTTTGAAGAACTGATGACCCCAAGACTGACGGTGTGAG	1620
Db	1851	ATTATGAGAAACGGGACGTTTGAAGAACTGATGACCCCAAGACTGACGGTGTGAG	1910
Qy	1621	GAGGTAATTCATCCAAAGTCTGGAGTGTGTTGTTATG	1659
Db	1911	GAGGTAATTCATCCAAAGTCTGGAGTGTGTTGTTATG	1949
RESULT 3			
US-10-311-034-45			
Sequence 45, Application US/10311034			
Publication No. US20040023242A1			
GENERAL INFORMATION:			
APPLICANT: INCYTE GENOMICS, INC.			
APPLICANT: YOE, Henry			
APPLICANT: LAL, Preeti			
APPLICANT: BANDMAN, Olga			
APPLICANT: BOROMSKY, Mark L.			
APPLICANT: AU-YOUNG, Janice			
APPLICANT: LU, Yan			
APPLICANT: GANDHI, Ameena R.			
APPLICANT: TRIBOULEY, Catherine M.			
APPLICANT: CHAWLA, Narinder K.			
APPLICANT: YAO, Monique G.			
APPLICANT: LU, Dying Aina M.			
APPLICANT: GREENWALD, Sara R.			
APPLICANT: RAMKUMAR, Jayalaxmi			
APPLICANT: GRIFFIN, Jennifer A.			
APPLICANT: KEARNEY, Liam			
APPLICANT: BUREFORD, Neil			
APPLICANT: NGUYEN, Daniel B.			
APPLICANT: TANG, Y. Tom			
APPLICANT: BAUGHN, Mariah R.			
APPLICANT: HE, Ann			
APPLICANT: THORNTON, Michael			
APPLICANT: HAPALITA, April			
APPLICANT: ARVIZU, Chandra S.			
APPLICANT: GURUBAJAN, Rajagopal			
APPLICANT: LO, Terence P.			
APPLICANT: KHAH, Farrah A.			
APPLICANT: RECIPON, Shirley A.			
APPLICANT: AZIMZAI, Yaida			
APPLICANT: POLICKY, Jennifer L.			
APPLICANT: DING, Li			
APPLICANT: GREYER, Megan			
APPLICANT: ELLIOTT, Vicki S.			
APPLICANT: THANGAVELEU, Kavitha			
APPLICANT: BATRA, Saijeev			
APPLICANT: ISON, Craig H.			
TITLE OF INVENTION: HUMAN KINASES			
FILE REFERENCE: PI-0125 PCT			

Query Match	99.8%	Score 1655.8;	DB 17;	Length 1662;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 1657; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0.

QY	781	AAAGACCCATCTTCGCTTCGTGCAAGACCTGAAATGAGGAGGAGAACTCCAGATTCCACATC	840
Db	781	AAAGACCCATCTTCGCTTCGTGATGACCTGATGATGAGGAGGAGAACTCCAGATTCCACATC	840
QY	841	TAACAAGTGGGCAAGCGGTGGCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAATA	900
Db	841	TACAAAGTGGGCAAGCGGTGGCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAATA	900
QY	901	GCCTGTGGGAATGCTTGCACTCTCATGAACTCGGCATCGTCTTATCGGAGACATGAACTTGAG	960
Db	901	GCCTGTGGGAATGCTTGCACTCTCATGAACTCGGCATCGTCTTATCGGAGACATGAACTTGAG	960
QY	961	AATGTGCTTCTGGAATGACCTGTGGGCAACTGACAGGTATCTGACCTTGGGGCTGGCCGTGAG	1020
Db	961	AATGTGCTTCTGGAATGACCTGTGGGCAACTGACAGGTATCTGACCTTGGGGCTGGCCGTGAG	1020
QY	1021	ATGAAGGGTGGCAAGCCCATCACCAAGAGGGCTGGAAACAAATGTTAATAGCTCTCTGAG	1080
Db	1021	ATGAAGGGTGGCAAGCCCATCACCAAGAGGGCTGGAAACAAATGTTAATAGCTCTCTGAG	1080
QY	1081	ATCCTTATGAAAAAGGTAAATTATTCCTATCTGTGACCTGGTTGCGCATGGAATGACG	1140
Db	1081	ATCCTTATGAAAAAGGTAAATTATTCCTATCTGTGACCTGGTTGCGCATGGAATGACG	1140
QY	1141	ATTATTGAAATGCTGTCTGAGACAAACAATTCAAAGATTAACAAGAAAAAGGTACGTAA	1200
Db	1141	ATTATTGAAATGCTGTCTGAGACAAACAATTCAAAGATTAACAAGAAAAAGGTACGTAA	1200
QY	1201	GAGGATCTGGAAGCAAGAATCTGTGCAAGACGAGGTCAATTCGACGATGATTAATTGACA	1260
Db	1201	GAGGATCTGGAAGCAAGAATCTGTGCAAGACGAGGTCAATTCGACGATGATTAATTGACA	1260
QY	1261	GAGGAAGCAAAAGATATTTGCAAGCTCTTCTGCTTAAGAAATCGAGACACGCTTAGGA	1320
Db	1261	GAGGAAGCAAAAGATATTTGCAAGCTCTTCTGCTTAAGAAATCGAGACACGCTTAGGA	1320
QY	1321	AGCAGAGAAAAGTCTGATGATCCGAGAAAACATATCTTTTAAACGATCAACTTCTCT	1380
Db	1321	AGCAGAGAAAAGTCTGATGATCCGAGAAAACATATCTTTTAAACGATCAACTTCTCT	1380
QY	1381	CGCCTGGAAGCTGAGCTCAATTGAAACCCCATTTGTGCCAGACCCCTTCAGTGGTTATGCC	1440
Db	1381	CGCCTGGAAGCTGAGCTCAATTGAAACCCCATTTGTGCCAGACCCCTTCAGTGGTTATGCC	1440
QY	1441	AAAGACATGCTGCAAAATGATGATTTCTGTGAGGTTGCGGGGGTGGAAATGATGACAA	1500
Db	1441	AAAGACATGCTGCAAAATGATGATTTCTGTGAGGTTGCGGGGGTGGAAATGATGACAA	1500
QY	1501	GATPACCAAGTCTTCAAAAACCTTGTGCAAGGGTGTCTTATGACATGACAGAGAA	1560
Db	1501	GATPACCAAGTCTTCAAAAACCTTGTGCAAGGGTGTCTTATGACATGACAGAGAA	1560
QY	1561	ATTATGAAACGGGACCTGTTGAGGAACCTGAATGACCCCAACAGACTTACGGGTTGTAG	1620
Db	1561	ATTATGAAACGGGACCTGTTGAGGAACCTGAATGACCCCAACAGACTTACGGGTTGTAG	1620
QY	1621	GAGGATTAATTCAACAGCTGAGCTGTGTTGTTATTTG	1659
Db	1621	GAGGATTAATTCAACAGCTGAGCTGTGTTGTTATTTG	1659

RESULT 4
 US-10-451-168-49
 / Sequence 49, Application US/10451168
 / Publication No. US20040091969A1
 / GENERAL INFORMATION:
 / APPLICANT: SMITHKLINE BEECHAM CORPORATION
 / APPLICANT: SMITHKLINE BEECHAM P.L.C.
 / APPLICANT: GLAXO GROUP LIMITED
 / TITLE OF INVENTION: NOVEL COMPOUNDS
 / FILE REFERENCE: GP50039
 / CURRENT APPLICATION NUMBER: US/10/451,168
 / CURRENT FILING DATE: 2003-11-12

conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	661	AAACTGGAACAAGGCGCTGAAGAAAGAAAGTGGCCAGAAATAGCTCTCTTGGAAAAG	720
Db	661	AAACTGGAACAAGGCGCTGAAGAAAGAAAGTGGCCAGAAATAGCTCTCTTGGAAAAG	720
QY	721	GAATCTCTGGAGAAAGGTCAAGAGCCCTTTCATGTCTCTCTGAGCCATAGGCTTTCAGAGC	780
Db	721	GAATCTCTGGAGAAAGGTCAAGAGCCCTTTCATGTCTCTCTGAGCCATAGGCTTTCAGAGC	780
QY	781	AAAGCCCATCTTGCCCTTGTCAAGAGCTGATGAATGAGGAGAGACCTCAAGTCCACATC	840
Db	781	AAAGCCCATCTTGCCCTTGTCAAGAGCTGATGAATGAGGAGAGACCTCAAGTCCACATC	840
QY	841	TACAACTGGGACCGGTGGCTTGGACATGAGCCGGGTGATCTTTTACTGGCCAGATA	900
Db	841	TACAACTGGGACCGGTGGCTTGGACATGAGCCGGGTGATCTTTTACTGGCCAGATA	900
QY	901	GCGTGTGGAGTGTGTGACCTCATGAACTGGGCAGTGGCTATTCGGGACATGAAGCTGTAG	960
Db	901	GCGTGTGGAGTGTGTGACCTCATGAACTGGGCAGTGGCTATTCGGGACATGAAGCTGTAG	960
QY	961	AATGTGCTTCTGGATGACCTTGCGCACTGCAAGTATTCGACTGGGCTGGCCGTGGAG	1021
Db	961	AATGTGCTTCTGGATGACCTTGCGCACTGCAAGTATTCGACTGGGCTGGCCGTGGAG	1021
QY	1021	AAGAAAGGTGGCAAGCCCATCACCAGAGGCTGAAACCATGTTATCATGAGCTCTGAG	1081
Db	1021	AAGAAAGGTGGCAAGCCCATCACCAGAGGCTGAAACCATGTTATCATGAGCTCTGAG	1081
QY	1081	ATTCCTAATGAAAGGTAAAGTATTCCTCATCTGTGAACTGGTTTGCAGTGGATATGAC	1141
Db	1081	ATTCCTAATGAAAGGTAAAGTATTCCTCATCTGTGAACTGGTTTGCAGTGGATATGAC	1141
QY	1141	ATTATTGAATGTTGCTGCGACGAACACCATTCMAAGATTACAGCAAAAAGTCCAGTAA	1201
Db	1141	ATTATTGAATGTTGCTGCGACGAACACCATTCMAAGATTACAGCAAAAAGTCCAGTAA	1201
QY	1201	GAGGATCTGAAACAAAGAACTCTGCAAGAAAGAGAGTAAATTCACGATATATCTTACAC	1261
Db	1201	GAGGATCTGAAACAAAGAACTCTGCAAGAAAGAGAGTAAATTCACGATATATCTTACAC	1261
QY	1261	GAGGAAACAAAGAAATTTGCAAGGCTCTTCTTGCTTAAGAAACCAAGCAAGCTTAGA	1321
Db	1261	GAGGAAACAAAGAAATTTGCAAGGCTCTTCTTGCTTAAGAAACCAAGCAAGCTTAGA	1321
QY	1321	AGCAGAAAGTCTGATATCCAGAGAAACATCATTTCTTTAAACATCACTTTCT	1381
Db	1321	AGCAGAAAGTCTGATATCCAGAGAAACATCATTTCTTTAAACATCACTTTCT	1381
QY	1381	CGCTGGAGAGCTGGCCATATGAAACCCCATTTGTGCGCAAGCCCTTCACTAGCTTATGCC	1441
Db	1381	CGCTGGAGAGCTGGCCATATGAAACCCCATTTGTGCGCAAGCCCTTCACTAGCTTATGCC	1441
QY	1441	AAAGACATGCTGAAATATGATTTCTCGAGAGTTCCGGGGGTGAAATTTGATGACAA	1501
Db	1441	AAAGACATGCTGAAATATGATTTCTCGAGAGTTCCGGGGGTGAAATTTGATGACAA	1501
QY	1501	GATTAACAGTCTTCAAAAACTTTGCGACAGGCTGTTCTTATAGCATGGCAGAGAA	1561
Db	1501	GATTAACAGTCTTCAAAAACTTTGCGACAGGCTGTTCTTATAGCATGGCAGAGAA	1561
QY	1561	ATTATGAAAGGGGACTGTTTGAAGATCGAATGACCCCAAGACCTAGCGGTTGTAG	1621
Db	1561	ATTATGAAAGGGGACTGTTTGAAGATCGAATGACCCCAAGACCTAGCGGTTGTAG	1621
QY	1621	GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTG	1659
Db	1621	GAGGTAATTCATCAAGTCTGGCGTGTGTTGTTATTG	1659

Query Match	99.8%	Score 1655.8;	DB 15;	Length 2249;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 1657; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0.

QY	721	GAATCTTGSAGAGGTGACGACCCCTTTCA	TGTCTCTCTGCGCTTAAGCTTTAGAGC	780
Db	1074	GAATCTTGSAGAGGTGACGACCCCTTTCA	TGTCTCTCTGCGCTTAAGCTTTAGAGC	1133
QY	781	AAGACCCATCTCTGCTTGCATGAGCCGTGAT	TGAATGGGAGAGACCTCAATTCATCATC	840
Db	1134	AAGACCCATCTCTGCTTGCATGAGCCGTGAT	TGAATGGGAGAGACCTCAATTCATCATC	1193
QY	841	TACACGTGGGACCCGCGGCTTGACATGAC	CGGGTGATCTTTTACTCGGCCAGATTA	900
Db	1194	TACACGTGGGACCCGCGGCTTGACATGAC	CGGGTGATCTTTTACTCGGCCAGATTA	1253
QY	901	GCCGTGGAGTGTCACTTCATGAACTCGCAT	TCTCTTAATGGGACATGAACCTCGAG	960
Db	1254	GCCGTGGAGTGTCACTTCATGAACTCGCAT	TCTCTTAATGGGACATGAACCTCGAG	1313
QY	961	AATGTGCTTCTGATGAGCTCGGACATGCA	CTGCAAGTTATCTGACCTGGGAGCTGGAG	1020
Db	1314	AATGTGCTTCTGATGAGCTCGGACATGCA	CTGCAAGTTATCTGACCTGGGAGCTGGAG	1373
QY	1021	ATGAAGGGTGGCAAGCCCATCACCAGAGG	CTGGAACCAATGTTTACATGAGCTCTGAG	1080
Db	1374	ATGAAGGGTGGCAAGCCCATCACCAGAGG	CTGGAACCAATGTTTACATGAGCTCTGAG	1433
QY	1081	ATCTTAATGAAAAAGGTAAATTCTCTAT	CTCTGAGACGTGTTCCATGGAGATGACG	1140
Db	1434	ATCTTAATGAAAAAGGTAAATTCTCTAT	CTCTGAGACGTGTTCCATGGAGATGACG	1493
QY	1141	ATTTATGAAATGGTTCCTGGACGAAACCA	TCATCAAGATTAACAAGAAAAAGCTGATA	1200
Db	1494	ATTTATGAAATGGTTCCTGGACGAAACCA	TCATCAAGATTAACAAGAAAAAGCTGATA	1553
QY	1201	GAGGATCTGAAGCAAAAGACTCTGCAAG	ACGAGTCAAAATTCAGCATGTATTACTTCA	1260
Db	1554	GAGGATCTGAAGCAAAAGACTCTGCAAG	ACGAGTCAAAATTCAGCATGTATTACTTCA	1613
QY	1261	GAGGAGCAAAAAGTATTTGAGGCTCTTT	GTGGCTTAAGAAACCAAGCAAGGCTTAGA	1320
Db	1614	GAGGAGCAAAAAGTATTTGAGGCTCTTT	GTGGCTTAAGAAACCAAGCAAGGCTTAGA	1673
QY	1321	AGGAGAGAAAGTCTGATGATCCAGAGAA	CATCATTTCTTTTAAAGATCAACTTCTCT	1380
Db	1674	AGGAGAGAAAGTCTGATGATCCAGAGAA	CATCATTTCTTTTAAAGATCAACTTCTCT	1733
QY	1381	CGCGTGAAGCTGGCCTTAATGAAACCCCA	ATTGTSCAGACCCCTTCAATGAGTTATGCC	1440
Db	1734	CGCGTGAAGCTGGCCTTAATGAAACCCCA	ATTGTSCAGACCCCTTCAATGAGTTATGCC	1793
QY	1441	AAAGCATCTGCTGAATTTGATGATTTCT	CTGAGGTTCGGGGGGTGGAATTTGATGACAA	1500
Db	1794	AAAGCATCTGCTGAATTTGATGATTTCT	CTGAGGTTCGGGGGGTGGAATTTGATGACAA	1853
QY	1501	GATTAACGATCTTCAAAAACCTTGCGAG	GGGAGTGTCTCTATAGCATGGCAGAGAA	1560
Db	1854	GATTAACGATCTTCAAAAACCTTGCGAG	GGGAGTGTCTCTATAGCATGGCAGAGAA	1913
QY	1561	ATTATAGAAACGGGACGTGTTGAGAACT	GAATGACCCCAACAGACTTAAGGGTGTGAG	1620
Db	1914	ATTATAGAAACGGGACGTGTTGAGAACT	GAATGACCCCAACAGACTTAAGGGTGTGAG	1973
QY	1621	GAGGGTAAATTCATCCAAAGTCTGGCTGT	GTTGTTATG 1559	
Db	1974	GAGGGTAAATTCATCCAAAGTCTGGCTGT	GTTGTTATG 2012	
RESULT 6				
US-10-217-745-1				
; Sequence 1, Application US/10217745				
; Publication No. US20030004328A1				
; GENERAL INFORMATION:				
; APPLICANT: Walke, D. Wade				
; APPLICANT: Wilganski, Nathaniel L.				
; APPLICANT: Turner, C. Alexander Jr.				

RESULT 6
US-10-217-745-1
Sequence 1, Application US/10217745
Publication NO. US2003000432BA1
GENERAL INFORMATION:
APPLICANT: Walke, D. Made
APPLICANT: Wilgansowski, Nathaniel L.
APPLICANT: Turner, C. Alexander Jr.

;; TITLE OF INVENTION: No. US20030004328A1e1 Human G-Coupled Protein Receptor Kinases and
;; TITLE OF INVENTION: Polynucleotides
;; TITLE OF INVENTION: Encoding the Same
;; FILE REFERENCE: LEX-0147-USA
;; CURRENT APPLICATION NUMBER: US/10/217,745
;; PRIOR APPLICATION NUMBER: 2002-08-12
;; PRIOR FILING DATE: 2001-03-08
;; NUMBER OF SEQ ID NOS: 5
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 1662
;; TYPE: DNA
;; ORGANISM: homo sapiens
US-10-217-745-1

Query Match 99.8%; Score 1655.4; DB 15; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1656; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGTGGACATGGGGGCGCTTGGACAACTGATCGCAACCGCTTACCTGCAAGCCCG 60
Db 1 ATGTGGACATGGGGGCGCTTGGACAACTGATCGCAACCGCTTACCTGCAAGCCCG 60
QY 61 AAGCCCTCGACTGCGACAGCAAAAGCTGACGCGGGGGGCGTAAAGCTGGCCCTGCCC 120
Db 61 AAGCCCTCGGACCTGCGACAGCAAAAGCTGACGCGGGGGGCGTAAAGCTGGCCCTGCCC 120
QY 121 GGGCTGAGGGCTGGCGGAGAGCTCGGCAAAAGCTGCTCCCTGAATTCACAGCTGTGT 180
Db 121 GGGCTGAGGGCTGGCGGAGAGCTCGGCAAAAGCTGCTCCCTGAATTCACAGCTGTGT 180
QY 181 GAGAGACAGCCCATGGTGGCGGCGCTTCCCTGATCTTCTGACCAAGTCCGACGTTT 240
Db 181 GAGAGACAGCCCATGGTGGCGGCGCTTCCCTGATCTTCTGACCAAGTCCGACGTTT 240
QY 241 CGCAAGGCGGCAACCTTCTGAGAGAGCTGCAAGAACTGGGAGCTGGCCCGGAGGAG 300
Db 241 CGCAAGGCGGCAACCTTCTGAGAGAGCTGCAAGAACTGGGAGCTGGCCCGGAGGAG 300
QY 301 ACCAAAGACAGCGGCTGCAAGAGGCTGAGTGTGAGAGTGGCCCGGAGGAG 360
Db 301 ACCAAAGACAGCGGCTGCAAGAGGCTGAGTGTGAGAGTGGCCCGGAGGAG 360
QY 361 AACCGGCAACCTTCTGAGAGAGCTGAGTGTGAGAGTGGCCCGGAGGAG 420
Db 361 AACCGGCAACCTTCTGAGAGAGCTGAGTGTGAGAGTGGCCCGGAGGAG 420
QY 421 GAAGAGCAGTGGCTGAGTGAAGCTGCGCAAGGCTGAGGAGGCTTCTTGGCAAG 480
Db 421 GAAGAGCAGTGGCTGAGTGAAGCTGCGCAAGGCTGAGGAGGCTTCTTGGCAAG 480
QY 481 CAGCCCTTTAAGATTTCGTGACAGCGCCCTTCAAGAAAGTTCTGCAAGTGC 540
Db 481 CAGCCCTTTAAGATTTCGTGACAGCGCCCTTCAAGAAAGTTCTGCAAGTGC 540
QY 541 TTGAGATGCAACCAAGTGCAGACAAAGTACTTCAAGTGTCAAGAGTGGGAAAGT 600
Db 541 TTGAGATGCAACCAAGTGCAGACAAAGTACTTCAAGTGTCAAGAGTGGGAAAGT 600
QY 601 GGTTTTGGGAGGTATGTCGCTCCAGGTAAACCACTGGGAGAGATGATGCTGTAAG 660
Db 601 GGTTTTGGGAGGTATGTCGCTCCAGGTAAACCACTGGGAGAGATGATGCTGTAAG 660
QY 661 AAATCTGACAAAGGCTGTAAGAAAGAGTGGCAAGAGTGGCTCTTGGAAAG 720
Db 661 AAATCTGACAAAGGCTGTAAGAAAGAGTGGCAAGAGTGGCTCTTGGAAAG 720
QY 721 GAAATCTTGAAGAGTGAAGAGCTTCTTATGCTCTTGGCTTATGCTTGAAGG 780
Db 721 GAAATCTTGAAGAGTGAAGAGCTTCTTATGCTCTTGGCTTATGCTTGAAGG 780
QY 781 AAGACCATCTGCTGCTTGTGATGAGGCTGATGATGAGGAGGAGCTCAAGTTCACATC 840

Db 781 AAGACCATCTGCTGCTTGTGATGAGGCTGATGATGAGGAGGAGCTCAAGTTCACATC 840
QY 841 TACAACTGGGCAAGCTGGCTGCAATGAGCCGGGTATCTTTTACTGAGCCAGATA 900
Db 841 TACAACTGGGCAAGCTGGCTGCAATGAGCCGGGTATCTTTTACTGAGCCAGATA 900
QY 901 GCGTGGGAGTGGCAAGCTGGCAATGAGCCGGGTATCTTTTACTGAGCCAGATA 960
Db 901 GCGTGGGAGTGGCAAGCTGGCAATGAGCCGGGTATCTTTTACTGAGCCAGATA 960
QY 961 AATGCTTCTGATGAGCTGGCAATGAGCCGGGTATCTTTTACTGAGCCAGATA 1020
Db 961 AATGCTTCTGATGAGCTGGCAATGAGCCGGGTATCTTTTACTGAGCCAGATA 1020
QY 1021 ATGAAGGCTGGCAAGCCCATCAAGAGGCTGCAAGGCTGCAAGGCTGCAAGGCTG 1080
Db 1021 ATGAAGGCTGGCAAGCCCATCAAGAGGCTGCAAGGCTGCAAGGCTGCAAGGCTG 1080
QY 1081 ATCTTAATGAAAGGTAAGTATCTTCTATCTGAGTGGTGGCATGAGGATGACAGC 1140
Db 1081 ATCTTAATGAAAGGTAAGTATCTTCTATCTGAGTGGTGGCATGAGGATGACAGC 1140
QY 1141 ATTATGAAATGCTGCTGCAAGCAACATCAATCAAGTAAAGTCAAGTAAAGTCA 1200
Db 1141 ATTATGAAATGCTGCTGCAAGCAACATCAATCAAGTAAAGTCAAGTAAAGTCA 1200
QY 1201 GAGATCTGAGAGAAAGCTCTGCAAGAGAGCTGCAAGTCAATTCAGATGATTA 1260
Db 1201 GAGATCTGAGAGAAAGCTCTGCAAGAGAGCTGCAAGTCAATTCAGATGATTA 1260
QY 1261 GAGAGAGCAAAAGATTTTGAAGGCTTCTTGGCTTAAAGTCAAGTCAAGTCA 1320
Db 1261 GAGAGAGCAAAAGATTTTGAAGGCTTCTTGGCTTAAAGTCAAGTCAAGTCA 1320
QY 1321 AGCAGAGAAAGTCTGATGATCCAGAGAAATCAATCTTCTTAAAGTCAAGTCA 1380
Db 1321 AGCAGAGAAAGTCTGATGATCCAGAGAAATCAATCTTCTTAAAGTCAAGTCA 1380
QY 1381 GCGCTGGAAGCTGCTTATGAAACCCCATTTTGGCAGAGCTTCAAGTGTATG 1440
Db 1381 GCGCTGGAAGCTGCTTATGAAACCCCATTTTGGCAGAGCTTCAAGTGTATG 1440
QY 1441 AAAGACATGCTGTAATGATTTCTGAGGTTGGGGGCTGGAATTTGATGACAA 1500
Db 1441 AAAGACATGCTGTAATGATTTCTGAGGTTGGGGGCTGGAATTTGATGACAA 1500
QY 1501 GATAGAGATTTCTCAAAAATTGCGACAGGCTGCTCTTATGACATGGCAGAGAA 1560
Db 1501 GATAGAGATTTCTCAAAAATTGCGACAGGCTGCTCTTATGACATGGCAGAGAA 1560
QY 1561 ATTATGAAAGGAGCTGTTGAGAACTGAATGACCCCAAGAGCTGAGGTTGAG 1620
Db 1561 ATTATGAAAGGAGCTGTTGAGAACTGAATGACCCCAAGAGCTGAGGTTGAG 1620
QY 1621 GAGGTAATTTCAATCAAGTCTGGCGGTGTTTATG 1659
Db 1621 GAGGTAATTTCAATCAAGTCTGGCGGTGTTTATG 1659

RESULT 7
US-09-964-469-1
; Sequence 1, Application US/09964469
; Patent No. US20020034803A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USBS
; FILE REFERENCE: C1000634D1V
; CURRENT APPLICATION NUMBER: US/09/964,469
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331

Mon Aug 16 09:34:13 2004

us-10-044-205a-3.rnpb

Page 8

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1  PRIOR FILING DATE: 2000-06-01
2  PRIOR APPLICATION NUMBER: 09/738,894
3  PRIOR FILING DATE: 2000-12-18
4  NUMBER OF SEQ ID NOS: 4
5  SOFTWARE: FastSeq for Windows Version 4.0.0
6  SEQ ID NO 1
7  LENGTH: 1662
8  TYPE: DNA
9  ORGANISM: Human
10 US-09-964-469-1

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Query Match	99.7%	Score 1654.2	DB 9	Length 1662
Best Local Similarity	99.8%	Pred. No. 0		
Matches 1656	Conservative	0	Mismatches 3	Indels 0
			Gaps	0

Qy	1	ATGTGTGACATATGGGAGGCGCTTGGACAAACTGATATGGCTACACCGCTACCTGATGAGAGCCCGG	30
Db	1	ATGTGTGACATATGGGAGGCGCTTGGACAAACTGATATGGCTACACCGCTACCTGATGAGAGCCCGG	60
Qy	61	AAGCCTCGGACTGTGCACACCAAAAGATGTACAGCGCGCGGGGTAGCTGGACCTGCTGCC	120
Db	61	AAGCCTCGGACTGTGCACACCAAAAGATGTACAGCGCGCGGGGTAGCTGGACCTGCTGCC	120
Qy	121	GGGCTGTAGAGGAGCTGTGGGAGAGCTTCGGCAGAGAGCTTCCCTGAACTTTCACAGCCTGTGT	180
Db	121	GGGCTGTAGAGGAGCTGTGGGAGAGCTTCGGCAGAGAGCTTCCCTGAACTTTCACAGCCTGTGT	180
Qy	181	GAGCAGCAGCCCATCGTTCGCGCTTCTCCGTGTACTTTCATGACAAATGTGCCACGTTTC	240
Db	181	GAGCAGCAGCCCATCGTTCGCGCTTCTCCGTGTACTTTCATGACAAATGTGCCACGTTTC	240
Qy	241	CGCAAGCGCGCAAACTTCTCTAGAGACGTCGACGACGACAACTGTGGAGCTGGCCAGAGAGGAGACC	300
Db	241	CGCAAGCGCGCAAACTTCTCTAGAGACGTCGACGACGACAACTGTGGAGCTGGCCAGAGAGGAGACC	300
Qy	301	ACCAAAAGCAGCGCGCTTGTGAGCACTTGTGTGAGTGTGCTTGTCCCGCGGG	360
Db	301	ACCAAAAGCAGCGCGCTTGTGAGCACTTGTGTGAGTGTGCTTGTCCCGCGGG	360
Qy	361	AACCGGCACACCTTCTCTAGACGACGCGGTGACCAAGTCGACAGCAGACCACTGTAG	420
Db	361	AACCGGCACACCTTCTCTAGACGACGCGGTGACCAAGTCGACAGCAGACCACTGTAG	420
Qy	421	GAAAGAGCAGTGTGCTGTGAGTAGCGCTGTGCAGAGGCTGAGGCGCANTGCTTTCTTGTAGAG	480
Db	421	GAAAGAGCAGTGTGCTGTGAGTAGCGCTGTGCAGAGGCTGAGGCGCANTGCTTTCTTGTAGAG	480
Qy	481	CAGCCTTTAAGATTTGTGTGACACAGCGCTTCTTACGACAAATTTCTGTGAGTGGAAAATC	540
Db	481	CAGCCTTTAAGATTTGTGTGACACAGCGCTTCTTACGACAAATTTCTGTGAGTGGAAAATC	540
Qy	541	TTTGAGATGTCAACACAGTGTGACAAATGTACTTCACTGAGTTTCAAGTGTCTGTGGGAAAAGT	600
Db	541	TTTGAGATGTCAACACAGTGTGACAAATGTACTTCACTGAGTTTCAAGTGTCTGTGGGAAAAGT	600
Qy	601	GGTTTTTGGGAGGATATGTGCGTCCAGGTGAAAACACTGTGGAAATGTGTAGCTGTAG	660
Db	601	GGTTTTTGGGAGGATATGTGCGTCCAGGTGAAAACACTGTGGAAATGTGTAGCTGTAG	660
Qy	661	AAATCTGTGACAAAGAGCGGTGACAAAGAAAGTGTGCGCAGAAAGATGTCTCTTGTGAAAAG	720
Db	661	AAATCTGTGACAAAGAGCGGTGACAAAGAAAGTGTGCGCAGAAAGATGTCTCTTGTGAAAAG	720
Qy	721	GAAATCTGTGAGAGGTCAAGCAGCCTTTTATTTCTCTCGGCTTAATGCTTTGTAGAGAC	780
Db	721	GAAATCTGTGAGAGGTCAAGCAGCCTTTTATTTCTCTCGGCTTAATGCTTTGTAGAGAC	780
Qy	781	AAGACCATCTCTGCTGTGTGATGAGGCTTAATGAGGAGGAACTTCAATTTTCACATC	840
Db	781	AAGACCATCTCTGCTGTGTGATGAGGCTTAATGAGGAGGAACTTCAATTTTCACATC	840
Qy	841	TACAACTGTGGCAGCGCTGGCTGTGACATAGCCGAGTATCTTTTACTCGGCTCAGATA	900

Db	841	TACACGTGGGCAAGCGTGGGCTCGGACATGAGCCGGGTGATCTTTTACTCGGCCACAGATA	900
Qy	901	GCCCTGGGGATCTGCACTCCATGAACTCGGCATCGTCTATCGGGACATGAAAGCCGAG	960
Db	901	GCCCTGGGGATCTGCAAGCTCCATGAACTCGGGCATCGCTATCGGGACATGAAAGCCCTGAG	960
Qy	961	AATGTGCTTCTGATGACCTCGGCACCTGCAAGTTATCTGACCTCGGGGCTGGCCGTGGAG	1020
Db	961	AATGTGCTTCTGATGACCTCGGCACCTGCAAGTTATCTGACCTCGGGGCTGGCCGTGGAG	1020
Qy	1021	ATGAAAGGGTGGCAACCCCATCAACCCAGAGGGCTGGAAACAATGGTTACATGGCTCTGAG	1080
Db	1021	ATGAAAGGGTGGCAACCCCATCAACCCAGAGGGCTGGAAACAATGGTTACATGGCTCTGAG	1080
Qy	1081	ATCCCATGGAAAAGTAAAGTTATTCCTATCTCTGTGACGTGTTTCCCATGGAGTCAGC	1140
Db	1081	ATCCCATGGAAAAGTAAAGTTATTCCTATCTCTGTGACGTGTTTCCCATGGAGTCAGC	1140
Qy	1141	ATTATGAAATGGTGTCTGACGAAACCAATTCGAAAGTTTACAGSAAAAGTCAAGTAA	1200
Db	1141	ATTATGAAATGGTGTCTGACGAAACCAATTCGAAAGTTTACAGSAAAAGTCAAGTAA	1200
Qy	1201	GAGGATCTGAACCAAGAACTCTGCAAGACAGAGTCAATTCACAGAGATGATCACTACA	1260
Db	1201	GAGGATCTGAAGCAAGAACTCTGCAAGACAGAGTCAATTCAGATATGATCACTACA	1260
Qy	1261	GAGGAACGAAAATATTTTGGAGGCTCTTCTGGCTAAGAAACCAAGACAGCGTTAGGA	1320
Db	1261	GAGGAAGGAAAATATTTTGGAGGCTCTTCTGGCTAAGAAACCAAGAGAGCGTTAGGA	1320
Qy	1321	AGCAGAGAAAAGTCTGATGATCCAGAGAAACATATTTCTTTAAACGATCAACTTCT	1380
Db	1321	AGGAGAGAAAAGTCTGATGATCCAGAGAAACATATTTCTTTAAACGATCAACTTCT	1380
Qy	1381	CGCCTGGAAGTGGCTTAATGAAACCCCAATTTGTGCAAGCCTTCAGTGGTTAAGCC	1440
Db	1381	CGCCTGGAAGTGGCTTAATGAAACCCCAATTTGTGCAAGCCTTCAGTGGTTAATGCC	1440
Qy	1441	AAAGCATGCTGAATTTGATGATTTCTCTGAGGTTCCGGGGGGTGGAAATTGATGACAA	1500
Db	1441	AAAGCATGCTGAATTTGATGATTTCTCTGAGGTTCCGGGGGGTGGAAATTGATGACAA	1500
Qy	1501	GATTAAGCAATCTTCAAAAACCTTTCGACAGGTGCTGTTCTTAAGCATGGCAGAGAA	1560
Db	1501	GATTAAGCAATCTTCAAAAACCTTTCGACAGGTGCTGTTCTTAAGCATGGCAGAGAA	1560
Qy	1561	ATTATTAAGAAACGGGACGTGTTGAGGAATGATGACCCCAAGACCTCAAGGTTGTAG	1620
Db	1561	ATTATTAAGAAACGGGACGTGTTGAGGAATGATGACCCCAAGACCTCAAGGTTGTAG	1620
Qy	1621	GAGGGTAAATCATCAAGTCTGGCGGTGTGTTGTTATG	1659
Db	1621	GAGGGTAAATCATCAAGTCTGGCGGTGTGTTGTTATG	1659

RESULT 8
US-10-425-962-1
; Sequence 1, Application US/10425962
; Publication No. US20030180786A1
; GENERAL INFORMATION:
; APPLICANT: GUSETER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THERBOP
; FILE REFERENCE: C1000636DIV2
; CURRENT APPLICATION NUMBER: US/10/425, 962
; CURRENT FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 09/964,469
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-16
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01

[illegible]

Db	901	GCCTGGGAGATGCTGACCTCCATGAACTCGGCAATCGTCTCATGCGACATGAAGCCTGAG	960
QY	961	AATGCTCTTGAGATGACCTCGCAACTGCAAGTTATCTGACCTGGGGGCTGGCCGTGGAG	102
Db	961	AATGCTCTTGAGATGACCTCGGCAACTGCAAGTTATCTGACCTGGGGGCTGGCCGTGGAG	102
QY	1021	ATGAAGGGTGGCAAGCCCATCAACCAGAAGCTGGAAACCAATGTTACATGGCTCTGAG	108
Db	1021	ATGAAGGGTGGCAAGCCCATCAACCAGAAGCTGGAAACCAATGTTACATGGCTCTGAG	108
QY	1081	ATCTCAATGGAAAAGGTAAAGTTATTCATATCCCTGTGACCTGGTCTTGGCATGGAGATGAGC	114
Db	1081	ATCTCAATGGAAAAGGTAAAGTTATTCATATCCCTGTGACCTGGTCTTGGCATGGAGATGAGC	114
QY	1141	ATTATGAAATGGTGTCTGACAGAACACCATTCMAAGATTACAGAAAAGGTCAGTAA	120
Db	1141	ATTATGAAATGGTGTCTGACAGAACACCATTCMAAGATTACAGAAAAGGTCAGTAA	120
QY	1201	GAGAGCTGAGCAAGAAAGACTCTGCAAGACAGAGTCAAAATTCAGCATGATTAATTCA	126
Db	1201	GAGAGCTGAGCAAGAAAGACTCTGCAAGACAGAGTCAAAATTCAGCATGATTAATTCA	126
QY	1261	GAGGAGCAAAAAGATATTTGCAAGCTCTTCTTGGCTTAAGAAACCAAGCAACGCTTGAG	132
Db	1261	GAGGAGCAAAAAGATATTTGCAAGCTCTTCTTGGCTTAAGAAACCAAGCAACGCTTGAG	132
QY	1321	AGCAGAAAAAATCTGATGATCCAGAAAACATCATATTTCTTAAACGATCACTTTCC	138
Db	1321	AGCAGAAAAAATCTGATGATCCAGAAAACATCATATTTCTTAAACGATCACTTTCC	138
QY	1381	CGCCTGGAGAGCTGGCTTAATGGAACCCCATTTGTCGACAGACCCCTCATGCTTTAGCC	144
Db	1381	CGCCTGGAGAGCTGGCTTAATGGAACCCCATTTGTCGACAGACCCCTCATGCTTTAGCC	144
QY	1441	AAAGACATCTGCGAAATTTGATATTTCTGCAAGTTGCGGGGGTGAATTTGATGACAA	150
Db	1441	AAAGACATCTGCGAAATTTGATATTTCTGCAAGTTGCGGGGGTGAATTTGATGACAA	150
QY	1501	GATTAAGACTTTCTCAAAAACCTTGGCAGAGGTGCTGTTCTTAAGCATGCGAGAAAGA	156
Db	1501	GATTAAGACTTTCTCAAAAACCTTGGCAGAGGTGCTGTTCTTAAGCATGCGAGAAAGA	156
QY	1561	ATTATAGAAAACGGAGCTGTTTGAAGAACTGAATGACCCCAACAGACCTTACGGGTGAG	162
Db	1561	ATTATAGAAAACGGAGCTGTTTGAAGAACTGAATGACCCCAACAGACCTTACGGGTGAG	162
QY	1621	GAGGGTAATTCATCAAGCTGAGGCTGTGTTGTTAATG	1659
Db	1621	GAGGGTAATTCATCAAGCTGAGGCTGTGTTGTTAATG	1659

; Sequence 273, Application US/10072012
; Publication No. 100040034001

GENERAL INFORMATION: 036200500353436AL

APPLICANT: Tchemnev, Velizar

APPLICANT: Spytkev, Kimbelly

APPLICANT: Zerkhan, Bryan

APPLICANT: Paturusien, Meera

APPLICANT: Shmukets, Richard

APPLICANT: Li, Li

APPLICANT: Gangolli, Esha

APPLICANT: Padiguru, Murali,shara

APPLICANT: Anderson, David W.

APPLICANT: Rastelli, Luca

APPLICANT: Miller, Charles E.

APPLICANT: Geislach, Valerie

APPLICANT: Taupler, Jr., Raymond J

APPLICANT: Gusev, Vladimir Y.

APPLICANT: Colman, Steven D.

APPLICANT: Wolcenc, Adam R.

APPLICANT: Pena, Carol E. A
APPLICANT: Futrak, Katarzyna
APPLICANT: Grosse, William M.
APPLICANT: Alsobrook II, John P.
APPLICANT: Lepley, Denise M.
APPLICANT: Rieger, Daniel K.
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: us/10/072,012
CURRENT FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: 60/265,102
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,517
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,412
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,395
PRIOR FILING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/266,406
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/266,767
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 60/267,057
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/266,975
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 60/267,459
PRIOR FILING DATE: 2001-02-08
Remaining Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 273
LENGTH: 1701
TYPE: DNA
ORGANISM: Homo sapiens
US-10-072-012-273

Query Match 95.8%; Score 1589.8; DB 13; Length 1701;

Best Local Similarity 98.6%; Pred. No. 0;

Matches 1642; Conservative 0; Mismatches 2; Indels 21; Gaps 3;

1 ATGTGACATGAGGAGCCCTGACACCTGATGCTCCAAACCGCTTACTGAGGCGCCG 60
13 ATGTGACATGAGGAGCCCTGACACCTGATGCTCCAAACCGCTTACTGAGGCGCCG 78
61 AAGCTTGGACCTGACAGCAAGAGAGCTGAGCGGCGGCGGAGTACCTGAGCCTGCGCC 120
79 AAGCTTGGACCTGACAGCAAGAGAGCTGAGCGGCGGCGGAGTACCTGAGCCTGCGCC 138
121 GGGGTGACAGGAGCTGAGCGGAGCTCGGACAGAGCTGCTCCGAACTTCCAGAGCTGTGT 180
139 GGGGTGACAGGAGCTGAGCGGAGCTCGGACAGAGCTGCTCCGAACTTCCAGAGCTGTGT 198
181 GAGCAGAGCCCATGAGTGGCTGCGCGCTCTTCCGTGACTTCTAGCCAAAGTGGCCAGCTTC 240
199 GAGCAGAGCCCATGAGTGGCTGCGCGCTCTTCCGTGACTTCTAGCCAAAGTGGCCAGCTTC 258
241 GCGAAGGAGCACTTCTAGAGAGAGTGCAGAACTGAGAGCTGAGCGGAGAGAGAGCC 300
259 GCGAAGGAGCACTTCTAGAGAGAGTGCAGAACTGAGAGCTGAGCGGAGAGAGAGCC 318
301 ACCAAGACAGCGAGCTGAGAGAGGAGTGCAGAACTTGTGAGTGGCTTGTGCGCGGAG 360
319 ACCAAGACAGCGAGCTGAGAGAGGAGTGCAGAACTTGTGAGTGGCTTGTGCGCGGAG 378
361 AACCGCAACCTTCTGAGCGAGCGGCTGAGCGAGCAATGTCAGAGAGAGCAACCTAGAG 420
379 AACCGCAACCTTCTGAGCGAGCGGCTGAGCGAGCAATGTCAGAGAGAGCAACCTAGAG 438
421 GAAAGCAGAGTGTGAGTGCAGAGCTGAGCGAGAGGCTGAGGCACTTCTTTCAGAGAG 480

439 GAAAGCAGAGTGTGAGTGCAGAGCTGAGCGAGAGGCTGAGGCACTTCTTTCAGAGAG 498
481 CAGCCCTTTAAGATTTTGTGAGCAAGCGCTTTCAGAGCAAGTTCTGAGTGAAGACTC 540
499 CAGCCCTTTAAGATTTTGTGAGCAAGCGCTTTCAGAGCAAGTTCTGAGTGAAGACTC 558
541 TTGAGATGCAACAGAGTGCAGAGAGTGCAGAACTTCACTGAGTGCAGTGTGAGAGAGT 600
559 TTGAGATGCAACAGAGTGCAGAGAGTGCAGAACTTCACTGAGTGCAGTGTGAGAGAGT 618
601 GCTTTTGGAGAGTATGTCCTGTCAGAGTGAAGAACTGAGAGAGTGAAGTGAAGCTGTAG 660
619 GCTTTTGGAGAGTATGTCCTGTCAGAGTGAAGAACTGAGAGAGTGAAGTGAAGCTGTAG 663
661 AAACCTGACAAAGAGCGCTGAGAGAGAGTGCAGAGAGTGCAGAGTGCAGAGAGTGCAG 720
664 AAACCTGACAAAGAGCGCTGAGAGAGAGTGCAGAGAGTGCAGAGTGCAGAGAGTGCAG 723
721 GAAATCTTGAAGAGTGCAGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 780
724 GAAATCTTGAAGAGTGCAGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 783
781 AAGACCATCTGCTGCTTGTGATGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGATC 840
784 AAGACCATCTGCTGCTTGTGATGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGATC 843
841 TCCAACTGAGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAG 900
844 TCCAACTGAGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAG 903
901 GCTTGTGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 960
904 GCTTGTGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 963
961 AATGCTTCTGAGTGAAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 1020
964 AATGCTTCTGAGTGAAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 1023
1021 AATGAGGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 1077
1024 AATGAGGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 1083
1078 GAGATCTTATGAGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 1137
1084 GAGATCTTATGAGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 1143
1138 AGCATTTATGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAG 1197
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1198 AAGAGGATCTGAGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 1257
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1264 AAGAGGATCTGAGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 1323
1318 GAGAGC---AAGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 1374
1324 GAGAGGATCTGAGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 1383
1375 TTTCTGCTGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 1434
1384 TTTCTGCTGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 1443
1435 TATGCAAGAGATGCTGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 1494
1444 TATGCAAGAGATGCTGAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 1503
1495 GAGCAAGATGAGATGCTTCAAAAGCTTGCAGAGTGCAGAGTGCAGAGTGCAGAGTGCAGAGT 1554

Db 1504 GACAAATATAGAGTTCTTCAAAAATTGCGACAGGTGCTTCTATATAGATGCGAG 1563
QY 1555 GAAAGAAATATAGAAACGGAGCTGTTGAGAACTGAATACCCCAAGACCTTACGGGT 1614
Db 1564 GAAAGAAATATAGAAACGGAGCTGTTGAGAACTGAATACCCCAAGACCTTACGGGT 1623
QY 1615 TGTGAGAGAGGTAAATTCATCCAGTCTGCGGTGTGTATG 1659
Db 1624 TGTGAGAGGTAAATTCATCCAGTCTGCGGTGTGTATG 1668

RESULT 10

US-10-217-745-3
; Sequence 3, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L.
; APPLICANT: Turner, C. Alexander Jr.
; TITLE OF INVENTION: No. US20030004328A1 Human G-Coupled Protein Receptor Kinases and
; TITLE OF INVENTION: Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: LEX-0147-USA
; CURRENT APPLICATION NUMBER: US/10/217,745
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: US/09/802,117
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-217-745-3

Query Match 63.1%; Score 1046.8; DB 15; Length 1062;
Best Local Similarity 99.8%; Pred. No. 3.8e-312;
Matches 1048; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGTGTGACATG3GGGCTCTGACAACTGATGCCAACAACCGCTTACTGACAGCCGG 60
Db 1 ATGTGTGACATG3GGGCTCTGACAACTGATGCCAACAACCGCTTACTGACAGCCGG 60
QY 61 AAGCCCTGCACTGCGACGCAAGAGCTGACGCGCGCGCGCTGACCTTGGCCCTTGC 120
Db 61 AAGCCCTGCACTGCGACGCAAGAGCTGACGCGCGCGCGCTGACCTTGGCCCTTGC 120
QY 121 GGGCTGAGGGCTGCGCGAGCTCGCGCAGAACTGCTCCGTAACCTTCCACAGCTGT 180
Db 121 GGGCTGAGGGCTGCGCGAGCTCGCGCAGAACTGCTCCGTAACCTTCCACAGCTGT 180
QY 181 GAGCAGCAGCCATGCTGCTGCGCTCTTCCGTGACTTCTAGCCACAGTGCACAGTTC 240
Db 181 GAGCAGCAGCCATGCTGCTGCGCTCTTCCGTGACTTCTAGCCACAGTGCACAGTTC 240
QY 241 CGCAAGGCGCACTCTCTAGAGAGAGTGAAGACTGGAGCTGCGCGAGGAGAGCC 300
Db 241 CGCAAGGCGCACTCTCTAGAGAGAGTGAAGACTGGAGCTGCGCGAGGAGAGCC 300
QY 301 ACCAAAGACGCGCTGCGAGGGCTGTGCGCACTTGTGAGGTGCGCCCGCGGG 360
Db 301 ACCAAAGACGCGCTGCGAGGGCTGTGCGCACTTGTGAGGTGCGCCCGCGGG 360
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Db 361 AACCCTGACCTTCTTCAAGCGCGGCTGCGCGCACTTGTGAGGTGCGCCCGCGGG 420
QY 421 GAAAGCGAGTGTGCGAGTGTGCGCGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 480
Db 421 GAAAGCGAGTGTGCGAGTGTGCGCGAGGTGAGGTGAGGTGAGGTGAGGTGAGGT 480
QY 481 CAGCCTTTAAGGATTTGTGACCAAGCGCTTCTACCAAGATTTGTGACGAGAACTG 540
Db 481 CAGCCTTTAAGGATTTGTGACCAAGCGCTTCTACCAAGATTTGTGACGAGAACTG 540

Db 481 CAGCCTTTAAGGATTTGTGACCAAGCGCTTCTACCAAGATTTGTGACGAGAACTG 540
QY 541 TTGAGAGTGAACCACTGTGACCAAGATTTCTGAGTTCAAGTGTGCGGAGAGT 600
Db 541 TTGAGAGTGAACCACTGTGACCAAGATTTCTGAGTTCAAGTGTGCGGAGAGT 600
QY 601 GGTGTTGCGGAGTATGTCGCTGAGTGAAGAACTGCGGAGAGTATGTCCTGTAAG 660
Db 601 GGTGTTGCGGAGTATGTCGCTGAGTGAAGAACTGCGGAGAGTATGTCCTGTAAG 660
QY 661 AAATGCAAGAGGCTGAGAGAAAGTGTGCGAGAGATGCTCTTGGAGAAAG 720
Db 661 AAATGCAAGAGGCTGAGAGAAAGTGTGCGAGAGATGCTCTTGGAGAAAG 720
QY 721 GAAATCTTGAAGAGTCAAGAGCTTCTGATGTTCTCTGCGCTATGCTTTGAGAGC 780
Db 721 GAAATCTTGAAGAGTCAAGAGCTTCTGATGTTCTCTGCGCTATGCTTTGAGAGC 780
QY 781 AAGACCATCTGCTGCTGATGAGCTGATGAGTGAAGTGAAGTGAAGTGAAGTGAAG 840
Db 781 AAGACCATCTGCTGCTGATGAGCTGATGAGTGAAGTGAAGTGAAGTGAAGTGAAG 840
QY 841 TACACGTGCGAGCGCTGCGCTGAGCATGAGCGGAGTATCTTTACTGCGCCAGATA 900
Db 841 TACACGTGCGAGCGCTGCGCTGAGCATGAGCGGAGTATCTTTACTGCGCCAGATA 900
QY 901 GCGTGTGAGTGTGCTGACCTTCAATGAACTGCGCATCTTATGCGAGCATGAGCTGAG 960
Db 901 GCGTGTGAGTGTGCTGACCTTCAATGAACTGCGCATCTTATGCGGAGCATGAGCTGAG 960
QY 961 AATGTGCTTGTGATGACCTGCGCACTGCAAGTATCTGACTGCGGCTGCGGAG 1020
Db 961 AATGTGCTTGTGATGACCTGCGCACTGCAAGTATCTGACTGCGGCTGCGGAG 1020
QY 1021 ATGAGGGGTGCGAAGCCCATCACCAGAG 1050
Db 1021 ATGAGGGGTGCGAAGCCCATCACCAGAG 1050

RESULT 11

US-09-964-469-3
; Sequence 3, Application US/09964469
; Patent No. US20020034803A1
; GENERAL INFORMATION:
; APPLICANT: GIBLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL000636D1V
; CURRENT APPLICATION NUMBER: US/09/964,469
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 36651
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(36651)
; OTHER INFORMATION: n = A,T,C or G
US-09-964-469-3

Query Match 37.2%; Score 617.4; DB 9; Length 36651;
Best Local Similarity 96.8%; Pred. No. 1.5e-178;
Matches 630; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 ATGTGTGACATG3GGGCTCTGACAACTGATGCCAACAACCGCTTACTGACAGCCGG 60
Db 1 ATGTGTGACATG3GGGCTCTGACAACTGATGCCAACAACCGCTTACTGACAGCCGG 60

Query Match	37.2%	Score 617.4	DB 15	Length 36651
Best Local Similarity	96.8%	Pred. No. 1.5e-178		
Matches 630	Conservative 0	Mismatches 21	Indels 0	Gaps 0
QY 1	ATGTGGACATAGGGGGGCCCTGTGACAACTTGATGTCCGCAACACCGCTTACCTTGACAGTCCCG 60			
Db 2076	ATGTGTGACATATGGGGGCCCTGTGACAACTTGATGTCCGCAACACCGCTTACCTTGACAGTCCCG 2135			
QY 61	AAECCTTGACATCTGCACACACAAAGAGCTGAGAGGGGGGGGGGGAGCTTGAGCCCTTGCC 120			
Db 2136	AAECCTTGACACTGCACACACAAAGAGCTGAGAGGGGGGGGGGGAGCTTGAGCCCTTGAGCC 2195			
QY 121	GGGCTGACAGAGCTGCAGAGCTCCGACAGAGAGCTGTCCCTGAACTTGCACAGCTGTGT 180			
Db 2196	GGGCTGACAGAGCTGCAGAGCTCCGACAGAGAGCTGTCCCTGAACTTGCACAGCTGTGT 2255			
QY 181	GACACAGACCCCATCGGTGTGCGCCCTCTTCCGTGACTTCTTAGCCACAGTGCACAGGTTC 240			
Db 2256	GACACACACCCCATCGGTGTGCGCCCTCTTCCGTGACTTCTTAGCCACAGTGCACAGGTTC 2315			
QY 241	CGAAGAGGGGCAACCTTCTTAGAGACGTGACGAATCGGAGAGCTGGCCGAGAGAGACCC 300			
Db 2316	CGAAGAGGGGCAACCTTCTTAGAGAGCTGACGAATCGGAGAGCTGGCCGAGAGAGACCC 2375			
QY 301	ACCAAGACAGGCGCGCTGACAGGGCTGTGTGTCACATTGTGTGAGTGCCTTGTCCCGGG 360			
Db 2376	ACCAAGACAGGCGCGCTGACAGGGCTGTGTGTCACATTGTGTGAGTGCCTTGTCCCGGG 2435			
QY 361	AAACCGCAACCTTCTTCAACGACAGGCGCGGACCAAGAGTGCACACAGCAGCAGCTAG 420			
Db 2436	AAACCGCAACCTTCTTCAACGACAGGCGCGGACCAAGAGTGCACACAGCAGCAGCTAG 2495			
QY 421	GAAAGCGAGTGGCTGCAGTGAAGCTGCGCAAGGTGAAGCATGCTTCTTGTGAAG 480			
Db 2496	GAAAGCGAGTGGCTGCAGTGAAGCTGCGCAAGGTGAAGCATGCTTCTTGTGAAG 2555			
QY 481	CAGCCCTTTAAGGATTTTGTGACCAAGCGCTTCTTCAACAAGTTTGTGAGTGAAGATC 540			
Db 2556	CAGCCCTTTAAGGATTTTGTGACCAAGCGCTTCTTCAACAAGTTTGTGAGTGAAGATC 2615			
QY 541	TTGAGAGTGAACCAAGTGTGACAAAGTACTTCACTGAGTTTCAAGTGTGGGAAAAGT 600			
Db 2616	TTGAGAGTGAACCAAGTGTGACAAAGTACTTCACTGAGTTTCAAGTGTGGGAAAAGT 2675			
QY 601	GGTTTGGGAGGTATGTGCGCTTCAGGTGAAAACACTGGGAAAGATGAT 651			
Db 2676	GGTTTGGGAGGTATGTGCGCTTCAGGTGAAAACACTGGGAAAGATGAT 2726			
RESULT 13				
US-09-851-686-2				
Sequence 2, Application US/09851686				
Patent No. US20020034767A1				
GENERAL INFORMATION:				
APPLICANT: Gomez, Jorge				
APPLICANT: Kumapuli, Priya				
TITLE OF INVENTION: Compositions and Methods for Modulating the Activity of G Protein				
TITLE OF INVENTION: Receptor Kinases GRK5 and GRK6				
FILE REFERENCE: JEFF-0118-DIV				
CURRENT FILING DATE: US/09/851,686				
PRIOR FILING DATE: 2001-10-01				
PRIOR APPLICATION NUMBER: US 08/464,954				
PRIOR FILING DATE: 1995-06-06				
PRIOR APPLICATION NUMBER: US 08/076,084				
PRIOR FILING DATE: 1993-06-11				
NUMBER OF SEQ ID NOS: 12				
SOFTWARE: PatentIn version 3.1				
SEQ ID NO 2				
LENGTH: 2848				
TYPE: DNA				
ORGANISM: Homo sapiens				
US-09-851-686-2				

QY 15 GGCCTCGAGCAACTGATGCGCAACCGGCTTACTGTGAGGCCCGGAGAGCCTTGAGACTG 74
 Db 65 GGGAGCTCGAGAACTCGTAGCGAACAGGATCTACTCACTCAAGGCCCGGAGAGGCTGGCGATG 12
 QY 75 CGACAGCAAAAG--AGCTGACACGGGCGGGGGTGAAGCTTGAGCCCTGCGCGAGCTGACAGG 13
 Db 125 AATATGCAAAAGCAAAAGCAGAAATATGGCGGACAGTGGCTCGAAGTTCTCCCTCACTACGCCA 184
 QY 132 CTGCGGGAAGCTTCGGCAGAAAGCTGTCCCTGAACTTCCAGACGCTGTGTAGCGAGAGCG 191
 Db 185 GTGCGAAGAGCTGGGCTCAGCTCGAGGCTGACTATTCAGACCTGTGTGAGAGGCGACGC 244
 QY 192 CATGGGTGGCGGCTCTTTCCTGACTTCTACGCCACAGTGGCCCAAGTTCGCGAAGGCGCG 251
 Db 245 CATGGAGCGCTGTCTTTCCTGAGAGTCTGTGCCACAGAGGCCGAGAGCTGAGCGCTGGCGT 304
 QY 252 AACCTTCTAGAGAGAGTGTGACAGACTGTGGAGCTGGCGGAGAGAGAGACCCACAAAGACAG 311
 Db 305 CCGCTTCTCGAATGGGATGGCGGAGATGAAATGATACCCCGGATGACAAAGCGAGAGCATG 364
 QY 312 CCGCGTGAAGGCGCTGTGTGCACTTGTGCGAGTCCCGTCCCGGAGAACCCGCAAC 371
 Db 365 TGGGCGGAGCG--TAAAGCGAATTTTGTAGCCACACGGGATCTTGACCTCATCTCCGA 421
 QY 372 CTTCCTAGACAGAGCCGCGTGGCCAGAGGCCAGAGCCACACTGAGAGAGAGCAT 431
 Db 422 GGTCCCCCGGAGACTGTGTAGAAC--TGCATCCAGCGGCTGAGAGAGGTCTCTCCAAAG 480
 QY 432 GCGCTGAGTACGCTGGCGAAAGCGCTGAGGCCATGGCTTTTGTGCAAGAGCAGCCCTTAA 491
 Db 481 ACGTTTTCAGAACTCAACCGGCTGA--CCAGAGATACGTAGCGTGGCCCTTTTGC 538
 QY 492 GGAATTTGATACAGAGGCGCTTCTACAGCAAGTTTCTGCGATGAACTCTTGAGANTCA 551
 Db 539 GCACTACCTGAGAGATCTTACTTCAACCGTTTCTGCGAGTGAAGTGGCTGGAAAGCA 598
 QY 552 ACGAGTGCAGCAAGTACTTCACTGAGTCAAGTGTGCGGAGAAAGTGGTTTGGGGA 611
 Db 599 GCGAGTGAACAAAACACTTTCAGGAGATACCGAGTCTGTGGCAAAAGTGGCTTTGGGGA 658
 QY 612 GGTATGTGCGCTTCAGGTGAGAAAAACCTGGAGAGATGATGCTGTAGAAAGTGTGACAA 671
 Db 659 GATGTGGCTCCACAGGTGGGCGCCACAGGTAAAGATGTGCTGCAAGACCTTAGGAA 718
 QY 672 GAACGCGCTGAAGAAAGATGTGCGAGAAATATGCTCTTTGGAAAAAGAAATTTTGA 731
 Db 719 AAGCGGATTCAGAGAGCGGAAAGGAGAGGACATAGCGGCTGAACAGAGACCAATCTCGGA 778
 QY 732 GAAGTGAAGAGCCCTTCAATGTCTCTCTGGGCTATGCTCTTGAAGCAAGACCCATCT 791
 Db 779 GAAATGGAACAATAGGTTTGTAGTGAAGCTTGGCTTACGCTATGAGACCAAGACGGGCT 838
 QY 792 CTGCGTTTGCATGAGGCTGATGAATGGGGGAGACCTCAAGTTTCAATTTACAAGTGG 851
 Db 839 GTGCTGTGTGTGCACTGATGAACGGGGGCGACCTCAAGTTTCAATCTTCCACATGGG 898
 QY 852 CAGCGGTGGCTGAGCATGAGAGCGGGGTGATCTTTTATCTGCGCCAGATATGCGCTGTGAGAT 911
 Db 899 CCAAGGCTGGCTTCCCGAAGCGCGGCGGTCTTCAAGCCGCGGAAATGTGCTGTGGCT 958
 QY 912 GCTGACCTTCATTAATCGGCAATGTCTATCGGGAATGAAAGCTGAGAAATGTCTCT 971
 Db 959 GAGAGACTTGAACCGGAGAGCATGTGTACAGGACCTGAAGCCCGAAGCAATCTTGCT 1018
 QY 972 GAATGACCTTGGCAACTGAGAGTTATCTGACTGTGGAGCTGGCGGTGAGAGAGAGGTGG 1031
 Db 1019 GGAATGACCAAGGTCACATCCGATCTCTGACTGTGAGACTTACCTGTGACATGTGCCCAAGGG 1078

QY	1032	CAAGCCATACCACGAGGGCTGAACCAATGGTTACATGCTCTTGAGANTCTTAATGGA	1091
Db	1079	CCAGACCATTAAGAGGACGTGTGGGACACGTGGGTTCATGCTCCGGAG--GTGGTGA	1133
QY	1092	AAAGGTAAGTATTCTCATCTCTGTGSACTGGTTTGGCANTGGATGACAGATTATTAAT	1155
Db	1136	GAATGAAACGGTACAGGTTCAAGCTTGACTGATGGTGGGGCTCGGCTCTCTACAGGAA	1199
QY	1152	GGTTGCTGACGACACACCATTTCAAGATTCAAGAGAAAAGTCAGTAAAGAGATCTGA	1211
Db	1196	GATCACAGGCGAGTGCCCTTCACAGAGGAAAGAAAGATCAAGCGGAGAGGTGGA	1255
QY	1212	GCAAAGAACCTCTGCAACACAGAGTCAATTTCAGCATGATTACTTCAAGAGAACAA	1271
Db	1256	GGGCGTGGTGAAGAGGTCCCGAGAGTATTCGAGCGGTTTCCCGCAGGCCCGCT	1315
QY	1272	AGATATTTGCAGGCTCTTCTGGCTTAAGAAACAGAGCAGCAAGCTTGAAGAGCAGAAA	1331
Db	1316	ACTTGTCTACAGCTCTCTCTGCAAGAACCTTCGCGAAGCCTCGAGGTGTGCTGGGGCAG	1375
QY	1332	GTCTGATGATCCACAGAAACATATTTCTTTAAAACATCACTTCTCGCTCGAAGC	1391
Db	1376	TGCCCGGAGGTGAAGAGACCCCTCTTTAAGAAAGCTGAACCTCAAGCGCTGGGAGC	1433
QY	1392	TGGCCTAATGACACCCCAATTGTGGCCAGACCTTCACTAGTGGTTATGCCAAGACATGC	1451
Db	1436	TGGCAGTCTGAGGCGCGGTCAAGCCTGACCCCGAGGCCATTATTACTGAAGCATGGTCT	1495
QY	1452	TGAATTATGATATTCTGAGAGTTTCGGGGGAGGGAATTTGATGACAAAGATMAAGAGTT	1511
Db	1496	GGACATTGAACAGTTCTTAAGCTCAAGGCGGTGGAGCTGAACTTACCGACACGACGTT	1555
QY	1512	CTTCAAAAACCTTTGCAACAGGTGTGTTCTTAATAGCATGACAGAGAATTTATGAAC	1571
Db	1556	CTACACGAAGTTGCCACAGGACGTGGCCCAATCCCTGGGCAACAGAGTGTGGAGAC	1615
QY	1572	GGACACTGTTTGGAGACGTAATGAC	1596
Db	1616	CGAGTCTTCCAGACCTGAATGTC	1640

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RESULT 14
US-09-873-367C-142
; Sequence 142, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; APPLICANT: Soppet, Daniel
; APPLICANT: Andress, Gregory
; APPLICANT: Augustus, Meena
; APPLICANT: Ebner, Reinhard
; APPLICANT: Carter, Kenneth
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-64
; CURRENT APPLICATION NUMBER: US/09/873,367C
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,891
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,842
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/244,867
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: U.S. 60/245,084
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 142
; LENGTH: 2648
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-873-367C-142

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Query Match 25.2%; Score 418.2; DB 10; Length 2848;
 Best Local Similarity 56.2%; Pred. No. 1.1e-117;
 Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;

15 GGCCTTGAGAACCTGATGCGCAACCGCTTACCTGAGAGCCGGAAGCCCTCGGACTG 74
 65 GAGGCTGAGAACATGCTGAGAACACGCTGCTCACTCAAGGCCCGGGAAGGTGGCGTGG 124
 75 CGACAGCAAG--AGCTGACGCGCGCGCGTACCTGAGCTGCGCTCGCGGCTGAGGG 131
 125 AATGCGCAAGGCAAGAAAGAAATGCGCGAGATGCTCCAGTCTCCATCAATAGCA 184
 132 CTGCGCGAGCTCCCGCAGAGCTGTCCCTGAACTTCCACAGCTGTGTGAGAGAGAGCC 191
 185 GTGCGAAGAGCTGCGCTGAGCTGAGCTGACCTGCTACCTGACAGCCCTGTGGAGGAGC 244
 192 CATGGGTGCGCGCTCTCTGCTGCTTCTAGCAGACAGTGCACAGTTCGCGCAAGCGCG 251
 245 CATGGGCGCTGCTGCTGCTGCGAGATTTGTGCGCAGAGCGCGAGCTGAGCGCTGGGT 304
 252 AACCTTCTGAGAGAGCTGAGAACCTGAGAGCTGCGCGAGAGGAGCCCAAGCAAG 311
 305 CGCTTCTGAGATGGGTGGCGAGATGAGATGACCCCGAGTGAAGAGGAGAGCATG 364
 312 CGGCTGCAAGGAGCTGTGCGCACTTGTGCGAGTGGCCCTGCGCGGGAAGCCGCAAC 371
 365 TGCGGCGGACG--TAAAGAGATTTTCTGAGCAAGGAGTCTTGACTCATCTCTGA 421
 372 CTTCCTCAGCAGGCGCTGCGCCAGCAAGTGCAGAGCCACACTGAGAGAGAGGAGT 431
 422 GGTCTCCCGAGAGCTGTGATGAGAC--TGCAACCGAGCGGCGAGAGAGGAGTCTCGCAAG 480
 432 GGTGCAAGTGAAGCTGCGCAAGGTGAGGCCATGCTTCTTGAAGAGAGCCCTTGA 491
 481 ACCTTTTCAAGAACTACCCGCGCTGA--CCCAAGATACCTGAGAGCTGAGCGCTTTTTC 538
 492 GGAATTCGAGCAGCGCTTCTGAGCAAGTTCCTGAGGAAATCTTCCAGATGCA 551
 539 GCACTACCTCGACAGCACTTACTTCAACCGTTCCTGAGTGAAGTGGCTGGAAGAGCA 598
 552 ACCAGTGTGAGCAAGTACTTCACTGAGTTGAGAGTGTGGGAAAGGTGTTTGGGGA 611
 599 GCGAGTGAACAAAAACACTTTCAGGCAATACGAGATCGGGAAGAGGTGCTTGGGGA 658
 612 GGTATGTCCTGCAAGTGAAGAACTCTGCGAAGTGTATGCTGTGAAGAACTGGA 671
 659 GGTGTGGCTGCTCAGGTGCGGCGCACAGGTAAAGTATGCTGTGAAGAAAGCTGAGAA 718
 672 GAAGCGGCTGAAGAAAGGTGGCGAAGATGGCTCTTGTGAAGAAAGAAATCTTGA 731
 719 AAGCGGATCAAGAAAGCGAAAGGAGGCGCAATGCGCTGAAGAGAGAGAGATCTGGA 778
 732 GAAGTGTGAGAGCTTCTCATGTCTCTGCGCTATGCTTTCAGAGCAAGACCATCT 791
 779 GAAGTGAACAGTAGTGTGTATGAGCTTGGCTTACGCCCTATGAGAACCAAGGACGCGCT 838
 792 CTGCTGTGATGAGCTGATGAATGGGAGAACTCAAGTCTCAATCAATCAACGCTGG 851
 839 GTGCTGTGATGAGCACTGATGAACGGGAGGCACTCAAGTCTCAATCAATCAACAGTGG 898
 852 CAGCGTGTGAGCACTGAGAGCGGGGATCTTCTTACTGCGCCAGATAGCTGTGGAT 911
 899 CGAGCTGTGCTTCCCGAAGCGCGGCGCTTCTTACCGCCCGGAGATCTGTGTGGCT 958
 912 GCTGACCTTCATGAACCTGCGATGCTATCGGGAATGAGAGCTGAGATGTGCTTCT 971
 959 GAGAGACCTGCAACCGGAGCGGATCTGTACAGGGAAGCTGAGAGCGGAGAACTTGTCT 1018
 972 GAGTGAACCTGGAATGAGATTTATGACTTGTGGGCTGCGCGTGTGAGATGAGAGTGG 1031
 1019 GAGTGAACAGGCGCAATCTCGATCTGAGCTGTGAGATCACTGTGTGATGTCCCGAGGG 1078
 1032 CAGGCTATGACCAAGGCGCTGAGAACCAATGATGTTATGAGCTCTGAGATCTTATGGA 1091

1079 CGAGACATCAAAAGGCGGTGTGGGACCGTGTGATGATGATGCTCGAG--GTGTGA 1135
 1092 AAGGTATGATTTCCATCTGATGATGATGATGATGATGATGATGATGATGATGAT 1151
 1136 GAATGAACGCTGACAGTTCAGGCTGATGATGATGATGATGATGATGATGATGATGAT 1195
 1152 GTTGTGAGAGAAACACATTTCAAGATTTCAAGAAAGTGTGATGATGATGATGATGAT 1211
 1196 GATGAGAGGCGAGTGTGCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1255
 1212 GCAAGAACTCTGAG 1271
 1256 GCGCTGTGAG 1315
 1272 AGATTTTCAAGGCTTCTTGTGCTTGAAGAAACAGAGAGAGAGAGAGAGAGAGAGAG 1331
 1316 ACTTGTGAG 1375
 1332 GTCTGATGATGAG 1391
 1376 TGCGCGAG 1435
 1392 TGCGCTTATGAG 1451
 1436 TGCGAGCTGAG 1495
 1452 TGAAATGATGATTTCTGAGGTTGCGGAGGTGAGAAATTTGATGACAAAGATGAGAG 1511
 1496 GATATGAG 1555
 1512 CTTCAGAAATCTTGTGAG 1571
 1556 CTACAGAGATTTGCAAGGCGAGTGTGCGCATCCCTGCGAGAGAGAGATGTGAGAG 1615
 1572 GGAAGTGTGAG 1596
 1616 CGAGTGTCTCAAGAGCTGAAATGTC 1640

RESULT 15
 US-10-159-856-4
 ; Sequence 4, Application US/10159856
 ; Publication No. US2003022869A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Susan M. Freier
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPRESSION
 ; FILE REFERENCE: R15-0365
 ; CURRENT APPLICATION NUMBER: US/10/159,856
 ; CURRENT FILING DATE: 2002-05-31
 ; NUMBER OF SEQ ID NOS: 134
 ; SEQ ID NO 4
 ; LENGTH: 2848
 ; TYPE: DNA
 ; ORGANISM: H. sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (63)...(1793)
 US-10-159-856-4

Query Match 25.2%; Score 418.2; DB 16; Length 2848;
 Best Local Similarity 56.2%; Pred. No. 1.1e-117;
 Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;

15 GGCCTTGAGAACCTGATGCGCAACCGCTTACCTGAGAGCCGGAAGCCCTCGGACTG 74
 65 GAGGCTGAGAACATGCTGAGAACACGCTGCTCACTCAAGGCCCGGGAAGGTGGCGTGG 124
 75 CGACAGCAAG--AGCTGACGCGCGCGCGTACCTGAGCTGCGCTCGCGGCTGAGGG 131
 125 AATGCGCAAGGCAAGAAAGAAATGCGCGAGATGCTCCAGTCTCCATCAATAGCA 184

QY 132 CTGGCGAGAGCTCCGCAAGAGCTGTCCCTGAACTTCCACAGCCTGTGTGACAGCAGCC 191
 Db 185 GTGCGAAGAGCTCGGCTCAGAGCTGATATCAAGGCTGTGCGAGCGCAGCGC 244
 QY 192 CATGAGTGGCGGCTCTTCCGTGACTTCTTACGACAGTGGCCCACTTCCGAGGCGCGC 251
 Db 245 CATTGGCGGCTGTGTGTCCGAGAGTTCTGTCCACAGAGCGGAGCTGAGCTCCGCTCGT 304
 QY 252 AACCTTCTTGAAGAGAGTGCAGAACTGGAGAGCTGGCCAGAGAGAGCCCAACAAAGCAG 311
 Db 305 CGCCTTCTGAGATGGGGTGGCCGAGTATGAAATGACCCCGAGTACAGAGAGAGAGCAGT 364
 QY 312 CGGCTGCGAGGAGCTGTGGCTCACTTGTCCAGTGGCCCTGGCCCGGAGAACCCGCAAGC 371
 Db 365 TGGCGGCGAG---TAAAGAGATTTTCTGAGCCACAGCGGCTCTGACCTTCATCCCTGA 421
 QY 372 CTTCTCAGCCAGGCGCGCTGGGCAACAAAGTCCAGAGCAGCCACACCTGAGAGAGAGAGT 431
 Db 422 GGTCCCGGAGAGCTGTGTGACGAGAC-TGCAACCCAGCGGCTGGAGCAGGAGTCCCTGCAAG 480
 QY 432 GGTGCAATGACGCTGGCGCAAGGCTGAGGCCATGGCTTTCTTGAAGAGCAGCCCTTAA 491
 Db 481 ACCCTTTCCAGGAACTCACCCGCTGA--CCACAGAGTACCTGAGCGTGGCCCTTTTGC 538
 QY 492 GGAATTTGAGACAGCGCCCTTACAGCAAGTTTCTGAGTGAATCTTTGAGATGCA 551
 Db 539 CGACTTCTCGAGCAGCTACTTACACCGTTTCTGAGTGAAGTGGCTGGAGAGGCA 598
 QY 552 ACCAGTGTACAGCAAGTACTTCACTGAGTTGAGAGTGGGGAGAAAGTGGTTTGGGGA 611
 Db 599 GCCAGTGAACAAAACCTTCAAGGCAATCCAGTGTCTGGGCAAAAGTGGCTTTGGGGA 658
 QY 612 GGTATGTCCGCTCCAGGTGAAAAACACTGGAGAGATGATGCTGTGTAAGAACTGGACA 671
 Db 659 GGTGTGCGCTGGCCAGGTGGGCGCACAGGTAAAGTATGCTGTGAGAGAGCTAGAGAA 718
 QY 672 GAAGCGGCTGAAGAAAGAGTGGGAGAGATGGCTCTTTGAAAAGGAAATCTTGA 731
 Db 719 AAAGCGATCAAGAGAGGAGAAAGGAGGCCATGGGCTGAACAGAGAGCAGATCTGGA 778
 QY 732 GAAGGTACAGAGCCCTTCAATTTGTCTGTGGCTTATGCTTGAAGAGAGAGCCATCT 791
 Db 779 GAAGGTGAAGATGATGTTGTGTAGTGGCTTGGCTTACGCTATGAGACCAAGAGAGCGCT 838
 QY 792 CTGCTTGTCAATGAGCTTATGATGATGGGAGAGACTCAAGTTCCACATCTACAGTGGG 851
 Db 839 GTGCTGTGTGACACTGATGAAGGGGGGCACTCAAGTTCCACATCTACAGTGGG 898
 QY 852 CACGCGGAGCTGGAATGAGCCGGGTGATCTTTTCTGGCCCAATAGACCTGTGGAT 911
 Db 899 CAGGCTGTGCTTCCCGAAGCGCGGCGGTCTTCTACGCGCCGAGATCTGTGGCT 958
 QY 912 GCTGACCTCCATGAATCTGGCATGCTCTATCGGAGCATGAAGCTGAGATGTGCTTCT 971
 Db 959 GAGAGACCTGACCGGAGAGCGATCTGTGACAGGAGACTGAAGCCGAGAGACATTTGCT 1018
 QY 972 GATATACCTGGCACTGAGAGTTATCTGACTGGGCTGGCCGTGAGATGAGAGGTTGG 1031
 Db 1019 GGATGACCAAGGCAATCCGATCTGACTGGGACTGAGCTGATGTGATGTGCCGAGGG 1078
 QY 1032 CAAGCCATCAACAGAGGAGCTGAGACAAATGGTTACATGGCTCTGAGATCTTAATGA 1091
 Db 1079 CCAAGCATCAAAAGGAGCTGTGGGACCGTGGGTTACATGGCTCCGAG--GTGGTGA 1135
 QY 1092 AAAGGTAAATTCTCTATCTGTGAGTGGTTTGCATGGGATGAGCATTTTAAAT 1151
 Db 1136 GAATGAACGATACAGTTCAAGCTGTGGGCGCTGGCTCTCTGTAGAGAT 1195
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 Db 1196 GATGCGAGCGAGTGGCTTCCAGCAGAGAGAAAGATCAAGCGGAGAGGTGGA 1255

QY 1212 GCAAGAACTGTGACAGAGAGTCAAAATTCAGCATGATTAATCTCAAGAGAGAAACAA 1271
 Db 1256 GCGGCTGTGTAAGAGATGCCAGAGAGTATTCGAGGCGCTTTTCCCGAGGCGCGCTC 1315
 QY 1272 AATATTTGAGAGCTCTTCTTGGCTTAAAGAAACAGAGCAAGCTTAGAGAGAGAGAAA 1331
 Db 1316 ACTTTGTCAAGAGCTCTCTGAGAGAGCCTGCGGAGAGCTGGGGTGTGTGGGGGAG 1375
 QY 1332 GTCTATATTCAGAGAAACATCATTTCTTAAAGATCAACTTTCCTGCTGGAGAGC 1391
 Db 1376 TGCCCGAGAGTGAAGAGCAACCCCTTTTAAAGAGTGAACCTTCAAGGAGTGGAGC 1435
 QY 1392 TGACCTAATGAACCCCATTTTGGCAGACCTTGAAGTGTGTATGCTCAAGAGATGCG 1451
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 QY 1452 TGAATTAATGAATTTCTGAGAGTTGGGGGGTGAATTTGATGACAAAGATTAACAGTT 1511
 Db 1496 GAGCATTTGAACAATTTCTTACAGGTCAAGGAGCTGAGAGCTTACGAGCAGAGACTT 1555
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 Db 1556 CTACCAAGATTTGCAAGAGAGAGTGTGCCATGCCCTGGCAGAGAGAGATGTGTGAGC 1615
 QY 1572 GAGACTGTTTGAAGAACTGAATGAC 1596
 Db 1616 CGAGTGTTCAGAGAGCTGAATGTC 1640

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 Job time : 527.034 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2004, 10:30:45 ; Search time 4319.34 Seconds

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Title: US-10-044-205a-3
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Scoring table: IDENTITY NTC

Gapop 10.0, Gapept 1.0

Searched: 3470272 segs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb_in:*

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	1655.8	99.8	6	AX64368	AX64368 Sequence
4	1655.8	99.8	1761	BD186115	BD186115 A novel g
5	1655.8	99.8	1799	AF439409	AF439409 Homo sapi
6	1655.8	99.8	2249	AR225819	AR225819 Homo sapi
7	1655.8	99.8	2249	AX252443	AX252443 Sequence
8	1655.8	99.8	3186	AX710216	AX710216 Sequence
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10	1655.4	99.8	1662	AR225817	AR225817 Sequence
11	1654.2	99.7	1662	AX252439	AX252439 Sequence
12	1654.2	99.7	1662	AR263766	AR263766 Sequence
13	1654.2	99.7	1662	AR343544	AR343544 Sequence
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15	1652.6	99.6	1662	AX166511	AX166511 Sequence
16	1652.6	99.6	1662	AX710213	AX710213 Sequence
17	1589.8	95.8	1701	AX921933	AX921933 Sequence
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38	418.2	25.2	2204	I23378	I23378 Sequence 12
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ALIGNMENTS

RESULT 1

AX797554

LOCUS AX797554 1659 bp DNA linear PAT 04-OCT-2003

DEFINITION Sequence 3 from Patent WO02095032.

ACCESSION AX797554

VERSION AX797554.1 GI:37518056

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE

1 Kapeller-Libermann, R. and Bandaru, R.

METHOD and compositions of human proteins and uses thereof

PATENT: WO 02095032-A 3 28-Nov-2002;

Pred. No. is the number of results predicted by chance to have a

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Source

Location/Qualifiers

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100.0%; Score 1659; DB 6; Length 1659;

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Best Local Similarity 100.0%; Pred. NO. 0;
Matches 1659; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db	61	AAGCCTTCGACATCGACAAAGAGATGCAAGCGAGCGAGGTAGCTGATGACCTTGCC	120
QY	121	GAGCTGCAAGGCTCGCGAGAGCTCCGACAGAGCTGCTCTTGAATTCCACAGCTGTGT	180
Db	121	GAGCTGCAAGGCTCGCGAGAGCTCCGACAGAGCTGCTCTTGAATTCCACAGCTGTGT	180
QY	181	GAGCAGACCCATCGATGATCGCGCTCTTCCGAGACTTCAGACCAATGCGCAGTTC	240
Db	181	GAGCAGACCCATCGATGATCGCGCTCTTCCGAGACTTCAGACCAATGCGCAGTTC	240
QY	241	CGCAGGCGGCAACCTCTTACAGAGACCTGACAGATG99AGCTGGCGAGAG99ACCC	300
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QY	301	ACCAAGACAGCGCGCTGCAAG99GCTGTGCGACTTGTGCGATGCCCCGCG999	360
Db	301	ACCAAGACAGCGCGCTGCAAG99GCTGTGCGACTTGTGCGATGCCCCGCG999	360
QY	361	AACCGCAACCTTCTTCAATCGACAGGCGGTGCGCAACCAATGCGCAAGCACAATGAG	420
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QY	421	GAAAGGAGATG9CTGCGAGT9ACGCTGCGCAAGGCTGAGGCAATG9CTTCTTGAAG	480
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QY	481	CAGCCTTTAAGATTTGTGACCAAGCGCTTCTTGAACAATTTCTGCAATG9AAATC	540
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QY	541	TTGCAATGCAACAGATGTCAGACAGTACTTCAATGATCAGAGTGTG9999AAAGT	600
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QY	601	GGTTTTGG99AGGTATGTCGCTGCAAGTGA9AAACCTG9AAGATGTATGCTGTAG	660
Db	601	GGTTTTGG99AGGTATGTCGCTGCAAGTGA9AAACCTG9AAGATGTATGCTGTAG	660
QY	661	AAATGCAACAAGAGCGCTAGAGAGAAAGGTGCGAGAAATG9CTCTTGGAAAG	720
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QY	781	AAGACCATCTTGCTGTCTATGAGCTGATGAATG9999AGACCTCAAGTTCACATC	840
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QY	841	TACACGTG99ACGCTGTGCTGGAATGAGCGGGTATCTTTACGTG999CGAGTA	900
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AX-797552
10076

LOCUS
DEFINITION

ACCESSIO

VERSION

KEYWORDS
SOURCE

ORGANIZATION

REFERENCES

AUTHOR

TITLE

JOURNAL

FEATURE:

501

1

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 LOCUS BD186115
 DEFINITION A novel gene relating to disease and use thereof.
 ACCESSION BD186115.1 GI:31878315
 VERSION WO 02103020-A/10.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 1761)
 Koyama, N., Tanida, S., and Yamamoto, K.
 A novel gene relating to disease and use thereof
 Patent: WO 02103020-A 10 27-DEC-2002;
 TAKEDA CHEMICAL INDUSTRIES LTD, NOBUYUKI KOYAMA, SEIICHI TANIDA, KOJI
 YAMAMOTO
 OS Homo sapiens (human)
 PN WO 02103020-A/10
 PD 27-DEC-2002
 PF 14-JUN-2002 WO 2002P005942
 PI 15-JUN-2001 JP OIP 182654
 NOBUYUKI KOYAMA, SEIICHI TANIDA, KOJI YAMAMOTO
 C12N15/54, C12N9/12, G01N33/50, G01N33/40, A61K39/395 CC
 A novel gene relating to disease and use thereof FH Key
 Location/Qualifiers

ORIGIN

Query Match	99.8%	Score 1655.8;	DB 6;	Length 1761;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 1657; Conservative	0;	Mismatches	2;	Indels 0;
		Gaps		0

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QY	121	GAGGCTGGAGAGGAGCTGGAGGAGCTGGCCCAAGAAAGTGTCTCTGAACTTCCACAGCTGTGT	180
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QY	181	GAGCAGCAGCCCATCGATCGATCGCGCTCTTTCCTGATCTTCTAGCAAGTGGCCCAAGCTTC	240
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QY	841	TAAACAGTGGGACAGCGTGGCTCTGGAACAGAGCAGGAGTAACTTTTAACTGGCGCCAGATA	900
Db	866	TAAACAGTGGGACAGCGTGGCTCTGGAACAGAGCAGGAGTAACTTTTAACTGGCGCCAGATA	925

[illegible]

AUTHORS Baehr, W. and Chen, C.-K.
 TITLE Direct Submission
 JOURNAL Submitted (23-OCT-2001) Ophthalmology, University of Utah, 15 North/2030 East, Salt Lake City, UT 84112, USA

FEATURES
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gene
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ORIGIN
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 Best Local Similarity 99.9%; Pred. No. 0;
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 1 ATGGTGAACATGGGGGCTTGGACAACTGATCGCAACCGCTTACCTGACAGCCCGG 60
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 61 AAGCCTCGGACTGCGACAGCAAGAGCTGACAGGGGCGGCGTGGCTGGCCCTGCCC 120
 198 AAGCCTCGGACTGCGACAGCAAGAGCTGACAGGGGCGGCGTGGCTGGCCCTGCCC 257
 121 GGGCTGAGGGCTGCGCGAGCTCCCGCAGAGCTGTCCTGAACTTCCACAGCTGTGT 180
 258 GGGCTGAGGGCTGCGCGAGCTCCCGCAGAGCTGTCCTGAACTTCCACAGCTGTGT 317
 181 GAGCAGAGCCCATGCTGCGCGCTCTTCTCTGCTGACCTTCTACCCAGTCCCAAGCTTC 240
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 241 CGCAAGCGCGCAACTCTTCTAGAGAGCTGAGCACTGGAGCTGGCCGAGAGAGAGCC 300
 378 CGCAAGCGCGCAACTCTTCTAGAGAGCTGAGCACTGGAGCTGGCCGAGAGAGAGCC 437
 301 ACCAAGACAGCGCGCTGACAGGGCTGATGACCACTTGTGAGTCCCTTCCCGGGG 360
 438 ACCAAGACAGCGCGCTGACAGGGCTGATGACCACTTGTGAGTCCCTTCCCGGGG 497
 361 AACCCGCAACCTTCTCTAGCCAGGCGTGGCCACCAAGTCCCAAGAGAGCACTGAG 420
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 421 GAAAGGAGATGGCTGAGTACGCTGCGCAAGGCTGAGGCACTGAGCTTCTTGGAGAG 480
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ORIGIN

Query Match 99.8%; Score 1655.8; DB 9; Length 1799;
 Best Local Similarity 99.9%; Pred. No. 0;
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 61 AAGCCTCGGACTGCGACAGCAAGAGCTGACAGGGGCGGCGTGGCTGGCCCTGCCC 120
 198 AAGCCTCGGACTGCGACAGCAAGAGCTGACAGGGGCGGCGTGGCTGGCCCTGCCC 257
 121 GGGCTGAGGGCTGCGCGAGCTCCCGCAGAGCTGTCCTGAACTTCCACAGCTGTGT 180
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 318 GAGCAGAGCCCATGCTGCGCGCTCTTCTCTGCTGACCTTCTACCCAGTCCCAAGCTTC 377
 241 CGCAAGCGCGCAACTCTTCTAGAGAGCTGAGCACTGGAGCTGGCCGAGAGAGAGCC 300
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 301 ACCAAGACAGCGCGCTGACAGGGCTGATGACCACTTGTGAGTCCCTTCCCGGGG 360
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 361 AACCCGCAACCTTCTCTAGCCAGGCGTGGCCACCAAGTCCCAAGAGAGCACTGAG 420
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 421 GAAAGGAGATGGCTGAGTACGCTGCGCAAGGCTGAGGCACTGAGCTTCTTGGAGAG 480
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 618 CAGCCTTTAAGATTTCTGACAGGAGCTTCTGACCAAGTCTTCTGAGTGGAACTC 677

QY 541 TTGAGATGCAACCAAGTGTGACAGAGTACTTCACTGAGTTGACAGTGTCTGGGAAAGGT 600
 DB 678 TTGAGATGCAACCAAGTGTGACAGAGTACTTCACTGAGTTGACAGTGTCTGGGAAAGGT 737
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ACCESSION AX252443
 VERSION AX252443.1 GI:15985735
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 Walke, D.W., Wilganski, N.L. and Turner, C.A.
 Human 9-coupled protein receptor kinases and polynucleotides
 TITLE encoding the same
 JOURNAL Patent: NO 0168865-A 5 20-SEP-2001;
 Lexicon Genetics Incorporated (US)
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 Best Local Similarity 99.9%; Pred. No. 0;
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RESULT 8
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 DEFINITION Sequence 4 from Patent WO03018815.
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 VERSION AX710216.1 GI:29786804
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 ORGANISM Homo sapiens

Query Match	99.8%	Score 1655.8;	DB 6;	Length 3186;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 1657; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

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DEFINITION	AF282269	3186 bp	mRNA	linear	PRI 21-NOV-2001
ACCESSION	AF282269				
VERSION	AF282269.1	GI:17026317			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Mumtaz, S., Ducceschi, M.H., Horner, T.J., Li, A., Craft, C.M. and Weiss, B.R.,				
AUTHORS	1 (bases 1 to 3186)				
	Memalia, Eutheria; Primates; Catarrhini; Homnidae; Homo.				
	Osawa, S.				

TITLE Species-specific differences in expression of G-protein-coupled receptor kinase (GRK) 7 and GRK1 in mammalian cone photoreceptor cells: implications for cone cell phototransduction

JOURNAL J. Neurosci. 21 (23), 9175-9184 (2001)

MEDLINE 21574315

PUBMED 111717351

REFERENCE 2 (bases 1 to 3186)

AUTHORS Osawa, S. and Weiss, E. R.

TITLE Direct Submission

JOURNAL Submitted (24-JUN-2000) Cell Biology and Anatomy, University of North Carolina, CB#7090, 108 Taylor Hall, Chapel Hill, NC 27599-7090, USA

FEATURES

source Location/Qualifiers

1..3186

/organism="Homo sapiens"

/mol_type="mRNA"

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/tissue_type="retina"

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ORIGIN

Query Match 99.8%; Score 1655.8; DB 9; Length 3186;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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2 ATGTGAGACATGGGGGCGCTGGACAACTGATGCGCAACGCGCTACTGAGGCGCG 144

3 ATGTGAGACATGGGGGCGCTGGACAACTGATGCGCAACGCGCTACTGAGGCGCG 120

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5 ATGTGAGACATGGGGGCGCTGGACAACTGATGCGCAACGCGCTACTGAGGCGCG 180

6 ATGTGAGACATGGGGGCGCTGGACAACTGATGCGCAACGCGCTACTGAGGCGCG 264

7 ATGTGAGACATGGGGGCGCTGGACAACTGATGCGCAACGCGCTACTGAGGCGCG 240

8 ATGTGAGACATGGGGGCGCTGGACAACTGATGCGCAACGCGCTACTGAGGCGCG 324

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Db 1705 GAGGTATATTCATCCAGTCTGGCTGTGTTTGTATTG 1743

RESULT 10
AR225817 1662 bp DNA linear PAT 20-DEC-2002
LOCUS AR225817
DEFINITION Sequence 1 from patent US 644456.
ACCESSION AR225817
VERSION AR225817.1 GI:27263947
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1662)
AUTHORS Walke,D.W., Wilganowski,N.L. and Turner,C.A. Jr.
TITLE Human,G-coupled protein receptor kinases and polynucleotides
encoding the same
JOURNAL Patent: US 644456-A 1 03-SEP-2002;
FEATURES Location/Qualifiers
source 1..1662
/organism="unknown"
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Query Match 99.8%; Score 1655.4; DB 6; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1656; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Query Match	99.7%	Score 1654.2;	DB 6;	Length 1662;
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Db	1501	GATPAGACGTTCTTCAAAAACCTTGGGGAAGGAGTGCTTCCTATAGCATGGCAGGAGAA	1560
QY	1561	ATTATPAGAAACGGGACTGTTTGAAGAACTGATGACCCCAAGACACTTACGGGTTGTGAG	1620
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QY	1621	GAGGGTATTTCAATCAAGCTCGGCTGGCTGTGTGTTATATG	1659
Db	1621	GAGGGTATTTCAATCAAGCTCGGCTGGCTGTGTGTTATATG	1659

Query Match	99.6%	Score 1652.6;	DB 6;	Length 1662;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1655; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1
TITLE	Pilowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R., Flanagan,P. and Clary,D.S.
JOURNAL	Novel human protein kinases and protein kinase-like enzymes Patent: WO 0138503-A 2 31-MAY-2001;
FEATURES	Sugen, Inc. (US)
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QY 1081 ATCTTAATGAAAAAGTAAATTAATTCATATCTGTGAGCTGTTTGCATGAGATCAGC 1140
 DB 1081 ATCTTAATGAAAAAGTAAATTAATTCATATCTGTGAGCTGTTTGCATGAGATCAGC 1140
 QY 1141 ATTTATGAATGTGCTGAGCAACATTCATTAATTAAGAAAAAGTCACTTAA 1200
 DB 1141 ATTTATGAATGTGCTGAGCAACATTCATTAATTAAGAAAAAGTCACTTAA 1200
 QY 1201 GAGATCTGAAGCAAAAGATTCAGAGCAAGAGTCAAAATTCAGATGATTAATTCACA 1260
 DB 1201 GAGATCTGAAGCAAAAGATTCAGAGCAAGAGTCAAAATTCAGATGATTAATTCACA 1260
 QY 1261 GAGAGCAAAAGATTTGCAAGAGCTTCTTGTGCTTAAAGCAAGCAAGCTTAAAG 1320
 DB 1261 GAGAGCAAAAGATTTGCAAGAGCTTCTTGTGCTTAAAGCAAGCAAGCTTAAAG 1320
 QY 1321 AGCAGAAAAAGTGTGAGATCCAGAAAAAGATTCATTTTAAACGATCACTTCT 1380
 DB 1321 AGCAGAAAAAGTGTGAGATCCAGAAAAAGATTCATTTTAAACGATCACTTCT 1380
 QY 1381 CGCTGGAAGCTGCTTAAATTTGAACCCCATTTGCGCAGACCTTCAAGTGTATGCT 1440
 DB 1381 CGCTGGAAGCTGCTTAAATTTGAACCCCATTTGCGCAGACCTTCAAGTGTATGCT 1440
 QY 1441 AAAGACATGCTGAATTTGATATTTCTGAGGTTGCGGAGGTTGAATTTGATGACAA 1500
 DB 1441 AAAGACATGCTGAATTTGATATTTCTGAGGTTGCGGAGGTTGAATTTGATGACAA 1500
 QY 1501 GATAGAGTGTCTTAAACCTTTCAGAGAGTGTCTTCTTATGATGAGAGAA 1560
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 QY 1621 GAGGTATTCATCCAGTCTGCGGTGTGTTGTTATG 1659
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Search completed: August 13, 2004, 16:48:51
 Job time : 4325.34 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: August 13, 2004, 06:21:35 ; Search time 444.751 Seconds
(without alignments)
15846.518 Million cell updates/sec

Title: US-10-044-205A-3

Perfect score: 1659
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Scoring table: IDENTITY NUC
Gapop 10.0 ; Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseq1990s:*
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9: geneseq2003cs:*
10: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1655.8	99.8	1662	6	AD46350
5	1655.8	99.8	1761	7	AB256943
6	1655.8	99.8	1821	9	AD39221
7	1655.8	99.8	2249	4	AAH78799
8	1655.8	99.8	3186	7	ACC44827
9	1654.2	99.7	1662	4	AAH78797
10	1654.2	99.7	1662	6	AAH28071
11	1652.6	99.6	1662	4	AA506702
12	1652.6	99.6	1662	7	ACC44826
13	1187.8	71.6	1191	7	AB256934
14	1094.2	66.0	1486	6	AAH46351
15	1046.8	63.1	1062	4	AAH78798
16	617.4	37.2	36651	6	AAH28072
17	419.8	25.3	2848	4	AAH24842
18	418.2	25.2	2204	2	AAH87426
19	418.2	25.2	2848	6	ABH61805
20	418.2	25.2	2848	6	ABH61805
21	403.8	24.3	2541	9	ADH53307
22	395.8	23.9	1983	2	AAH87427
23	389.4	23.5	2206	2	AAH87425

24	377.8	22.8	2519	7	ACA03892	ACA03892	CDNA upre
25	374.6	22.6	2519	9	ADB47372	ADB47372	Human CDN
26	373	22.5	2511	2	AAV71032	AAV71032	Grt5-gree
27	373	22.5	2529	2	AAV71024	AAV71024	Grt5-gree
28	373	22.5	2557	6	AAH36142	AAH36142	Human G p
29	373	22.5	2557	7	ACA56700	ACA56700	Human sig
30	369	22.2	1996	5	AAH80696	AAH80696	DNA encod
31	368.2	22.2	2557	6	ABK49404	ABK49404	CDNA enco
32	366.6	22.1	2557	4	AAH24842	AAH24842	Nucleotid
33	327.2	19.7	3836	4	ABL19581	ABL19581	Drosophila
34	320.6	19.3	2017	2	AAH90219	AAH90219	GRK4 poly
35	320.6	19.3	2113	2	AAH90218	AAH90218	GRK4 poly
36	311.6	18.8	1879	2	AAH90221	AAH90221	GRK4 poly
37	311.6	18.8	1886	2	AAH90221	AAH90221	GRK4 poly
38	311.6	18.8	1875	2	AAH90220	AAH90220	GRK4 poly
39	262.4	15.8	2947	5	AAH86360	AAH86360	DNA encod
40	253.2	15.3	1324	2	AAH90223	AAH90223	GRK4 poly
41	246.8	14.9	1420	2	AAH90222	AAH90222	GRK4 poly
42	158.4	9.5	493	8	ACH50623	ACH50623	Human mam
43	153.4	9.2	3154	8	ACD44895	ACD44895	Human sig
44	151	9.1	2037	6	ABT06290	ABT06290	Human NOV
45	151	9.1	2067	6	AAH96675	AAH96675	Human hu

ALIGNMENTS

RESULT 1	ABSS7375	standard; cDNA; 2198 BP.
ID	ABSS7375	
AC	ABSS7375	
XX	ABSS7375	
DT	04-FEB-2003	(first entry)
XX		
DE	CDNA encoding human GPCR kinase (GPCR) 69087.	
XX		
KW	Human; G protein coupled receptor kinase; GPCR 69087;	
KW	cellular proliferative disorder; differentiative disorder;	
KW	haematopoietic neoplastic disorder; leukaemia; sarcoma;	
KW	metastatic disorder; cytostatic; gene therapy; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
FM	Key	Location/Qualifiers
FT	CDS	291..1952
FT		/*tag= a
FT		/product= "GPCR 69087"
FT		/note= "The coding sequence given as SEQ ID No:3 is specifically claimed in Claim 1"
XX		
XX	US2002123464-A1.	
XX		
XX	05-SEP-2002.	
XX		
PF	22-OCT-2001; 2001US-00044205.	
XX		
PR	19-OCT-2000; 2000US-0241884P.	
PR	20-OCT-2000; 2000US-0241877P.	
PR	23-OCT-2000; 2000US-0242428P.	
XX		
XX	(MILL-) MILLENNIUM PHARM INC.	
PA		
PI	Kapeller-Libermann R; Bandaru R;	
XX		
XX	WPI; 2003-066811/06.	
DR	P-PSDB; ABG72173.	
XX		
PT	Novel isolated G protein coupled receptor kinase, 69087, nuclear	
PT	signaling protein, 15821 or mitogen activated protein kinase phosphatase,	
PT	15418, useful for treating cellular proliferative or differentiative	
PT	disorders.	
XX		

PS Claim 1; Fig 1; 98pp; English.

The present invention relates to the isolation of a novel human G protein-coupled receptor (GPCR) kinase (GPCRK) designated 69087, a novel human nuclear signalling protein designated 15821, and a novel human mitogen-activated protein kinase (MAPK) phosphatase MAPKP designated 15418, and the polynucleotide sequences encoding them. The sequences of the invention are useful for treating and diagnosing disorders such as cellular proliferative and differentiative disorders (e.g. haematopoietic neoplastic disorders, leukaemia, carcinoma, sarcoma or metastatic disorders). They are also useful in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics), and in methods of treatment (e.g. therapeutic and prophylactic). The sequences may also be used to screen public databases to identify other family members or related sequences. The polypeptide sequences are useful as immunogens to generate antibodies that bind the polypeptides. The polynucleotide sequences are useful for mapping their respective genes on a chromosome, identifying gene regions associated with cellular proliferative or differentiative disorders, and in gene therapy. The present sequence encodes human GPCRK 69087

SQ Sequence 2198 BP; 558 A; 557 C; 607 G; 476 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1659;	DB 7;	Length 2198;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1659; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

OY	ATGATGACATCGGGGGCCCTGGACAAACCTATCGCCACAACCGCTACCTCGAGGCCCGG	60
Db	ATGATGACATCGGGGGCCCTGGACAAACCTATCGCCACAACCGCTACCTCGAGGCCCGG	350
OY	AAAGCCCTGGACTGGACAAGCAAAAGCTGACGGCGGAGCGCTGACCTGCTGCCC	120
Db	AAAGCCCTGGACTGGACAAGCAAAAGCTGACGGCGGAGCGCTGACCTGCTGCCC	410
OY	GGGTGTAGAGGCTGTGGGAGCTCCGCGAAGCTGCTCCCTGAATCTTCACAGCTGTGT	180
Db	GGGTGTAGAGGCTGTGGGAGCTCCGCGAAGCTGCTCCCTGAATCTTCACAGCTGTGT	470
OY	GAGCAGACGCCATGGTCCCGCCTCTTCGTGACTTCTTAGCACAAGTGCACCGTTC	240
Db	GAGCAGACGCCATGGTCCCGCCTCTTCGTGACTTCTTAGCACAAGTGCACCGTTC	530
OY	CGCAGGCGCACTTCTTAGAGACTGTGAATCTGGAGCTGCGCAGAGAGGACCC	300
Db	CGCAGGCGCACTTCTTAGAGACTGTGAATCTGGAGCTGCGCAGAGAGGACCC	590
OY	ACCAAAACACGAGCGCTGCAGGGGCTGTGTGCATTTGTGAGTGTGCCCTGCCCGGAG	360
Db	ACCAAAACACGAGCGCTGCAGGGGCTGTGTGCATTTGTGAGTGTGCCCTGCCCGGAG	650
OY	AAACCGCAACCTTCTTAGACCAAGCGTGTGCACCAATGTCACAGACCACTGAG	420
Db	AAACCGCAACCTTCTTAGACCAAGCGTGTGCACCAATGTCACAGACCACTGAG	710
OY	GAAAGAGAGTGGCTGACAGTGAAGCTGTGCAGAGGCTGAGGCCATGCTTTCTTGAAG	480
Db	GAAAGAGAGTGGCTGACAGTGAAGCTGTGTGCAGAGGCTGAGGCCATGCTTTCTTGAAG	770
OY	CAGCCCTTTAAGGATTTGTGACCAAGCGCTTCTTACGACAAATTTCTGACGTGAAATC	540
Db	CAGCCCTTTAAGGATTTGTGACCAAGCGCTTCTTACGACAAATTTCTGACGTGAAATC	830
OY	TTTCAGATGCAACAGGTGTCAACAATCTTCACTGAATTCAGAGTGTGGGGAAAAGT	600
Db	TTTCAGATGCAACAGGTGTCAACAATCTTCACTGAATTCAGAGTGTGGGGAAAAGT	890
OY	GGTTTGTGGGAGGTATGTGCGCTGCAGGTGAAAACCACTGGAGATGTATGTGCTTAG	660
Db	GGTTTGTGGGAGGTATGTGCGCTGCAGGTGAAAACCACTGGAGATGTATGTGCTTAG	950
OY	AAATCGACACAGAGCGCTGAAGAAAGAGTGGCGAAGATGTGCTCTTCTTGAAG	720

Db	951	AAATCTGGACAAAGAGGCTGAGAGGCCCTTTCATTTGCTCTCTGGCCTTATGCTTTTGAGAGC	780
Qy	721	GAATCTTGGAGAGAGGTGACAGAGCCCTTTCATTTGCTCTCTGGCCTTATGCTTTTGAGAGC	780
Db	1011	GAATCTTGGAGAGAGGTGAGAGCCCTTTCATTTGCTCTCTGGCCTTATGCTTTTGAGAGC	1070
Qy	781	AAAGACCATCTCTGCTCTGTCATGAGCTTGAGAAATGGGGAGAAACCTCAAGTCTCCACATC	840
Db	1071	AAAGACCATCTCTGCTCTGTCATGAGCTTGAGAAATGGGGAGAAACCTCAAGTCTCCACATC	1130
Qy	841	TACACGTGGGCACAGCGCTGAGCATGAGACCGAGTGATCTTTTACTCGGCCACAGATA	900
Db	1131	TACACGTGGGCACAGCGCTGAGCATGAGACCGAGTGATCTTTTACTCGGCCACAGATA	1190
Qy	901	GCCTGGGGATGCTGCACTCCATGAATCTCGGCATCGTCTATGCGGACATGAACTTGAG	960
Db	1191	GCCTGGGGATGCTGCACTCCATGAATCTCGGCATCGTCTATGCGGACATGAACTTGAG	1250
Qy	961	AATGTGCTTCTTGATGATCCTGGGCATATGAGAGTTATCTGACTCGGGGTGGCCGTGGAG	1020
Db	1251	AATGTGCTTCTTGATGATCCTGGGCATATGAGAGTTATCTGACTCGGGGTGGCCGTGGAG	1310
Qy	1021	ATGAAAGGTGGCAAGCCCATACCCAGAGGGCTGGAGCAATGGTTATCAGTACTCTGAG	1080
Db	1311	ATGAAAGGTGGCAAGCCCATACCCAGAGGGCTGGAGCAATGGTTATCAGTACTCTGAG	1370
Qy	1081	ATCTTAATGAAAAAGTAAAGTTATCTCTATCTGTGGAATGCTGTTTCCATGGAGTCAGC	1140
Db	1371	ATCTTAATGAAAAAGTAAAGTTATCTCTATCTGTGGAATGCTGTTTCCATGGAGTCAGC	1430
Qy	1141	ATTATTGAATGCTGTGCTGAGAGAACCATCTTCAAAAGTTATCAAGAAAAAGGTACAGTAA	1200
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Qy	1201	GAGGATCTGGAAGCAAAAGAACTCTGCAAGAAGAGTCAATCTCAGCATGATTAACCTTCA	1260
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Qy	1261	GAGGAGCAAAAAGATATTTGCAAGGCTCTTCTTGCTAAAGAACCGAGCAAGCTTAGGA	1320
Db	1551	GAGGAGCAAAAAGATATTTGCAAGGCTCTTCTTGCTAAAGAACCGAGCAAGCTTAGGA	1610
Qy	1321	AGCAAGAAAAAGTGTGATGATCCCAAGAAACATCATTTCTTTAAACGATCACTTCCCT	1380
Db	1611	AGCAAGAAAAAGTGTGATGATCCCAAGAAACATCATTTCTTTAAACGATCACTTCCCT	1670
Qy	1381	CGCGTGAAGAGCTGCGCTAAATTTGAACCCCACTTTGTGCGACAGCCCTCACTGGTTTATGCC	1440
Db	1671	CGCGTGAAGAGCTGCGCTAAATTTGAACCCCACTTTGTGCGACAGCCCTCACTGGTTTATGCC	1730
Qy	1441	AAAGACATGCTGGAATTTGATGATTTCTGTAGGTTGCGGGGAGTGAATTTGATGACAA	1500
Db	1731	AAAGACATGCTGGAATTTGATGATTTCTGTAGGTTGCGGGGAGTGAATTTGATGACAA	1790
Qy	1501	GATTAAGCACTTCTCAAAAACCTTTGCGACAGGTCGTGTTCTTATAGATGAGAGGAAGA	1560
Db	1791	GATTAAGCACTTCTCAAAAACCTTTGCGACAGGTCGTGTTCTTATAGATGAGAGGAAGA	1850
Qy	1561	ATTATAGAAAGCGGACGTTTGAGGAACTGATGACCCCAACAGACTCAAGGAGTTGAG	1620
Db	1851	ATTATAGAAAGCGGACGTTTGAGGAACTGATGACCCCAACAGACTCAAGGAGTTGAG	1910
Qy	1621	GAGGCTAATTCATCAAGCTGAGCGTGTGTTGTATTTG	1659
Db	1911	GAGGCTAATTCATCAAGCTGAGCGTGTGTTGTATTTG	1949
RESULT 2			
ABQ86178			
ID ABQ86178 standard; DNA; 1662 BP.			
AC ABQ86178;			

XX 10-SEP-2002 (first entry)
 DT
 XX
 DE Novel human gene. SEQ ID 49.
 XX
 KW Human; cytostatic; vulnery; antiarteriosclerotic; antiparkinsonian;
 KW neurotropic; neuroprotective; immunosuppressive; haemostatic;
 KW antiinflammatory; cardiant; antitumor; antihypertensive;
 KW cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
 KW wound healing disorders; atherosclerosis; Parkinson's disease;
 KW Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
 KW inflammation; neoplastic disease; nervous system disorder;
 KW cardiovascular disorders; pancreatitis; respiratory disorder;
 KW hyperproliferation; systemic autoimmune disease; hyper-immunity;
 KW developmental abnormality; gastrointestinal ulceration; neuropathy;
 KW haematological disease; metabolic disease; sperm dysfunction;
 KW thyroid disorder; hypothyroidism; brain damage; colitis;
 KW congenital; transduction deficiency; neurological disease; stroke;
 KW angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;
 KW trachea; thymus; lymph node; muscular system; obesity; anorexia;
 KW growth abnormality; precocious puberty; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200250105-A1.
 XX
 PD 27-JUN-2002.
 XX
 PF 17-DEC-2001; 2001WO-US049232.
 XX
 PR 19-DEC-2000; 2000US-0256710P.
 PR 20-DEC-2000; 2000US-0257048P.
 PR 09-JAN-2001; 2001US-0260482P.
 PR 30-JAN-2001; 2001US-0264922P.
 PR 06-FEB-2001; 2001US-0266797P.
 PR 19-MAR-2001; 2001US-0276888P.
 PR 04-APR-2001; 2001US-0281535P.
 PR 08-MAY-2001; 2001US-0289622P.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Agarwal P, Birkeland M, Cogswell JP, Kahnick KP, Lai Y;
 PI Mathensen SA, Rizvi SK, Smith RP, Scruton JC, Xie Q;
 DR WPI; 2002-508784/54.
 DR P-PSDB; ABP61013.
 XX
 PT Secreted proteins and polynucleotides useful as vaccines for preventing
 PT or treating various diseases e.g. cancer, wounds, atherosclerosis,
 PT Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.
 XX
 PS Claim 2(a); Page 255-256; 335pp; English.

CC trachea, thymus, lymph node and muscular system, obesity, anorexia,
 CC growth abnormalities, and alleviation of precocious puberty. The
 CC sequences given in records AB086130-AB086184 represent novel human cDNA's
 CC of the invention
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 Query Match 99.8%; Score 1655.8; DB 6; Length 1662;
 Best Local Similarity 99.9%; Pred. No. 0;
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 QY 61 AAGCCCTCGACTGCGACAGCAAGAGCTGCGAGCGCGCGCGTGAAGCTGCGCGG 120
 DB 61 AAGCCCTCGACTGCGACAGCAAGAGCTGCGAGCGCGCGCGTGAAGCTGCGCGG 120
 QY 121 GAGCTGAGGAGGCTGCGAGGAGCTGCGAGGAGCTGCGAGGAGCTGCGAGGAGCT 180
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 QY 541 TTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
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 QY 601 GGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
 DB 601 GGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
 QY 661 AAATCTGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
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 QY 721 GAAATCTGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
 DB 721 GAAATCTGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
 QY 781 AAGACCATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 DB 781 AAGACCATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
 QY 841 TACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
 DB 841 TACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
 QY 901 GCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960


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Db      61  AAGCCTCGGACTGAGACCAAGAGCTGAGCGGCGGAGTACCTGCGCCCTGCCC 120
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Db      121  GGGCTGCAAGGCTGAGGAGCTCCGCAAGCTGTCCCTGAATCTTCAAGAGCTGTGT 180
Qy      181  GAGCAGACGACCATTCGTGCTGCGGCTCTTCTGCTGATCTTCTGACCAAGTCCCACTTC 240
Db      181  GAGCAGACGACCATTCGTGCTGCGGCTCTTCTGCTGATCTTCTGACCAAGTCCCACTTC 240
Qy      241  CGCAAGGCGGCAACCTTCTTGAAGACGTGAGCACTGGAGCTGGCCGAGAGGAGACCC 300
Db      241  CGCAAGGCGGCAACCTTCTTGAAGACGTGAGCACTGGAGCTGGCCGAGAGGAGACCC 300
Qy      301  ACCAAGACAGGCGCTGCAAGGCGCTGAGCTGCTGAGCACTGAGTCCGCGGCGGCGG 360
Db      301  ACCAAGACAGGCGCTGCAAGGCGCTGAGCTGCTGAGCACTGAGTCCGCGGCGGCGG 360
Qy      361  AACCCGCAACCTTCTTCAAGCTGAGCGCTGAGCACTGAGTCCGCGGCGGCGG 420
Db      361  AACCCGCAACCTTCTTCAAGCTGAGCGCTGAGCACTGAGTCCGCGGCGGCGG 420
Qy      421  GAAGACGAGTGTGCTGAGTACGCTGAGGAGGCTGAGGCTGAGTCTTCTTGAAG 480
Db      421  GAAGACGAGTGTGCTGAGTACGCTGAGGAGGCTGAGGCTGAGTCTTCTTGAAG 480
Qy      481  CAGCCCTTAAAGATTTCTGACACGCGCTTCTTCAAGCACTTCTGCAAGTGAATCTC 540
Db      481  CAGCCCTTAAAGATTTCTGACACGCGCTTCTTCAAGCACTTCTGCAAGTGAATCTC 540
Qy      541  TTGAGAGTCAACCAAGTGTGACCAAGTCTTCAAGTCTGAGTCTGAGGAGAGGT 600
Db      541  TTGAGAGTCAACCAAGTGTGACCAAGTCTTCAAGTCTGAGTCTGAGGAGAGGT 600
Qy      601  GGTTTGGGAGGTATGTCGCTCCAGGTAAAAACACTGGAGAGTATGCTGTAAAG 660
Db      601  GGTTTGGGAGGTATGTCGCTCCAGGTAAAAACACTGGAGAGTATGCTGTAAAG 660
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Db      721  GAAATCTTGAAGAGTCAAGCGCTTCAATGCTCTCTCTGCGCTTGAAGAGC 780
Qy      781  AAGACCAATCTCTGCTGTGATGAGCTGATGAATGGGAGAGCTTCAAGTCCATC 840
Db      781  AAGACCAATCTCTGCTGTGATGAGCTGATGAATGGGAGAGCTTCAAGTCCATC 840
Qy      841  TACAACGTGGCAAGCGCTGAGCAATGAGCGGAGTCTTCTGCGCCCAAGTA 900
Db      841  TACAACGTGGCAAGCGCTGAGCAATGAGCGGAGTCTTCTGCGCCCAAGTA 900
Qy      901  GCTCTGAGAGTCTGCACTCTCAATGAATCGGATGCTTATCGGAGCATGAAGCTGAG 960
Db      901  GCTCTGAGAGTCTGCACTCTCAATGAATCGGATGCTTATCGGAGCATGAAGCTGAG 960
Qy      961  AATGTGCTCTGAGTACCTCGGCACTGAGAGTATCTGACCTGGGAGCTGCGCTGAG 1020
Db      961  AATGTGCTCTGAGTACCTCGGCACTGAGAGTATCTGACCTGGGAGCTGCGCTGAG 1020
Qy      1021  ATGAAGGCTGCAAGCGCTCAACCAAGAGGCTGAGCAATGCTTCAATGCTGAG 1080
Db      1021  ATGAAGGCTGCAAGCGCTCAACCAAGAGGCTGAGCAATGCTTCAATGCTGAG 1080
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Qy      1261  GAGGAGCAAGAAAGATATTGAGGCTCTTCTGCTGATGAAGAACAGAGCAAGCTTGA 1320
Db      1261  GAGGAGCAAGAAAGATATTGAGGCTCTTCTGCTGATGAAGAACAGAGCAAGCTTGA 1320
Qy      1321  AGCAGAGAAAGTCTGATGATCCAGAGAAATCATTTCTTAAAGATCAACTTTCT 1380
Db      1321  AGCAGAGAAAGTCTGATGATCCAGAGAAATCATTTCTTAAAGATCAACTTTCT 1380
Qy      1381  GCGCTGAGAGCTGAGCTTAAATGAACCCCATTTGTCGACAGCTTCAAGTGTATGCC 1440
Db      1381  GCGCTGAGAGCTGAGCTTAAATGAACCCCATTTGTCGACAGCTTCAAGTGTATGCC 1440
Qy      1441  AAGAGCATGCTGAAATGATGATTTCTGAGGTTGCGGAGGAGTGAATTTGATGACAA 1500
Db      1441  AAGAGCATGCTGAAATGATGATTTCTGAGGTTGCGGAGGAGTGAATTTGATGACAA 1500
Qy      1501  GATAGCAATTTCTTCAAAAATTTGAGACAGTGTCTGCTTATGATGACAGAGAA 1560
Db      1501  GATAGCAATTTCTTCAAAAATTTGAGACAGTGTCTGCTTATGATGACAGAGAA 1560
Qy      1561  ATTATGAAGAGGAGCTGTTGAGAACTGAAATGACCCCAAGACTTACGAGTGTGAG 1620
Db      1561  ATTATGAAGAGGAGCTGTTGAGAACTGAAATGACCCCAAGACTTACGAGTGTGAG 1620
Qy      1621  GAGGATTAATTCATCCAGTCTGAGCTGTGTTGTTGTTATG 1659
Db      1621  GAGGATTAATTCATCCAGTCTGAGCTGTGTTGTTGTTATG 1659

RESULT 4
AAD46350
ID      AAD46350 standard; cDNA, 1662 bp.
XX
AC      AAD46350;
XX
DE      27-JAN-2003 (first entry)
XX
XX      Human cone opsin kinase (GRK7) cDNA.
XX
KW      Human; enzyme; cone opsin kinase; G-protein coupled receptor kinase 7;
KW      GRK7; cone visual signaling; visual sensitivity; visual resolution;
KW      night blindness; colour blindness; Oguchi disease; pineal gland activity;
KW      chronobiological desynchrony; depression; anxiety; memory loss; headache;
KW      mental foginess; fatigue; jet lag; circadian rhythm; ophthalmological;
KW      gene therapy; antidepressant; analgesic; gene; db.
XX
OS      Homo sapiens.
XX
FH      Key
FT      CDS
FT      1..1662
FT      /tag=a
FT      /product="Human GRK7 protein"
XX
XX      WO200272541-A2.
XX
PD      19-SEP-2002.
XX
PF      07-MAR-2002; 2002WO-US007025.
XX
PR      07-MAR-2001; 2001US-0274006P.
XX
PA      (IMMUNEX CORP.
XX
PI      Bird TA, Spencer M, Mosley BA,
XX
XX      WPI; 2002-723307/78.
XX
XX      P-PsDB; AAE28952.
DR

```


QY	1	ATGCTGAGACATGGGAGGACCTCTGGACAACTGATATGCCCAACACGGCTACTCTGACAGGACCCG	60
Db	1	ATGCTGAGACATGGGAGGACCTCTGGACAACTGATATGCCCAACACGGCTACTCTGACAGGACCCG	60
QY	61	AAGCCCTCGGACTGGAGACAGCAAGAGCTGCAAGGCGGGGCGGTAACTGGCCCTCTGCCC	120
Db	61	AAGCCCTCGGACTGGAGACAGCAAGAGCTGCAAGGCGGGGCGGTAACTGGCCCTCTGCCC	120
QY	121	GGGCTGACAGGGCTCGGCGGAGAGCTCCGCAAGAGCTGCTGCTTGAATTCTTCAACAAGCTGTGT	180
Db	121	GGGCTGACAGGGCTCGGCGGAGAGCTCCGCAAGAGCTGCTGCTTGAATTCTTCAACAAGCTGTGT	180
QY	181	GAGCAGCAGCCCATGCTGTGCTGCGCTCTTCCGTGATCTTCTTAGCACAAGTGTCCACGTTTC	240
Db	181	GAGCAGCAGCCCATGCTGTGCTGCGCTCTTCCGTGATCTTCTTAGCACAAGTGTCCACGTTTC	240
QY	241	CGCAAGGCGGCAACCTCTTGAAGAGACGTGACAGAACTGAGAACTGTGGAACTGTGGCGAGAGGAACTCC	300
Db	241	CGCAAGGCGGCAACCTCTTGAAGAGACGTGACAGAACTGAGAACTGTGGAACTGTGGCGAGAGGAACTCC	300
QY	301	ACCAAGACACGTCGCTGTGAGGAGGCTGTGTGTGCACTTGTGCGAATGTGCTTGTGCTCCCGGGG	360
Db	301	ACCAAGACACGTCGCTGTGAGGAGGCTGTGTGTGCACTTGTGCGAATGTGCTTGTGCTCCCGGGG	360
QY	361	AACCCGCAACCCCTTCCTTAGCAGGCGCGTGTGACCAAGTGCAGAGCAGCACTGACTAG	420
Db	361	AACCCGCAACCCCTTCCTTAGCAGGCGCGTGTGACCAAGTGCAGAGCAGCACTGACTAG	420
QY	421	GAAAGAGAGTGTGCTGACGTACGCTTGCAGAAAGCTGAGGCTGATGTGCTTTCTTGAAGAG	480
Db	421	GAAAGAGAGTGTGCTGACGTACGCTTGCAGAAAGCTGAGGCTGATGTGCTTTCTTGAAGAG	480
QY	481	CAGCCCTTTAAGATTTTGTGACCAAGGCTTTCTTAGACAAGTTTCTGACGTGAAATCTC	540
Db	481	CAGCCCTTTAAGATTTTGTGACCAAGGCTTTCTTAGACAAGTTTCTGACGTGAAATCTC	540

QY	541	TTGAGATGCAACCAAGGTGTCAGACAATGATCTTCACTAGATTGAGATGCTGGGAAAGGT	600
Db	541	TTGAGATGCAACCAAGGTGTCAGACAATGATCTTCACTAGATTGAGATGCTGGGAAAGGT	600
QY	601	GGTTTTGGGAGAGTATGTGCGCTCCAGGTGAAAAACACTGGAGAGATGATGTCTGTAAAG	660
QY	661	AAACTGGAACAAGACGGCTGGAAGAAAGGTGGCCGAGAAAGATGGCTCTCTGGAAGAAG	720
Db	661	AAACTGGAACAAGACGGCTGGAAGAAAGGTGGCCGAGAAAGATGGCTCTCTGGAAGAAG	720
QY	721	GAAATCTTGGAGAAAGGTAGAGAGCCCTTTCATTTGCTCTGSCCTAATGCTTTGAGAGC	780
Db	721	GAAATCTTGGAGAAAGGTAGAGAGCCCTTTCATTTGCTCTGSCCTAATGCTTTGAGAGC	780
QY	781	AAGACCCATCTCTGCTTTCATGAGCCTGATGAATGGGGAGAGCTCAAGTTCACATTC	840
Db	781	AAGACCCATCTCTGCTTTCATGAGCCTGATGAATGGGGAGAGCTCAAGTTCACATTC	840
QY	841	TACAACTGTGGCAACCGCTGGCTTGGAATGAGACGGGGTGAATCTTTTACCTGGCCCAATA	900
Db	841	TACAACTGTGGCAACCGCTGGCTTGGAATGAGACGGGGTGAATCTTTTACCTGGCCCAATA	900
QY	901	GCCGTGGGATGCTGCACCTCATGAACTGGCATGCTATGSGGACATGAAAGCTGAG	960
Db	901	GCCGTGGGATGCTGCACCTCATGAACTGGCATGCTATGSGGACATGAAAGCTGAG	960
QY	961	AATGTGCTTCTGAGATGACCTCGGCACTGCAAGTTATCTGACTTGGGGCTGGCGGTGAG	1020
Db	961	AATGTGCTTCTGAGATGACCTCGGCACTGCAAGTTATCTGACTTGGGGCTGGCGGTGAG	1020
QY	1021	ATGAAAGGTGGCAAGCCCATATCCAGAGGGCTGGAACCAATGGTTACATGGCTCTCGAG	1080
Db	1021	ATGAAAGGTGGCAAGCCCATATCCAGAGGGCTGGAACCAATGGTTACATGGCTCTCGAG	1080
QY	1081	ATCCATATGAAAGGTAAAGTTATTCGTAACCTCGTGAAGCTGGTTGSCATGGGATGACGC	1140
Db	1081	ATCCATATGAAAGGTAAAGTTATTCGTAACCTCGTGAAGCTGGTTGSCATGGGATGACGC	1140
QY	1141	ATTATATGAAATGTTGTGTCGAGCAACACATTTCAAGATTTCAAGAAAAAGTCTGATAA	1200
Db	1141	ATTATATGAAATGTTGTGTCGAGCAACACATTTCAAGATTTCAAGAAAAAGTCTGATAA	1200
QY	1201	GAGATCTGAAGCAAGAACTCTGCAAGACAGGTCAAAATTCAGCATGATACTTCA	1260
Db	1201	GAGATCTGAAGCAAGAACTCTGCAAGACAGGTCAAAATTCAGCATGATACTTCA	1260
QY	1261	GAGGAACCAAAATATATTTGAGAGGCTTTCTTGGCTAAGAAACAGAGCAACGTTTAA	1320
Db	1261	GAGGAACCAAAATATATTTGAGAGGCTTTCTTGGCTAAGAAACAGAGCAACGTTTAA	1320
QY	1321	AGCAGAGAAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAACTTTCT	1380
Db	1321	AGCAGAGAAAAGTCTGATGATCCAGGAAACATCATTTCTTTAAACGATCAACTTTCT	1380
QY	1381	CGCCTGGAAGCTGCTTAATTGAACCCCAATTTGTGCCAGACCTTCAAGTGGTTATACC	1440
Db	1381	CGCCTGGAAGCTGCTTAATTGAACCCCAATTTGTGCCAGACCTTCAAGTGGTTATACC	1440
QY	1441	AAAGACATGCTGAATATGATGATTTCTCTGAGGTTGGGGGGGTGGAATTTGATACAAA	1500
Db	1441	AAAGACATGCTGAATATGATGATTTCTCTGAGGTTGGGGGGGTGGAATTTGATACAAA	1500
QY	1501	GATTAAGCAAGTTCTTCAAAAACCTTGGCAAGAGTGTGTTCTATAGCATGGCAGGAAGA	1560
Db	1501	GATTAAGCAAGTTCTTCAAAAACCTTGGCAAGAGTGTGTTCTATAGCATGGCAGGAAGA	1560
QY	1561	ATTATATGAAACGGACCTGTTTGAAGAACTGATGACCCCAACAGACTAGGGTTGTGAG	1620
Db	1561	ATTATATGAAACGGACCTGTTTGAAGAACTGATGACCCCAACAGACTAGGGTTGTGAG	1620
QY	1621	GAGGGTAATTCATCCAAAGTCTGGCGTGTGTTGTATATG	1659

DB 1621 GAGGTAATTCATCCAACTCGCGCTGTTGTTATTG 1659

RESULT 5
AB256943
ID AB256943 standard; DNA; 1761 BP.
XX
AC AB256943;
XX
XX 04-APR-2003 (first entry)
XX
DE Human gene sequence relative to the invention # SEQ ID 11.
XX
XX Human; heart disease; cancer; omentopathy; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 26..1687
ET /tag= a
XX
XX WO2002103020-A1.
XX
XX 27-DEC-2002.
XX
XX 14-JUN-2002; 2002MO-JP005942.
XX
XX 15-JUN-2001; 2001JP-00182654.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Koyama N, Tanida S, Yamamoto K;
XX
XX WPI; 2003-157045/15.
XX
XX P-PSDB; ABP60079.
XX
XX Novel disease-associated gene of the RGS gene family and its product,
XX applicable in diagnosis of and screening for drugs for heart diseases,
XX cancers and omentopathy.
XX
XX Example 3; Page 85-86; 96pp; Japanese.
XX
XX The invention relates to a novel disease associated gene and its uses.
XX The gene and its encoded protein are useful for diagnosis of and
XX screening for drugs for heart diseases, cancers and omentopathy. The
XX current sequence represents a human gene sequence relative to the
XX invention
XX
XX Sequence 1761 BP; 441 A; 441 C; 504 G; 375 T; 0 U; 0 Other;
XX
Query Match 99.8%; Score 1655.8; DB 7; Length 1761;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGTGACATGGGGGCTCTGACCACTGATGCCAACACCGCTACCTGAGCGCCG 60
DB 26 ATGGTGACATGGGGGCTCTGACCACTGATGCCAACACCGCTACCTGAGCGCCG 85
QY 61 AAGCCTCGAGCTGCGACAGCAAGAGCTGCGAGCGGCGGGGTAGCTGCGCCCTGCGC 120
DB 86 AAGCCTCGAGCTGCGACAGCAAGAGCTGCGAGCGGCGGGGTAGCTGCGCCCTGCGC 145
QY 121 GGGCTGCGAGGCTGCGCGAGCTCTCGGCAAGAGCTGTCCCTGAATTTCCACAGCCTGTG 180
DB 146 GGGCTGCGAGGCTGCGCGAGCTCTCGGCAAGAGCTGTCCCTGAATTTCCACAGCCTGTG 205
QY 181 GAGGAGGAGCCATGCGTGCAGCGCTTCTGACTTCTGACCTTCAAGCCAGTGCCTCA 240
DB 206 GAGGAGGAGCCATGCGTGCAGCGCTTCTGACTTCTGACCTTCAAGCCAGTGCCTCA 265
QY 241 CGCAAGGCGGCACTTCTGAGAGAGTGCAGACTGGAGCTGCGCGAGGAGGAGCC 300

DB 266 CGCAAGCGGCAACCTTCTGAGAGCACTGACAACTGGAGCTGGCCGAGGAGGCC 325
QY 301 ACCAAGACAGCGCGCTGCAAGGGCTGTGGCCACTTGTGAGTGCCTCTCCCGGCG 360
DB 326 ACCAAGACAGCGCGCTGCAAGGGCTGTGGCCACTTGTGAGTGCCTCTCCCGGCG 385
QY 361 AACCGGCAACCTTCTGAGAGCACTGACAACTGGAGCTGGCCGAGGAGGCCACTGAG 420
DB 386 AACCGGCAACCTTCTGAGAGCACTGACAACTGGAGCTGGCCGAGGAGGCCACTGAG 445
QY 421 GAAAGCGAGTGTGCGAGTACGCTGCGCAAGGCTGAGGCAATGCTTTCTTGCAGAG 480
DB 446 GAAAGCGAGTGTGCGAGTACGCTGCGCAAGGCTGAGGCAATGCTTTCTTGCAGAG 505
QY 481 CAGCCCTTTAAGATTTTGTGACCAAGCGCTTTTACGACAACTTGTGAGTGAAGCTC 540
DB 506 CAGCCCTTTAAGATTTTGTGACCAAGCGCTTTTACGACAACTTGTGAGTGAAGCTC 565
QY 541 TTGAGATGCAACAGTGTGACCAAGTACTTCACTGAGTTGAGAGTGTGAGGAGAGT 600
DB 566 TTGAGATGCAACAGTGTGACCAAGTACTTCACTGAGTTGAGAGTGTGAGGAGAGT 625
QY 601 GGTTTGGGAGATATGTGCGCTGCGTCAAGTGAAGAACTGGAGAGATGATGCTTGA 660
DB 626 GGTTTGGGAGATATGTGCGCTGCGTCAAGTGAAGAACTGGAGAGATGATGCTTGA 685
QY 661 AATCTGGAACAGACCGGCTGAGAGAAAGTGGCCGAGAGATGCTCTTGGAAAG 720
DB 686 AATCTGGAACAGACCGGCTGAGAGAAAGTGGCCGAGAGATGCTCTTGGAAAG 745
QY 721 GAAATCTTGAAGAGTGTGAGAGCTTCACTGCTGAGGCTTATGCTTGGAGAG 780
DB 746 GAAATCTTGAAGAGTGTGAGAGCTTCACTGCTGAGGCTTATGCTTGGAGAG 805
QY 781 AAGACCATCTCTGCTTGTGATGAGCTTGAATGAGTGGAGAACCTCAATTCACATC 840
DB 806 AAGACCATCTCTGCTTGTGATGAGCTTGAATGAGTGGAGAACCTCAATTCACATC 865
QY 841 TACAGCTGGGAGCGTGGCTGACATGAGCCGGGTATCTTTTACTGGGCCAGATA 900
DB 866 TACAGCTGGGAGCGTGGCTGACATGAGCCGGGTATCTTTTACTGGGCCAGATA 925
QY 901 GCTGTGGAGTGTGACCTGACATGACCTGAGCATGTCTATGCGGAGACATGAGCCGAG 960
DB 926 GCTGTGGAGTGTGACCTGACATGACCTGAGCATGTCTATGCGGAGACATGAGCCGAG 985
QY 961 AATGTCTTGTGATGACCTGCGCAACTGCAAGTATCTGACCTGCGCTGGCGTGGAG 1020
DB 986 AATGTCTTGTGATGACCTGCGCAACTGCAAGTATCTGACCTGCGCTGGCGTGGAG 1045
QY 1021 ATGAAGGTGGAGGCGGACCATGACCCGAGAGGGCTGGAACCAAGTGTACATGCGCTGAG 1080
DB 1046 ATGAAGGTGGAGGCGGACCATGACCCGAGAGGGCTGGAACCAAGTGTACATGCGCTGAG 1105
QY 1081 ATCTTAATGAGAAAGTAAATTAATCTATCTGTGAGCTGCTTGGCAATGGAGTCAAC 1140
DB 1106 ATCTTAATGAGAAAGTAAATTAATCTATCTGTGAGCTGCTTGGCAATGGAGTCAAC 1165
QY 1141 ATTTATGAATGTGCTGAGAGCAACACCATTTAAGATTTACAGAGAAAGTCAATAA 1200
DB 1166 ATTTATGAATGTGCTGAGAGCAACACCATTTAAGATTTAAGAGAAAGTCAATAA 1225
QY 1201 GAGGATCTGAAGCAAGAACTGCGAAGAGAGGTAATTTCCAGCATGATTAATTTTACA 1260
DB 1226 GAGGATCTGAAGCAAGAACTGCGAAGAGAGGTAATTTCCAGCATGATTAATTTTACA 1285
QY 1261 GAGGAGCAAGAAATATTTGAGGCTCTTCTGCTAAGAAACAGAGCAACCTTGAAGA 1320
DB 1286 GAGGAGCAAGAAATATTTGAGGCTCTTCTGCTAAGAAACAGAGCAACCTTGAAGA 1345
QY 1321 AGCAGAGAAAGTGTGATGATCCAGAGAAACATATTTCTTTAAAGATCAACTTCTCT 1380
DB 1346 AGCAGAGAAAGTGTGATGATCCAGAGAAACATATTTCTTTAAAGATCAACTTCTCT 1405

QY 1381 CGCCGAGACGCTGCTTATTTGACCCCACTTTGCGCAACCTTATGCTTTATGCC 1440
 DB 1406 CGCCGAGACGCTGCTTATTTGACCCCACTTTGCGCAACCTTATGCTTTATGCC 1465
 QY 1441 AAGGACGCTGCTTATTTGACCCCACTTTGCGCAACCTTATGCTTTATGCC 1500
 DB 1466 AAGGACGCTGCTTATTTGACCCCACTTTGCGCAACCTTATGCTTTATGCC 1525
 QY 1501 GATAGACGCTTCTTCAAAACCTTTGCGCAACCTTATGCTTTATGCC 1560
 DB 1526 GATAGACGCTTCTTCAAAACCTTTGCGCAACCTTATGCTTTATGCC 1585
 QY 1561 ATTATGACGCTTCTTCAAAACCTTTGCGCAACCTTATGCTTTATGCC 1620
 DB 1586 ATTATGACGCTTCTTCAAAACCTTTGCGCAACCTTATGCTTTATGCC 1645
 QY 1621 GAGGTAATTCATGCAAGCTGCGCTGCTTTATGCTTTATGCC 1659
 DB 1646 GAGGTAATTCATGCAAGCTGCGCTGCTTTATGCTTTATGCC 1684

RESULT 6
 ADC39221
 ID ADC39221 standard; cDNA; 1821 BP.
 AC ADC39221;
 XX
 DT 18-DEC-2003 (first entry)
 DE Novel human NOVX polypeptide coding sequence SEQ ID NO: 165.
 KW ds; gene; antidiabetic; cytostatic; immunomodulator; anorectic;
 KW antiparkinsonian; anti-HIV; antiaesthetic; antiinflammatory; hypotensive;
 KW antidiabetic; anorectic; cancer; lymphoma; uterine cancer; prostate cancer;
 KW diabetes; obesity; cachexia; wasting disorder; Alzheimer's disease;
 KW Parkinson's disease; multiple sclerosis; hypertension; atherosclerosis;
 KW hemophilia; graft-versus-host disease;
 KW Albright hereditary osteodystrophy.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 73..1732
 FT /tag= a
 XX
 PN WO2003010327-A2.
 XX
 PD 06-FEB-2003.
 PF 02-MAY-2002; 2002WO-US014199.
 XX
 XX 02-MAY-2001; 2001US-0288063P.
 PR 03-MAY-2001; 2001US-0288395P.
 PR 07-MAY-2001; 2001US-0289087P.
 PR 09-MAY-2001; 2001US-0289817P.
 PR 11-MAY-2001; 2001US-0290154P.
 PR 14-MAY-2001; 2001US-0290753P.
 PR 15-MAY-2001; 2001US-0291181P.
 PR 16-MAY-2001; 2001US-0291243P.
 PR 18-MAY-2001; 2001US-0292001P.
 PR 21-MAY-2001; 2001US-0292374P.
 PR 22-MAY-2001; 2001US-0292587P.
 PR 23-MAY-2001; 2001US-0293107P.
 PR 25-MAY-2001; 2001US-0293747P.
 PR 29-MAY-2001; 2001US-0294109P.
 PR 30-MAY-2001; 2001US-0294434P.
 PR 31-MAY-2001; 2001US-0294827P.

PR 12-JUL-2001; 2001US-0304879P.
 PR 31-JUL-2001; 2001US-0308901P.
 PR 14-AUG-2001; 2001US-0312270P.
 PR 17-AUG-2001; 2001US-0313416P.
 PR 10-SEP-2001; 2001US-0318463P.
 PR 27-SEP-2001; 2001US-0325683P.
 PR 18-OCT-2001; 2001US-0330292P.
 PR 28-NOV-2001; 2001US-0333873P.
 PR 03-DEC-2001; 2001US-0336909P.
 PR 03-DEC-2001; 2001US-0337552P.
 PR 21-FEB-2002; 2002US-0359245P.
 PR 01-MAY-2002; 2002US-00136826.
 XX
 PA (CUBA-) CURAGEN CORP.
 XX
 PI Miller CE, Kekuda R, Malysankar UM, Li L, Pena CE, Sylek KA;
 PI Gorman L, Guo X, Fernandez ER, Smithson G, Stone DJ, Zerkow BD;
 PI Paturajan M, Anderson DW, Mezes PS, Peyman JA, Macdougall JR;
 PI Padigaru M, Rastelli L, Shenoy SG, Gerlach VL, Shinkens RA, Zhong M;
 PI Edinger SR, Ellerman K;
 XX
 DR MPI. 2003-239445/23.
 DR P-PSDB; ADC39222.
 XX
 PT New NOVX polypeptides and polynucleotides, useful in gene therapy,
 PT particularly for treating or preventing a syndrome associated with a
 PT human disease e.g. diabetes, obesity, cancer, Alzheimer's disease,
 PT hypertension or hemophilia.
 XX
 PS Claim 20; SEQ ID NO 165; 748bp; English.
 XX
 CC The invention relates to new isolated NOVX polypeptides, the genes
 CC encoding them or sequences having at least 95% identity to the amino acid
 CC or nucleotide sequences. The NOVX polypeptide is useful as a therapeutic,
 CC particularly in the manufacture of a medicament for treating a syndrome
 CC associated with a human disease, which includes a pathology associated
 CC with NOVX polypeptide. The NOVX polypeptide is particularly useful for
 CC treating, preventing or alleviating pathology associated with NOVX
 CC polypeptide in a mammal, e.g. a human. The NOVX nucleic acid and
 CC polypeptide are especially useful for treating or preventing e.g.
 CC diabetes, obesity, cancers (e.g. lymphoma, uterine cancer or prostate
 CC cancer), dyslipidemia, anorexia, wasting disorders, Alzheimer's disease,
 CC Parkinson's disorder, cachexia, cardiomyopathy, AIDS, asthma, Crohn's
 CC disease, multiple sclerosis, hypertension, atherosclerosis, hemophilia,
 CC graft-versus-host disease or Albright hereditary osteodystrophy. The DNA
 CC encoding the protein is useful in gene therapy for treating the above
 CC conditions. These are also useful in developing powerful assay system for
 CC functional analysis of various human disorders, as well as in diagnostic
 CC applications. This sequence represents one of the NOVX genes of the
 CC invention.
 CC
 SQ Sequence 1821 BP; 453 A; 459 C; 524 G; 385 T; 0 U; 0 Other;
 XX
 QY Query Match 99.8%; Score 1655.8; DB 9; Length 1821;
 Db Best Local Similarity 99.8%; Pred. No. 0;
 QY Matches 1657; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Db 1 AAGGTGACATGAGGAGCCCTGAGCAACCTGATGCGCAACCGCTTACCTGAGCGCGG 60
 73 ATGTGACATGAGGAGCCCTGAGCAACCTGATGCGCAACCGCTTACCTGAGCGCGG 112
 QY 61 AAGCTCTGAGCTGCGACGCAAGAGCTGCGAGCGCGCGGCTGAGCTGCGCGGCTGCC 120
 Db 133 AAGCTCTGAGCTGCGACGCAAGAGCTGCGAGCGCGCGGCTGAGCTGCGCGGCTGCC 192
 QY 121 GGGCTGAGGCGCTGCGAGAGTCTCCGCAAGCTGCTCCGAACTTCCAGCAAGCTGCTG 180
 Db 193 GGGCTGAGGCGCTGCGAGAGTCTCCGCAAGCTGCTCCGAACTTCCAGCAAGCTGCTG 252
 QY 181 GAGGACGAGCGCATGCGGTGCGCGCTCTTCTGAGCTTCTGAGCAAGTCCAGGCTTC 240
 Db 253 GAGGACGAGCGCATGCGGTGCGCGCTCTTCTGAGCTTCTGAGCAAGTCCAGGCTTC 312

QY	1	ATGTGGGACATGGGGGGCCCTTGACAACTGATGTGCACACCGCTTACTGTGAGGCCGG	60
Db	354	ATGTGTGACATGGGGGGCCCTTGACAACTGATGTGCACACCGCTTACTGTGAGGCCGG	413
QY	61	AAGCCCTGCGACTGTGCGACAGCAAGAAAGCTGACGCGCGCGGTGAGCTGTGCGCTTCGCC	120
Db	414	AAGCCCTGCGACTGTGCGACAGCAAGAAAGCTGACGCGCGCGGTGAGCTGTGCGCTTCGCC	473
QY	121	GCGCTGAGAGGGCTGTGCGCGAGCTCCGCGAAGAGCTGTCCCTGAACTTCCACAGCCTGTGT	180
Db	474	GCGCTGAGAGGGCTGTGCGCGAGCTCCGCGAAGAGCTGTCCCTGAACTTCCACAGCCTGTGT	533
QY	181	GAGCAGAGGCCCATGCGTGTGCGCGCGCTTTCCTGTGACTTCTTGAGCCAGTGTCCACGTTT	240
Db	534	GAGCAGAGGCCCATGCGGTGTGCGCGCGCTTTCCTGTGACTTCTTGAGCCAGTGTGTCC	593
QY	241	CCCAAGCGCGCACTTCTCTAGAGAGTGCAGAACTGAGAGCTGTGCGCGCGAGGAGGCC	300
Db	594	CCCAAGCGCGCACTTCTCTAGAGAGTGCAGAACTGAGAGCTGTGCGCGCGAGGAGGCC	653
QY	301	ACCAAGAAGCAGCGCGCTGTGAGGGGCTGTGTGGCCACTTGTGTGAGTGTCCCTCCCGGG	360
Db	654	ACCAAGAAGCAGCGCGCTGTGAGGGGCTGTGTGGCCACTTGTGTGAGTGTCCCTCCCGGG	713
QY	361	AACCCGCAACCTTCTCTAGCGAGCGCTGTGCCCACTCAAGTGCAGAGAGCGACACTGTAG	420
Db	714	AACCCGCAACCTTCTCTAGCGAGCGCTGTGCCCACTCAAGTGCAGAGAGCGACACTGTAG	773
QY	421	GAGAGCGAGGTGCTGTGAGTGCAGCTGTGCGAGAGGCTGTGAGGCGCATGTCTTCTTTCAGAG	480
Db	774	GAGAGCGAGGTGCTGTGAGTGCAGCTGTGCGAGAGGCTGTGAGGCGCATGTCTTCTTTCAGAG	833
QY	481	CAGCCCTTAAAGATTTGTGTGACCGCGCGCTTCTTACGACAACTTCTGTGAGTGAATTC	540
Db	834	CAGCCCTTAAAGATTTGTGTGACCGCGCGCTTCTTACGACAACTTCTGTGAGTGAATTC	893
QY	541	TTGAGAGTGCACCAAGTGTGCAGCAAGTACTTCACTGATGTGAGTGTGCGGAGAAAGT	600
Db	894	TTGAGAGTGCACCAAGTGTGCAGCAAGTACTTCACTGAGTGTGAGTGTGCGGAGAAAGT	953
QY	601	GGTTTGGGAGGATGTGTGCGGTCCAGGTGAAAAACCTGTGAAAGATGTATGTCTGTAG	660
Db	954	GGTTTGGGAGGATGTGTGCGGTCCAGGTGAAAAACCTGTGAAAGATGTATGTCTGTAG	1013
QY	661	AAACTGTGACAAAGACGCGCTGAAGAAAGAAAGTGTGAGAAATGTGCTCTTGGAAAAAG	720
Db	1014	AAACTGTGACAAAGACGCGCTGAAGAAAGAAAGTGTGAGAAATGTGCTCTTGGAAAAAG	1073
QY	721	GAATCTTGTGAGAGTGTGAGACGCCCTTTCATGTGTCTCTGTGACTATGTGCTTGAAGC	780
Db	1074	GAATCTTGTGAGAGTGTGAGACGCCCTTTCATGTGTCTCTGTGACTATGTGCTTGAAGC	1133
QY	781	AAGACCATCTGTGCTTGTGATGAGCTGTGAATGATGGGGGAGACTTCAAGTTCCACATTC	840
Db	1134	AAGACCATCTGTGCTTGTGATGAGCTGTGAATGATGGGGGAGACTTCAAGTTCCACATTC	1193
QY	841	TACAACTGTGGGACGCGTGTGCTGTGACATGAGCGCGGGTATCTTTTACTGTGCGCCAGATA	900
Db	1194	TACAACTGTGGGACGCGTGTGCTGTGACATGAGCGCGGGTATCTTTTACTGTGCGCCAGATA	1253

QY	901	GCCTGTGGAGTCTGCACCTGCATGAACTCGGACCTGCTAACTGAGGACATGAAGCCTGAG	960
Db	1254	GCCTGTGGAGTCTGCACCTGCATGAACTCGGACCTGCTAACTGAGGACATGAAGCCTGAG	1313
QY	961	AATGTGCTTCCTGGATGATACCTCGGCAACCTCAGATTTATCTGACCTG396GCTGGCGTGAAG	1020
Db	1314	AATGTGCTTCCTGGATGATACCTCGGCAACCTCAGATTTATCTGACCTG666GCTGGCGTGAAG	1373
QY	1021	ATGAGGGGTGGCAAGCCATCAACCCAGAGGGCTGGAACATATGTTATATG6GCTCTGAG	1080
Db	1374	ATGAGGGGTGGCAAGCCATCAACCCAGAGGGCTGGAACATATGTTATATG6GCTCTGAG	1433
QY	1081	ATCTCTAATGCAAAAAGTAATGTTATCTGTAACCTGCGTGAACCTGTTGGCATG3ATGCAAC	1140
Db	1434	ATCTCTAATGCAAAAAGTAATGTTATCTGTAACCTGCGTGAACCTGTTGGCATG6ATGCAAC	1493
QY	1141	ATTATATGAATATGTGTGTGCGAGCAACACCATTCATTAAGATTAACAAGAAAAGTCAGTAAA	1200
Db	1494	ATTATATGAATATGTGTGTGCGAGCAACACCATTCATTAAGATTAACAAGAAAAGTCAGTAAA	1553
QY	1201	GAGGATCTGAGCAAGAACCTTGCAAGACAGAGTCAAAATTCAGATGATTAACCTTACAC	1266
Db	1554	GAGGATCTGAGCAAGAACCTTGCAAGACAGAGTCAAAATTCAGATGATTAACCTTACAC	1613
QY	1261	GAGGAAGCAAAAAGTATTTGACAGGCTCTCTTGGCTAAGAAACAGAGCAACGCTTAGA	1320
Db	1614	GAGGAAGCAAAAAGTATTTGACAGGCTCTCTTGGCTAAGAAACAGAGCAACGCTTAGA	1672
QY	1321	AGCAGAGAAAAGTCGATGATCCAGAGAAACATCATTTCTTTAAACGATCACTTTCT	1386
Db	1674	AGCAGAGAAAAGTCGATGATCCAGAGAAACATCATTTCTTTAAACGATCACTTTCT	1733
QY	1381	CGCTGTGAAGCTGCTCTAATGTAACCCCATTTGGTGCAGACCCCTTCACTGGATTTATGCC	1440
Db	1734	CGCTGTGAAGCTGCTCTAATGTAACCCCATTTGGTGCAGACCCCTTCACTGGATTTATGCC	1793
QY	1441	AAAGACATCGCTGAAAATTGATGATTTCTCTGAGGTTCG396G3GTGAAATTTGATGACAAA	1500
Db	1794	AAAGACATCGCTGAAAATTGATGATTTCTCTGAGGTTCG666G3GTGAAATTTGATGACAAA	1853
QY	1501	GATPAGCAGTCTTCAAAAACTTGTGCGACAGTGTCTTTCTATAGATGCGAGGAAAGA	1566
Db	1854	GATPAGCAGTCTTCAAAAACTTGTGCGACAGTGTCTTTCTATAGATGCGAGGAAAGA	1911
QY	1561	ATTATAGAAAACGGACCTGTTGAGGAACGTAATGACCCCAACAGACTCAGGCTTGAG	1621
Db	1914	ATTATAGAAAACGGACCTGTTGAGGAACGTAATGACCCCAACAGACTCAGGCTTGAG	1977
QY	1621	GAGGTAATTCAATCCAGAGTGTGCGCTGTGTGTTGTTATG	1659
Db	1974	GAGGTAATTCAATCCAGAGTGTGCGCGTGTGTGTTGTTATG	2012
RESULT 8			
ID	ACC44827	standard; cDNA; 3186 BP.	
XX	ACC44827;		
XX	04-JUN-2003	(first entry)	
DE	Human G protein-coupled receptor kinase encoding cDNA SEQ ID NO.4.		
XX	Human, G protein coupled receptor kinase; GRK; cytosolic; antidiabetic;		
KM	neuroprotective; nootropic; cardiovascular; anti-Parkinsonian; cardiant;		
KM	vasotropic; antidiabetic; gene therapy; cancer; diabetes; CNS disorder;		
KM	central nervous system disorder; cardiovascular disorder; asthma; COPD;		
KM	chronic obstructive pulmonary disorder; anxiety; mood disorder; enzyme;		
KM	Alzheimer's disease; Parkinson's disease; congestive heart failure;		
KM	myocardial infarction; ischaemic disease; hypertensive vascular disease;		
KM	gene; ss.		

QY	361	AATCCGGAACCCCTCTCAAGCAGGCGCTGGCCACCAATGCTCAAGACCACTAG	420
Db	445	AAACCCGAAACCCCTCTCAAGCAGGCGCTGGCCACCAATGCTCAAGACCACTAG	504
QY	421	GAAGAGGAGATGGCTGCAAGTGAAGCTGGCAAGGCTGAAGGCTTCTTGGAGAG	480
Db	505	GAAGAGGAGATGGCTGCAAGTGAAGCTGGCCAAAGCTGAAGGCTTCTTGGAGAG	564
QY	481	CAGCCCTTTAAGATTTGTGTGACCAAGCCGCTTCAAGACATTTCTGCAGTGAAAATC	540
Db	565	CAGCCCTTTAAGATTTGTGTGACCAAGCCGCTTCAAGACATTTCTGCAGTGAAAATC	624
QY	541	TTTCAGATGGAACCAAGTGTCAACAATTACTCAATGATTCAGATGTGGGAAAAGT	600
Db	625	TTTCAGATGGAACCAAGTGTCAACAATTACTCAATGATTCAGATGTGGGAAAAGT	684
QY	601	GGTTTGTGGGAGGTATGTGACCGTCCAGGCTGAAAACATCGGAGAAATGTATGCTGTAA	660
Db	685	GGTTTGTGGGAGGTATGTGACCGTCCAGGCTGAAAACATCGGAGAAATGTATGCTGTAA	744
QY	661	AAATCGAACAAGACGGCTGAAGAAGAAAGTGTGCAAGATATGCTCTTGGAAAAG	720
Db	745	AAATCGAACAAGACGGCTGAAGAAGAAAGTGTGCAAGATATGCTCTTGGAAAAG	804
QY	721	GAATCTTGGAAAAGTCAAGACCCCTTATTTCTCTCTGAGCTTATGACCTTTGAGAG	780
Db	805	GAATCTTGGAAAAGTCAAGACCCCTTATTTCTCTCTGAGCTTATGACCTTTGAGAG	864
QY	781	AAGACCCATCTGCTGCTTGCATGAGCCCTGATGAATATGGGGGAGACCTCAATGTCATATC	840
Db	865	AAGACCCATCTGCTGCTTGCATGAGCCCTGATGAATATGGGGGAGACCTCAATGTCATATC	924
QY	841	TACAACTGTGGCAAGCGCTGGCTTGGCAATGAGCCGGGTATCTTTACTCGGCCCAATA	900
Db	925	TACAACTGTGGCAAGCGCTGGCTTGGCAATGAGCCGGGTATCTTTACTCGGCCCAATA	984
QY	901	GCCGTGGGATATGCTGACCTCCATGAATCTGGATATCGTATGTGGGACATGAACTGTAG	960
Db	985	GCCGTGGGATATGCTGACCTCCATGAATCTGGATATCGTATGTGGGACATGAACTGTAG	1044
QY	961	AATGTCTTCTGATGACTCTGGCCAACTGCAAGTTATGTACCTGGGGCTGGCCGTGGAG	1020
Db	1045	AATGTCTTCTGATGACTCTGGCCAACTGCAAGTTATGTACCTGGGGCTGGCCGTGGAG	1104
QY	1021	ATGAAGGTGGCAAGCCCTCAACCCAGAGGGCTGGAAACAAATGGTATCATAGCTCTGAG	1080
Db	1105	ATGAAGGTGGCAAGCCCTCAACCCAGAGGGCTGGAAACAAATGGTATCATAGCTCTGAG	1164
QY	1081	ATCTTAATGAAAAAGGTAAGTTATCTATCTGTGAGCTGTGGTTCATGGGATGACG	1140
Db	1165	ATCTTAATGAAAAAGGTAAGTTATCTATCTGTGAGCTGTGGTTCATGGGATGACG	1224
QY	1141	ATTATGAAATGTTGTCTGAGCAAGACCAATTCAAAGATTTACAAGAAAAAGTCAATAA	1200
Db	1225	ATTATGAAATGTTGTGTGAGCAAGACCAATTCAAAGATTTACAAGAAAAAGTCAATAA	1284
QY	1201	GAGATCTGAAGCAAGAACTCTGCAAGCGAGGTCAAAATTCAGATGATTAATCTTACA	1260
Db	1285	GAGATCTGAAGCAAGAACTCTGCAAGCGAGGTCAAAATTCAGATGATTAATCTTACA	1344
QY	1261	GAGAAAGCAAAAAGATTGTGAGGCTCTCTTGGCTAAAGAAACAGAGCAACGCTTAGA	1320
Db	1345	GAGAAAGCAAAAAGATTGTGAGGCTCTCTTGGCTAAAGAAACAGAGCAACGCTTAGA	1404
QY	1321	AGCAGAGAAAAGTCTGATGATCCAGAGAAACATATTTCTTTAAAGATCACTTCTCT	1380
Db	1405	AGCAGAGAAAAGTCTGATGATCCAGAGAAACATATTTCTTTAAAGATCACTTCTCT	1464
QY	1381	CGCTGGAAAGCTGGCTTAATTTGAACCCCAATTTGTGCAAGACCTTGAAGTATATCC	1440
Db	1465	CGCTGGAAAGCTGGCTTAATTTGAACCCCAATTTGTGCAAGACCTTGAAGTATATCC	1524

QY 901 GCTGTGGGATGCTGCACTTCATGAACCTTGCCATTCGCGAATGAACTGAG 960
 DB 901 GCTGTGGGATGCTGCACTTCATGAACCTTGCCATTCGCGAATGAACTGAG 960
 QY 961 AATGTGCTTCTGGATGACCTTGCGAACTGCAAGTATCTGACCTGCGGCTGCGAG 1020
 DB 961 AATGTGCTTCTGGATGACCTTGCGAACTGCAAGTATCTGACCTGCGGCTGCGAG 1020
 QY 1021 ATGAGGGTGGCAACCCATCACCAGAGGCTGGAACCAATGTTAATGCTGCTGAG 1080
 DB 1021 ATGAGGGTGGCAACCCATCACCAGAGGCTGGAACCAATGTTAATGCTGCTGAG 1080
 QY 1081 ATCTTAATGAAAAGTAAAGTATTCCTTCTGAGCTGTTGCTGCTGAGTACG 1140
 DB 1081 ATCTTAATGAAAAGTAAAGTATTCCTTCTGAGCTGTTGCTGCTGAGTACG 1140
 QY 1141 ATTTATGAATGTTGCTGAGCAACACATTCCTTCAAGTAAAGTCAAGTAA 1200
 DB 1141 ATTTATGAATGTTGCTGAGCAACACATTCCTTCAAGTAAAGTCAAGTAA 1200
 QY 1201 GAGGATCGAAGCAAAAGTCTGCAAGCAAGGTCAAATTCGAGCATGATTA 1260
 DB 1201 GAGGATCGAAGCAAAAGTCTGCAAGCAAGGTCAAATTCGAGCATGATTA 1260
 QY 1261 GAGGAGCAAAAGTATTTGCAAGGCTCTTCTGCTTGAAGAACCAAGCAACCTTGA 1320
 DB 1261 GAGGAGCAAAAGTATTTGCAAGGCTCTTCTGCTTGAAGAACCAAGCAACCTTGA 1320
 QY 1321 AGCAGAGAAAAGTCTGATGATCCAGAAACATCATTTCTTAAAGATCACTTCT 1380
 DB 1321 AGCAGAGAAAAGTCTGATGATCCAGAAACATCATTTCTTAAAGATCACTTCT 1380
 QY 1381 CGCTTGAAGCTGACCTTAATTAACCCCATTTGTCGAGACCCCTTCAAGCTTATG 1440
 DB 1381 CGCTTGAAGCTGACCTTAATTAACCCCATTTGTCGAGACCCCTTCAAGCTTATG 1440
 QY 1441 AAAGCATGCTGAATTAATGATTTCTTGAAGTCTGCGGCTGGAATTTGACAA 1500
 DB 1441 AAAGCATGCTGAATTAATGATTTCTTGAAGTCTGCGGCTGGAATTTGACAA 1500
 QY 1501 GATTAAGCATCTTCAAAAACCTTGCGACAGTGTCTGCTATGAGATGCGAGAA 1560
 DB 1501 GATTAAGCATCTTCAAAAACCTTGCGACAGTGTCTGCTATGAGATGCGAGAA 1560
 QY 1561 ATTATGAAGACGGAGCTGTTGAGAACTGAATGACCCCAAGACCTTACGCTGTGAG 1620
 DB 1561 ATTATGAAGACGGAGCTGTTGAGAACTGAATGACCCCAAGACCTTACGCTGTGAG 1620
 QY 1621 GAGGTATTCATCCAGGCTGCGGCTGCTGTTGTTATTTG 1659
 DB 1621 GAGGTATTCATCCAGGCTGCGGCTGCTGTTGTTATTTG 1659

RESULT 10
 AAD28071 ID AAD28071 standard; cDNA, 1662 BP.
 XX AAD28071;
 XX 22-APR-2002 (first entry)
 DE Human kinase cDNA.
 KW Human; kinase; G-protein coupled receptor kinase; tissue differentiation;
 KM chromosome 3; therapeutic; immune response; drug screening; enzyme; ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FT CDS 1..1662
 FT /*tag= a
 FT /product= "Human kinase protein"

PN W020192496-A2.
 XX 06-DEC-2001.
 PD 31-MAY-2001; 2001WO-US017510.
 XX 01-JUN-2000; 2000US-0208331P.
 PR 18-DEC-2000; 2000US-00738894.
 XX (APPL-) APPLERA CORP.
 PA
 PI Guegler K, Di Francesco V, Beasley EW,
 XX WPI; 2002-130533/17.
 DR P-PDB; ABE17136.
 PT New isolated human kinase proteins and nucleic acids, useful as a major
 PT target for drug action and development, particularly for screening
 PT modulators of the kinase peptides.
 XX
 PS Claim 4; Fig 1; 87bp; English.
 CC The invention relates to human kinase proteins that are related to G-
 CC protein coupled receptor kinase subfamily. Human kinase gene is located
 CC on chromosome 3. The kinase peptide and nucleic acid are useful in the
 CC development of human therapeutic and diagnostic compositions. The peptide
 CC is useful as a major target for drug action and development, and is
 CC valuable to the field of pharmaceutical development to identify and
 CC characterize modulators of the kinase. The proteins may also be used to
 CC raise antibodies or to elicit an immune response, as a reagent in assays
 CC designed to quantitatively determine levels of the protein in biological
 CC fluids and as markers for tissues in which the corresponding protein is
 CC preferentially expressed (either constitutively or at a particular stage
 CC of tissue differentiation or development or in a disease state). The
 CC kinase proteins are also useful for providing a target for diagnosing a
 CC disease or predisposition to disease mediated by a target for diagnosing a
 CC disease or predisposition to disease mediated by a target for diagnosing a
 CC in biological assays. The nucleic acids are also useful in making vectors
 CC containing the gene regulatory regions of the nucleic acid molecules and
 CC for drug screening to identify compounds that modulate kinase nucleic
 CC acid expression. The present sequence is human kinase cDNA expressed in
 CC cells, germinal center B cells, colon, kidney and lung
 XX

Sequence 1662 BP; 419 A; 411 C; 480 G; 352 T; 0 U; 0 Other;
 Query Match 99.7%; Score 1654.2; DB 6; Length 1662;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1656; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGCTGGAATGAGGAGGCTGCAAGCAACCTGATTCGCCAAACCCGCTTACCTGAGCCCG 60
 DB 1 ATGCTGGAATGAGGAGGCTGCAAGCAACCTGATTCGCCAAACCCGCTTACCTGAGCCCG 60
 QY 61 AAGCCCTCGAATCGACAGCAAAAGCTGCAAGCGGCGGCTGAGCTGCGCTCGCC 120
 DB 61 AAGCCCTCGAATCGACAGCAAAAGCTGCAAGCGGCGGCTGAGCTGCGCTCGCC 120
 QY 121 GGGTTCAGAGGCTCGGAGGCTCGGCAAGAGCTGTCTTCAAGCTTCAAGAGCTGTGT 180
 DB 121 GGGTTCAGAGGCTCGGAGGCTCGGCAAGAGCTGTCTTCAAGCTTCAAGAGCTGTGT 180
 QY 181 GAGCAGAGCCCATCGGTGCGGCTCTTCCCTGATCTTCTGACCAAGTCCCAAGTTC 240
 DB 181 GAGCAGAGCCCATCGGTGCGGCTCTTCCCTGATCTTCTGACCAAGTCCCAAGTTC 240
 QY 241 CGCAAGGCGGCAACCTTCTTAAGAGAGCTGCAAGACTGGAAGTGGAGAGGAGCC 300
 DB 241 CGCAAGGCGGCAACCTTCTTAAGAGAGCTGCAAGACTGGAAGTGGAGAGGAGCC 300
 QY 301 ACCAAGACAGCGGCTGCAAGGAGCTGAGTGGCACTTGTGCAAGTCCCTGCGCGAG 360
 DB 301 ACCAAGACAGCGGCTGCAAGGAGCTGAGTGGCACTTGTGCAAGTCCCTGCGCGAG 360


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QY 361 AACCCGCAACCCCTTCTCTGAGCCGAGCCGTCACCAAGTCCGCAAGAGCACTAG 420
Db 361 AACCCGCAACCCCTTCTCTGAGCCGAGCCGTCACCAAGTCCGCAAGAGCACTAG 420
QY 421 GAAAGGAGAGTGGCTGACAGTACGCTGCGAAGGCTGAGGCGCATGCTTTCTTGAAG 480
Db 421 GAAAGGAGAGTGGCTGACAGTACGCTGCGAAGGCTGAGGCGCATGCTTTCTTGAAG 480
QY 481 GAGCCCTTAAAGATTTGCTGACGAGGCTTCTACGACAAATTTCTGCAAGTGAATC 540
Db 481 GAGCCCTTAAAGATTTGCTGACGAGGCTTCTACGACAAATTTCTGCAAGTGAATC 540
QY 541 TTGCGAGTGAACCAAGTCAAGAGTCACTGAGTTCAGAGTCTGAGGAAAGT 600
Db 541 TTGCGAGTGAACCAAGTCAAGAGTCACTGAGTTCAGAGTCTGAGGAAAGT 600
QY 601 GGTTTTGGGAGATATGTCCTCCAGGTGAAAAACATGGGAAAGATGATGCTGTAG 660
Db 601 GGTTTTGGGAGATATGTCCTCCAGGTGAAAAACATGGGAAAGATGATGCTGTAG 660
QY 661 AAATCGACAAAGAGCGGCTGAAGAAAGTGGCGAGAGATGGCTCTTCTTGAAG 720
Db 661 AAATCGACAAAGAGCGGCTGAAGAAAGTGGCGAGAGATGGCTCTTCTTGAAG 720
QY 721 GAAATCTTGAAGAGTCAAGGCTTCAATGCTCTGCTGCTGCTGCTGCTGCTGAGC 780
Db 721 GAAATCTTGAAGAGTCAAGGCTTCAATGCTCTGCTGCTGCTGCTGCTGAGC 780
QY 781 AAGACCCATCTCTGCTTGTCAATGAGCCTGATGATGAGGAGAGACCTTCAAGTCAATC 840
Db 781 AAGACCCATCTCTGCTTGTCAATGAGCCTGATGATGAGGAGAGACCTTCAAGTCAATC 840
QY 841 TACAACTGGGACGCGCTGCTGCAATGAGCGGCTGATCTTTTACTGCGCCGAGAT 900
Db 841 TACAACTGGGACGCGCTGCTGCAATGAGCGGCTGATCTTTTACTGCGCCGAGAT 900
QY 901 GCTCTGGAGATGCTGACCTCCATGACCTGGGACATGCTGATCGGAGCATGAGAGCTGAG 960
Db 901 GCTCTGGAGATGCTGACCTCCATGACCTGGGACATGCTGATCGGAGCATGAGAGCTGAG 960
QY 961 AATGCTCTTCTGATGACCTCGGCAATGCGATTAATCTGCACTGGGCTGCGCGTGAAG 1020
Db 961 AATGCTCTTCTGATGACCTCGGCAATGCGATTAATCTGCACTGGGCTGCGCGTGAAG 1020
QY 1021 ATGAGAGGTGGCAAGCCCATCACCAGAGGCTGGAACCAATGCTTCAATGCTGAG 1080
Db 1021 ATGAGAGGTGGCAAGCCCATCACCAGAGGCTGGAACCAATGCTTCAATGCTGAG 1080
QY 1081 ATCTTAATGAGAAAGTAAATGATATCTTCTGATGAGTGGTTCATGAGTGAAGC 1140
Db 1081 ATCTTAATGAGAAAGTAAATGATATCTTCTGATGAGTGGTTCATGAGTGAAGC 1140
QY 1141 ATTATGAATGATGTTGCTGACGACCAACCATTTCAAGATTAAGGAAAGTCAATGA 1200
Db 1141 ATTATGAATGATGTTGCTGACGACCAACCATTTCAAGATTAAGGAAAGTCAATGA 1200
QY 1201 GAGGATCTGAACCAAGATCTGCAAGCGAGTCAATTTCCAGATGAATCTTCA 1260
Db 1201 GAGGATCTGAACCAAGATCTGCAAGCGAGTCAATTTCCAGATGAATCTTCA 1260
QY 1261 GAGGAGCAAAAGATATTTGAGAGCTCTTCTTGGCTAAAGAAACAGAGCAAGCTTGA 1320
Db 1261 GAGGAGCAAAAGATATTTGAGAGCTCTTCTTGGCTAAAGAAACAGAGCAAGCTTGA 1320
QY 1321 AGCAGAGAAAGTCTGATGATCCAGAGAAACATCTTTTAAACGATCACTTTCT 1380
Db 1321 AGCAGAGAAAGTCTGATGATCCAGAGAAACATCTTTTAAACGATCACTTTCT 1380
QY 1381 CGCTGAGAGCTGCTTAATGAACCCCAATTTGGCCAGACCTTCACTGCTTTATG 1440
Db 1381 CGCTGAGAGCTGCTTAATGAACCCCAATTTGGCCAGACCTTCACTGCTTTATG 1440
QY 1441 AAAGACATGCGTGAATGATTTCTGAGGTTGCGGAGGTGAATTTGATGACAA 1500

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Db 1441 AAAGACATGCGTGAATGATTTCTGAGGTTGCGGAGGTGAATTTGATGACAA 1500
QY 1501 GATTAAGAGTCTTCAAAAACCTTGGGACAGAGTCTGTTCTATAGATGAGCAAGAA 1560
Db 1501 GATTAAGAGTCTTCAAAAACCTTGGGACAGAGTCTGTTCTATAGATGAGCAAGAA 1560
QY 1561 ATTATGAAGAGGAGCTGTTTGAAGAACTGAATGACCCCAAGACCTTACGGTTGAG 1620
Db 1561 ATTATGAAGAGGAGCTGTTTGAAGAACTGAATGACCCCAAGACCTTACGGTTGAG 1620
QY 1621 GAGGTAATTCATCCAGTCTGCGCTGCTGCTTGTATG 1659
Db 1621 GAGGTAATTCATCCAGTCTGCGCTGCTGCTTGTATG 1659

RESULT 11
AAS06702
ID AAS06702 standard; cDNA, 1662 BP.
XX
AC AAS06702;
XX
DT 12-SEP-2001 (first entry)
DE
XX Polynucleotide sequence encoding human protein kinase #2.
XX Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
XX metabolic disorder; immune related disease; neurological disorder;
XX neurodegenerative disorder; inflammatory disorder; infectious disease;
XX reproductive disorder; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN NC0200138503-42.
XX
PD 31-MAY-2001.
XX
XX 22-NOV-2000; 2000MO-US032085.
XX
XX 24-NOV-1999; 99US-0167482P.
XX
PA (SUGEN-) SUGEN INC.
XX
PI Plozman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
PI Flanagan P, Clary D;
XX
XX WPI: 2001-343950/36.
XX
XX P-PSDB; AAU03502.
XX
XX Nucleic acids encoding human kinase polypeptides, useful for preventing
XX diagnosing and/or treating e.g. cancer, immune, cardiovascular and
XX neuronal-associated diseases, and microbial infections.
XX
XX Example 1; Fig 1; 433pp; English.
XX
XX AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel
XX protein kinases have been identified as members of the tyrosine or
XX serine/threonine kinase (PTK and STK) families. The polynucleotides
XX encoding protein kinases and the polypeptides may be used in the
XX prevention, diagnosis and treatment of diseases associated with
XX inappropriate kinase expression. For example, they may be used to treat
XX cancers (especially cancers of haematopoietic origin), cardiovascular
XX disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
XX immune related diseases (e.g. rheumatoid arthritis), neurological
XX disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
XX Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
XX disease (e.g. HIV) and reproductive disorders (e.g. infertility).
XX Additionally, polynucleotides encoding protein kinases may be used for
XX gene therapy and as DNA probes in diagnostic assays. The protein kinase
XX polypeptides may be used as antigens in the production of antibodies
XX against the protein kinases and in assays to identify modulators of
XX protein kinase expression and activity
XX

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Sequence 1662 BP; 421 A; 411 C; 479 G; 351 T; 0 U; 0 Other;

Query Match	99.6%	Score 1652.6;	DB 4;	Length 1662;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 1655; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0

QY	ATGCTGGACATATGGGGGCGCTTGTGCAAACTTGATCGCAACAACCGCTTACTCTGACGGCCCG	60
Db	1 ATGCTGGACATATGGGGGCGCTTGTGCAAACTTGATCGCAAAACCGCTTACTCTGACGGCCCG	60
QY	61 AAGCCCTCGACATGCGACAGCAAAAGCTGACAGCGGGGGGGGGGTAAAGCTTGGCTTGCCT	120
Db	61 AAGCCCTCGACATGCGACAGCAAAAGCTGACAGCGGGGGGGGGGTAAAGCTTGCCTTGCCT	120
QY	121 GGGCTGCAAGGCTGTGGCGGGAAGCTTCGGCGAAGAGCTGCTCCCTGAATTCCACAGGCTGTGT	180
Db	121 GGGCTGCAAGGCTGTGGCGGGAAGCTTCGGCGAAGAGCTGCTCCCTGAATTCCACAGGCTGTGT	180
QY	181 GACACACACACCCATCGAGTGGCGCGGCTCTTCCGTGACTTCTAGCCACAGTGGCCACGTTTC	240
Db	181 GACACACACCCATCGAGTGGCGCGGCTCTTCCGTGACTTCTAGCCACAGTGGCCACGTTTC	240
QY	241 CGCAGCGGGCAACCTTCTTAAAGACGTGACAACTGAGGAGCTTGAGCCGAGAGGGAGCC	300
Db	241 CGCAGCGGGCAACCTTCTTAAAGACGTGAGAACTGAGAACTTGAGCCGAGAGGGAGCC	300
QY	301 ACCAAAGACACGGCGCTGACAGGGGCTGTGGCCACTTTGTGCGATGGTCCCTGCCCCGAGG	360
Db	301 ACCAAAGACACGGCGCTGACAGGGGCTGTGTGCGCACTTTGTGCGAAGTGGCCCCCTGCCCCG	360
QY	361 AACCCGCAACCTTCTCTACAGCAGGCGCGTGGGCCACCAAGTGTGCAAGCGACACACTAG	420
Db	361 AACCCGCAACCTTCTCTACAGCAGGCGCGTGGGCCACCAAGTGTGCAAGCGACACACTAG	420
QY	421 GAAAGCGACAGTGTGTGAGTACGCTGTGGCAAGGCTTAAGGCCCATGCTTTCTTGCAGAG	480
Db	421 GAAAGCGACAGTGTGTGAGTACGCTGTGGCCAAAGCTTAAGGCCCATAGCTTTCTTGCAGAG	480
QY	481 CAGCCCTTAAAGATTTCTGTGACAGCGGCGCTTCTAAGCAAGTTTCTGCAGTGTGAATCTC	540
Db	481 CAGCCCTTAAAGATTTCTGTGACAGCGGCGCTTCTAAGCAAGTTTCTGCAGTGTGAATCTC	540
QY	541 TTGAGATGCAACCAATGTACAGACAAAGTACTTCACTAGATTCAAGTGTGGGGAAAGGT	600
Db	541 TTGAGATGCAACCAATGTACAGACAAAGTACTTCACTAGATTCAAGTGTGGGGAAAGGT	600
QY	601 GGTTTTGGGGAGATGTGCGCTTCAAGTGAATAACTGGAAAGATGATATGCTGTAG	660
Db	601 GGTTTTGGGGAGATGTATGTGCGCTTCAAGTGAATAAACTGGAAAGATGATATGCTGTAG	660
QY	661 AAATCTGACAAAGAGCGGCTGAAGAAAGAGTGGCGAAGAGATGAGTCTCTTGGAAAG	720
Db	661 AAATCTGACAAAGCGGCTGAAGAAAGAGTGGCGAAGAGATGAGTCTCTTGGAAAG	720
QY	721 GAAATCTTGGAGAAGGTACAGAGCCCTTTGATTGTCTCTGAGCTTATGCTTGAAGC	780
Db	721 GAAATCTTGGAGAAGGTACAGAGCCCTTTGATTGTCTCTGAGCTTATGCTTGAAGC	780
QY	781 AAGACCATCTCTGCTTGTGATGAGCGCTGAAGATGGGGGAAAGCTCAAGTTTCAATC	840
Db	781 AAGACCATCTCTGCTTGTGATGAGCGCTGAAGAAAGTGGGGGAAAGCTCAAGTTTCAATC	840
QY	841 TACAACTGTGGGCAAGCGGTGTGAGATGAGCGGAGTGACTTTTAATCTGAGCCCAATTA	900
Db	841 TACAACTGTGGGCAAGCGGTGTGAGCATGAGCGGAGTGAATCTTTAATCTGAGCCCAATTA	900
QY	901 GCGTGTGGAGATGTGACCTGACATGAACTTGGCAATCGTCTATGTGGGCAATGAAGCTTAG	960
Db	901 GCGTGTGGAGATGTGACCTGACATGAACTTGGCAATCGTCTATGTGGGCAATGAAGCTTAG	960
QY	961 AATGTGCTTGTGATGACCTGCGCACTGCAAGTTATCTGACCTGGGGCTGAGCGGTGAG	1020
Db	961 AATGTGCTTGTGATGACCTGCGCACTGCAAGTTATCTGACCTGGGGCTGAGCGGTGAG	1020

Oy		1021	ATGAAGGGTGGAAAGCCCATCAACCCAGAAGGCTTGAAACAATGGTTTCATGCTCCTCGAG	108
Db		1021	ATGAAGGGTGGAAAGCCCATCAACCCAGAAGGCTTGAAACAATGGTTTCATGCTCCTCGAG	108
Oy		1081	ATCCTAATGAAAAGTAGTAATTCTCATCTGTGAGACMGTTTTGCCATGGATGCAAG	1140
Db		1081	ATCCTAATGAAAAGTAGTAATTCTCATCTGTGAGACMGTTTTGCCATGGATGCAAG	1140
Oy		1141	ATTATGAATAATGTGTGCTGAGCAACACCATTCCAAGATTCAAGAAAAAGTCAAGTAA	1200
Db		1141	ATTATGAATAATGTGTGCTGAGCAACACCATTCCAAGATTCAAGAAAAAGTCAAGTAA	1200
Oy		1201	GAGGATCTGAAACCAAABAATCTCTGACAGAGAGGTCAAAATTCACAGATGATTAAC	1260
Db		1201	GAGGATCTGAAACCAAABAATCTCTGACAGAGAGGTCAAAATTCACAGATGATTAAC	1260
Oy		1261	GAGAAAGCAAAAAGATATTGACAGGCTCTCTTGGCCTTAAGAAAACAGAGCAACCTTAGA	1320
Db		1261	GAGAAAGCAAAAAGATATTGACAGGCTCTCTTGGCCTTAAGAAAACAGAGCAACCTTAGA	1320
Oy		1321	AGCAGAGAAAAGTCTGATGATCCAGAGAACATATTTCTTTAAAGATCAACTTCT	1380
Db		1321	AGCAGAGAAAAGTCTGATGATCCAGAGAACATATTTCTTTAAAGATCAACTTCT	1380
Oy		1381	CAGCTGGAAGAGTGGCCCATTAATTAACCCCCTTATGTGCCAGACCCCTTCAAGTGTATGCC	1440
Db		1381	CAGCTGGAAGAGTGGCCCATTAATTAACCCCCTTATGTGCCAGACCCCTTCAAGTGTATGCC	1440
Oy		1441	AAGAATCATCGTGAATAATGATATTCTCTGAGGTGCGGGGGTGGAAATTGATGACAA	1500
Db		1441	AAGAATCATCGTGAATAATGATATTCTCTGAGGTGCGGGGGTGGAAATTGATGACAA	1500
Oy		1501	GATTAAAGCATTTCTTCAAAAACCTTGGCAGACAGTGTCTGTCCATATGATGACAGAGAA	1560
Db		1501	GATTAAAGCATTTCTTCAAAAACCTTGGCAGACAGTGTCTGTCCATATGATGACAGAGAA	1560
Oy		1561	ATTATAGAAAAGGGAATGTTTGAGAACTGATATGACCCCAACAGACTTACGAGTGTGAG	1620
Db		1561	ATTATAGAAAAGGGAATGTTTGAGAACTGATATGACCCCAACAGACTTACGAGTGTGAG	1620
Oy		1621	GAGGTAATTCATCCAAAGCTGAGCGTGTGTTGTTATTG	1659
Db		1621	GAGGTAATTCATCCAAAGCTGAGCGTGTGTTGTTATTG	1659
RESULT 12				
ACC44826				
ID	ACC44826	standard; cdna; 1662 bp.		
XX	ACC44826;			
AC				
DT	04-JUN-2003	(first entry)		
XX				
Human G protein-coupled receptor kinase encoding cDNA SEQ ID NO:1.				
Human; G protein coupled receptor kinase; GRK; cytosolic; antidiabetic; neuroprotective; nootropic; cardiovascular; anti-Parkinsonian; cardiac; vasotrophic; antihistaminic; gene therapy; cancer; diabetes; CNS disorder; central nervous system disorder; cardiovascular disorder; asthma; COPD; chronic obstructive pulmonary disorder; anxiety; mood disorder; enzyme; Alzheimer's disease; Parkinson's disease; congestive heart failure; myocardial infarction; ischemic disease; hypertensive vascular disease; gene; ss.				
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XX				
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 ID ABZ56934 standard; DNA; 1191 BP.
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 AC ABZ56934;
 XX
 DT 04-APR-2003 (first entry)
 XX
 DE Human RGSNO9 encoding DNA # SEQ ID 2.
 XX
 KW Human; RGSNO9; heart disease; cancer; omentopathy; gene; ds.
 OS Homo sapiens.
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 PD 27-DEC-2002.
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 PF 14-JUN-2002; 2002MO-JP005942.
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 PR 15-JUN-2001; 2001JP-00182654.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Koyama N, Tanida S, Yamamoto K;
 XX
 DR WPI; 2003-157045/15.
 DR P-PSDB; ABP60078.
 XX
 PT Novel disease-associated gene of the RGS gene family and its product,
 PT applicable in diagnosis of and screening for drugs for heart diseases,
 PT cancers and omentopathy.
 XX
 BS Claim 6; Page 81-82; 96pp; Japanese.
 XX
 CC The invention relates to a novel disease associated gene and its uses.
 CC The gene and its encoded protein are useful for diagnosis of and
 CC screening for drugs for heart diseases, cancers and omentopathy. The
 CC current sequence represents the human RGSNO9 encoding DNA sequence
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 SQ Sequence 1191 BP; 274 A; 320 C; 363 G; 234 T; 0 U; 0 Other;
 Query Match 71.6%; Score 1187.8; DB 7; Length 1191;
 Best Local Similarity 99.8%; Pred. No. 3.7e-286;
 Matches 1189; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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AAH78798
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AC AAH78798;
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DE 08-MAR-2002 (first entry)
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KW G-protein coupled receptor kinase; GRK; human; ss; gene therapy;
KW drug screening; gene expression characterization; NHP;
KW novel human protein.
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XX
PR 10-MAR-2000; 2000US-0188449P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Walke DW, Wilganski NL, Turner CA;
XX
DR WPI; 2001-570872/64.
DR P-PSDB; AAG77816.
DR

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XX New polynucleotides encoding human proteins that share sequence
PT similarity with animal kinases e.g. G-protein coupled receptor kinases,
PT useful for drug screening, diagnosis and in gene therapy of biological
PT disorders.

PS Claim 4; Page 32; 34pp; English.

CC The present cDNA sequence encodes a human G-protein coupled receptor
CC kinase (GRK), also designated NHP (novel human protein) in the
CC specification, which is claimed in the invention. The invention comprises
CC novel human nucleotide and protein sequences which have similarity to G-
CC protein coupled receptor kinases. Oligonucleotides derived from the
CC nucleotides of the invention are useful as hybridisation probes for
CC screening libraries and assessing gene expression patterns. The
CC nucleotides of the invention are also useful in drug screening and gene
CC therapy for the modulation of GRK expression. The nucleotides of the
CC invention can be used to genetically engineer host cells to express GRK
CC products in vivo. The nucleotide sequences of the invention are also
CC useful in addressable arrays for identifying and characterising the
CC temporal and tissue specific expression of a gene and in microarrays to
CC screen collections of genetic material from patients who have a
CC particular medical condition. The proteins of the invention are useful
CC for generating antibodies, as reagents in diagnostic assays, for
CC identifying other cellular gene products related to GRK, and as reagents
CC in assays for screening for compounds that are useful in the treatment of
CC mental, biological or medical disorders/diseases

SO Sequence 1062 BP; 237 A; 296 C; 330 G; 199 T; 0 U; 0 Other;

Query Match 63.1%; Score 1046.8; DB 4; Length 1062;
Best Local Similarity 99.8%; Pred. No. 5.6e-251;

Matches 1048; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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GenCore version 5.1.6
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Run on: August 13, 2004, 12:57:35 ; Search time 2906.37 Seconds

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	7	300.2	18.1	1058	13	BQ057469	BQ057469 AGENCOURT
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ALIGNMENTS

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DEFINITION Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:DJ0046K2 product:G PROTEIN-COUPLED RECEPTOR KINASE GPR6 (EC 2.7.1.1) homolog [Mus musculus], full insert sequence.

ACCESSION AK051405
VERSION AK051405.1 GI:26094516
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636

REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20493374

PUBMED
REFERENCE
AUTHORS

11042159

TITLE

JOURNAL

RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multipipillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913

JOURNAL
MEDLINE

REFERENCE

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

JOURNAL

Nature 409, 685-690 (2001)

TITLE

⁵ The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL
REFERENCE
AUTHORS

6 (bases 1 to 2978)

Adachi, J., Aizawa, K., Akamura, T., Akawa, T., Bono, H., Caliniceanu, F., Fukuda, S., Furuno, M., Hagihara, T., Harai, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hironaka, T., Hoti, F., Imotani, K., Ishi, Y., Itoh, M., Kikawa, I., Kusurawa, T., Kato, H., Kawai, J., Kojima, T., Kondo, S., Komori, H., Kouda, M., Koyama, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohsato, N., Oozaki, Y., Saito, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takai-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE
JOURNAL

Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome and Experimental Research Group, RIKEN Genomic Sciences Center (GSC), 3-1-1 Koyohama Institute, 1-7-22 Sueniwa-cho, Tsukuba-shi, Yokohama, Kanagawa 230-0045, Japan (E-mail: yoshihide-hayashizaki@gscl.riken.go.jp, URL: <http://www.genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: <http://fantom.gsc.riken.go.jp/>.

FEATURES

source

Location/Qualifiers

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ORIGIN

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Dh 248 GGCACCAGATGTGTGACATGCTCCCCCATATACGACGATGTGAAGAACTTTCGACTCAGCCCTTG 307

Qy 158 CCGTGAACCTTTCACAGGCTGTGTGTGAGCAGCAGGCCATCGAGTGTGCGGCTCTTCCGTGACT 217

Dh 308 AGCTGTACTACAGCAGCTATGTGAGCCGACGCCATTGTGGGCGCTGTATTATTTGTGTAGT 367

Qy 218 TCTTAGCCACAGTGGCCCACTTCCGCAAGCGGCAACTTCTTGAAGAGCTGTGCAAACT 277

Dh 368 TGTGTGTATGAGAGACTTGAGCTTGACCCCGGTGTACTCTCTTCTGTAAGGAGTGTGTAAAT 427

Qy 278 GGAAGCTGTGCCAGAGAGGAGCCACCAACAAAGACAGCGGTGTGAGAGGAGGAGCTGTGGCCACTT 337

Dh 428 ATGAGGTGAGCCCTCATGTATGAGAACGGAAAGATGTGGCGCC---GACTATATGCAAGAACT 484

Qy 338 GTGCGAGTGTCCCTGTCCCGGAGAACCCGCAACCTTCTCTTACAGCAGGCGCTGTGGCCACA 397

Dh 485 TTCTGAGCCACAAAGGATCTGTGACTGTATCTCTTGAAGTTCACAGGCACTGTGTGAGTAACT 544

Qy 398 AGTGTCCAAAGACCACTGATGAGAAAGCCAGTGGCTGTGCAATGATGACCTGTGCCAAGGCTG 457

Dh 545 GTGCCACGCGGCTTAAAGGACAGAGAACCTGTCAAAAGACTTCTTCAAGAGCTGACCCGAGCTG 604

Qy 458 AGGCGCATGTCTTCTTGTGAGAGACAGCCCTTAAAGATTTGTGTGACAGCGGCTTCTACG 517

Dh 605 A--CCCAAGATCTGTGAGCAGCGCCCTTTTGGCCAGTAACTGTGACAGCATCTACTCA 662

Qy 518 ACGAGTTTCTGTGAGTGAACCTTCTTGAGATGACCAACAGTGTCAAGAACTTCTACTG 577

Dh 663 ACCGTTTTCTGTGATGTGAAGTGTGCTGAAAGGCAACAGTGTGACAAAGAAACACTTCCAGGC 722

Qy 578 AGTTTCAAGTGTCTGTGGGAAAGATGTGTTTGGGAGAGTATGTGTCGAGTGTGAAAGAAACA 637

Dh 723 AGTACCGAGTCTGTGGCAAAAGTGTGCTTTGGGAGAGTATGTGCTGTGCAAGTGTGCGGAGAA 782

Qy 638 CTGGGAAAGATGTATGTCTGTAAAGAACTGACAAAGAGCGGCTGAAGAAAGATGTGGCG 697

Dh 783 CAGGCAAAATGTACGATGTGCAAGAAAGTGTGAAGAAAGAGCGGATTAAGACGAAAGGAGG 842

Qy 698 AGAAGATGTCTCTTGTGAAGAAAGAAATTTGTGAGAAAGTGTGACAGCCCTTCACTGTCT 757

Dh 843 AGGCGATGTGCTTCAACAGAGAAACAGATCTTGTGAGAAAGTGAACGTATGTGTATGTGA 902

Qy 758 CTCTGGCCCTATGTGAGAGCAAGCCATCTGTGCTGTGTGATGTGAGAGCTGATGAATG 817

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Qy 938 TGTATGTGAGACATGAGACCTGTGAGATGTGTTCTGTGATGACTGTGGCACTGTGAGTTAT 997

Dh 1083 TGTACAGGGATCTTAAAGCCAGAGAAATATCTTCTGTGATGACATGTGCCACCAATTCGAGATCT 1142

Qy 998 CTGACTGTGGGCTGTGCTGTGTGAGATGAGAGGTGTGAAGGCCATCAACCAAGGAGGCTGTGAA 1057

Dh 1143 CGGACCTGTGAGCTGTGCGGTGATGTGCTGTGAGGAGCGACATCAAAAGCGGTGTGGGGA 1202

Qy 1058 CCAATGTATCATGTGCTGTGTGATCTTATGTGAAGAAAGTATGATTTCTATCTGTGG 1117

Dh 1203 CTGTGGGCTATATGTGCTTCCAGAGGTGTGAGG---AATGAGCGCTTCAAGTTCACTGTG 1259

Qy 1118 ACTGTGTTTCGATGGAGATGACATTTATGAATGTGCTGTGACGAAACACCATTTCAAG 1177

Db 1260 ACTGTGGCGCTAGGCTCTCTTACGAGATGATGAGGTAGTGCCCTTCCACG 1319
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 QY 1298 AGAAACAGAGAGAGAGCTGAGAGAGAGAGAAAGTGTATGATCCAGAGAAATCAT 1357
 Db 1440 ACCCTGCTAGAGCGCTGGGGTGTCTGAGAGTGGCGCCGTGAGTAAAGAGAGACCC 1499
 QY 1358 TCTTTAAACAGATCACTTTCTCGCTGAGAGCTGAGCTTAAATGAAACCCCATTTGTC 1417
 Db 1500 TTTTCAAGAAAGTAAATTTCAAGCGGCTGGAGCTGAGCTGATAGAGCACTTTTAAAG 1559
 QY 1418 CAGACCTTCAGTGGTATTATGCAAGAGCATGCTGAAATGATGATTTCTGAGGTTTC 1477
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 Db 1680 TGTCCATCCCTGCGAGAGATGAGATGAGTGAAGAGAGAGCTTCCAGAGAGTCAATGTC 1738

RESULT 2
 BC057206 2989 bp mRNA linear HTC 19-NOV-2003
 LOCUS Mus musculus G protein-coupled receptor kinase 6, mRNA (CDNA clone
 IMAGE:5328461), containing frame-shift errors.
 ACCESSION BC057206.1 GI:34784381
 VERSION BC057206.1 GI:34784381
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
 1 (bases 1 to 2989)
 Strussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carminci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwen, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hu, Y., S.W.,
 Villalón, D.K., Muzny, D.M., Soderberg, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywicki, M.I., Skalska, U., Small, D.E.,
 Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.,
 generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 22388257
 1247932
 2 (bases 1 to 2989)
 AUTHORS
 Strausberg, R.
 Direct Submission
 Submitted (29-AUG-2003) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer

REMARK

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
 Contact: MGC help desk
 Email: gcgabs-remail.nih.gov
 Tissue Procurement: Leibar Henniphausen Ph.D., Priscilla Futh
 Ph.D.

CDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mgc@nih.gov

Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Grant, S., Guan, X., Gupta, J., Haghghi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R.,
 Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantipop, S., Thomas, P.J., Touchman, J.W.,
 Tsurgou, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

FEATURES

source

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ORIGIN

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 Matches 873; Conservative 0; Mismatches 685; Indels 27; Gaps 6;
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 Db 170 GGAGCTGAGAAATCTGATGCAACACGCTGCTCTCAAGGCCCGGAAGTGTGTGG 229
 QY 75 CGACACCAAG--AGCTGAGCGGGCGGCGGTGAGCTGAGCCCTGCGGGCTGAGGG 131
 Db 230 GAATTCGAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 289
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 Db 290 GTGTGAGAGCTGTGACTAGCTTGAAGCTGATCAAGCAAGCTTATGTAGCGCGAG 349
 QY 192 CATGCTGCGCGCTCTTCCGTGATCTTCAAGCAAGTCCCAAGTTCGCAAGGCGG 251
 Db 350 CATTTGGGCGCTGTATTATTTGTGAGTTTGTGTGCTAGAGAACTGAGCTGACCGG 409
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 Db 410 TGCCTTCTGATGAGGTGTGATATGAGTGAAGCCCTGATGAGAGGAGAAAGCAG 469
 QY 312 CGGCTGAGAGGAGTGTGAGCACTTGTGAGAGTGCCTGCGCGGAGAACCCGGAAC 371
 Db 470 TGGGCGCC--GATATGCAAGATTTTGTAGCCACAGAGGTCTTACTATCTTGA 526
 QY 372 CTTCCTAGCCAGGCGGTGGCCACAGATGCAAGAGCAAGCAAGTGAAGAGAGGAGT 431

QY 762 GGCCTATGCTTTGAGAGAGACCCATCTGCTTGTGATGAGCTGATGAATGGGG 821
 DB 764 GGCTTACGCTTATGAGACCAAGACCGCTGTGCTGTGCTGATCACTGATGAACGGGG 705
 QY 822 AGACCTCAAGTTCCACATCTTCAACAGCTGGGACCGGTGCTGSACTAGACCGGGGAT 881
 DB 704 CCACTCAAGTTCCACATCTTCAACAGCTGGGACCGGTGCTGSACTAGACCGGGGAT 645
 QY 882 CTTTATCTGCGCCAGATATGCTGTGGGATGCTGACCTTCATGAACTCGGACCTCTA 941
 DB 644 CTTTATGCGCCAGATATGCTGTGGGATGCTGACCTTCATGAACTCGGACCTCTA 585
 QY 942 TCGGACATGAAAGCCTGAGATGTGCTTCTGATGATGCTGCACTGAGTTATCTGA 1001
 DB 584 CAGGACCTGAAAGCCCGAGAACCTTCTGTGATGAACTGCACTGAGTTATCTGA 525
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 DB 524 CTTGGGCTGCGCTGAGATGAAAGGTGGCAAGCCATCACCGAGGCTGGAACCA 465
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 DB 407 GTGGGCTGCGCTGAGATGCTTATGAGATGCTGAGGCTGAGGCTTCTGAGAGAG 348
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 DB 227 TCCGAGAGGCTTGGGCTGTGCTGAGGAGCTGAGGCTGAGAGAGAGAGAGAG 168
 QY 1362 TAAAGCATGCACTTCTGCTGAGAGAGCTGAGCTTATGAAAGAGAGAGAGAG 1421
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 QY 1422 C 1422
 DB 107 C 107

RESULT 4
 LOCUS BC027597 2329 bp mRNA linear HTC 01-MAY-2002
 DEFINITION Homo sapiens, similar to G protein-coupled receptor kinase 2-like
 (Drosophila), clone IMAGE:4830673, mRNA.
 ACCESSION BC027597
 VERSION BC027597.1 GI:20379554
 KEYWORDS HTC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 2329)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (08-APR-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Miklos Palikovitcs, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki

ORIGIN

Query Match 18.8%; Score 311.6; DB 11; Length 2329;
 Best Local Similarity 57.4%; Pred. No. 5,5e-60;
 Matches 623; Conservative 0; Mismatches 454; Indels 9; Gaps 3;

FEATURES

source

Toshituki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systembiology.org>
 contact: amadansystembiology.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Ketterman, Anuradha
 Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>
 Series: IRAP Plate: 34 Row: 1 Column: 14
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 488346
 This clone has the following problem: frame shifted.
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 /mol_type="mRNA"
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 /clone="IMAGE:4830673"
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 QY 597 AGGTGTTTTGGAGAGTATGCTGCTGAGTAAACACTGAGAAATGATGCTG 656
 DB 1041 AGCGGATTTGAGAGGTTTCCCTGTCAAGTGCAGGACAGAAATGATGCTG 1100
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 DB 1161 GAAAAGATTTCTGAGAGAAAGTGAAGAGTAAAGTAAAGTAAAGTAAAGTAA 1220
 QY 777 GAGCAAGACCATCTGCTGCTTGTATGATGAGCTGATGAATGAGGAGAGCTCAAGTTCA 836
 DB 1221 AACCAAGATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1280
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 DB 1341 GCTGTGTGGGCTTGAAGATTACAGAGGAAAGATTGATACAGAGCTTGAAGCC 1400
 QY 957 TGAAGATGCTTCTGATGAGCTGAGCACTGAGAGTATGATCTGAGGAGCTGAGCC 1016
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 QY 1017 GAGATGAGAGGTGAGAGAGCATCAAGAGAGGCTGAGCAAGATGATGATGAGCTGC 1076
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 DB 1695 TTGAGAGATGCCAAATCTATCTGAGAGATGTTACTCAACAAAGATCAAGCAACGCTT 1754
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 QY 1374 CTTTCTGCTGGAAGCTGCGCTTAATTGAACCCCATTTGSCAGACCCCTTCAGTGT 1433
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 QY 1494 TCACAAAGATAGCAGTTCTTCAAAAACCTTTGCGACAGGTGCTGCTTACATAGCA 1553
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 QY 1554 GGAAGA 1559
 DB 1995 GAATGA 2000

RESULT 5
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 LOCUS BX392018 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
 DEFINITION Homo sapiens CDNA clone CS0D1010YD11 3-PRIME, mRNA sequence.
 ACCESSION BX392018
 KEYWORDS BX392018.1 GI:30607809
 SOURCE EST.
 ORGANISM Homo sapiens (human)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 917)
 L1, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: sequef@genoscope.cns.fr Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 3090.f For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0BA1046ZH12_CS04416_1&cluster=3090.f.
 Contact: Feng Liang Email: fliang@lifetech.com URL:
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
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 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)

ORIGIN

primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

Query Match 18.5%; Score 307; DB 13; Length 917;
 Best Local Similarity 63.8%; Pred. No. 3,7e-59;

Matches 482; Conservative 0; Mismatches 270; Indels 3; Gaps 1;

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 QY 519 CAGTTTCTGAGTGAAGAACTCTTGAGATCAACAGTGTCAAGATTAATCACTGA 578
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 DB 676 ATACCAAGTCTGGGCAAAAGTGTGTTGGGAGGTATGTCCCTTCAGGTGAAAAAC 617
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 DB 616 AGTAAGATGATATGCTGTGAAGAACTGGAACAGACCGCTGAAGAAAGTGTGCA 557
 QY 699 GAAGATGCTCTCTTGAAGAAAGTGTGGAAGTGTGGAAGTGTGGAAGTGTGGAAG 758
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RESULT 6
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 LOCUS AY406080
 DEFINITION Homo sapiens GPRK5 gene, VIRUTAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY406080
 VERSION AY406080.1 GI:39762054
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
1 (bases 1 to 1721)
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Mang, G., Zheng, X.H., White, T.J., Shtinsky, J.J.,
Adams, M.D. and Cargill, M.
Interfering nonneutral evolution from human-chimp-mouse orthologous
gene tios

JOURNAL
PUBMED
14671302
Science 302 (5652), 1960-1963 (2003)

REFERENCE
AUTHORS
2 (bases 1 to 1721)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Mang, G., Zheng, X.H., White, T.J., Shtinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

FEATURES
Location/Qualifiers
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Query Match 18.4%; Score 304.6; DB 29; Length 1721;
Best Local Similarity 49.5%; Pred. No. 1.9e-58;
Matches 559; Conservative 0; Mismatches 561; Indels 9; Gaps 3;

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529 CAGTGAACCTTTCAGATGCAACAGTGTGACAGCAAGTCTTCTGAGTTTCAAGT 588
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522 NNN 581
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762 AAGTTCCATCTTACCAAGTGGAGCAGCTGAGCTGAGAGAGAGAGAGAGAGAG 821
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822 GCGGCGAGATAGCTGAGAGAGTCAAGCTTCAAGAGAGAGAGAGAGAGAGAGAG 881
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AGENCY: NIH-MGC 6739297 NIH-MGC_99 Homo sapiens cDNA clone IMAGE:5813090
5', mRNA sequence.
ACCESSION
B0057469
VERSION
B0057469.1 GI:19816809
KEYWORDS
EST.
SOURCE
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ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 1058)
NIH-MGC <http://mgi.nci.nih.gov/>,
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-ri@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
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ORIGIN

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 /note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
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 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACAGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 library."

Query Match 18.1%; Score 300.2; DB 13; Length 1058;
 Best Local Similarity 63.9%; Pred. No. 1.3e-57;
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 5 GACCCAGAGTACTGAGCGTGGCCCTTTTGGCCGACTCTGACAGCATCTACTTAA 64
 519 CAAGTTCTGAGTGAAGAACTCTTGAGATGCAACAGTGTGACAAAGTACTTCACTGA 578
 65 CGTTTCTGAGTGAAGTGGCTGAAAGGCGACAGTGAACAAAACCTTCAGGCA 124
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 LOCUS B0061148
 DEFINITION AGENCOURT_6862941 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5920180

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 accession B0061148.1 GI:19884933
 version EST.
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 source Homo sapiens (human)
 organism Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1019)
 NIH-MGC <http://mgc.nci.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Lou Staudt
 CDNA library preparation: Rubin laboratory
 CDNA library arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA sequencing by: Agencourt Bioscience Corporation
 clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
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 high quality sequence stop: 704.
 Location/Qualifiers

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 /note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dt priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACAGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 library."

ORIGIN

Query Match 18.0%; Score 299.2; DB 13; Length 1019;
 Best Local Similarity 63.8%; Pred. No. 2.4e-57;
 Matches 470; Conservative 0; Mismatches 264; Indels 3; Gaps 1;

459 GGCATGCTCTTCTGCAAGACACCCCTTAAAGATTTCGTGACAGCCGCTTCTACGA 518
 5 GACCCAGAGTACTGAGCGTGGCCCTTTTGGCCGACTCTGACAGCATCTACTTAA 64
 519 CAAGTTCTGAGTGAAGAACTCTTGAGATGCAACAGTGTGACAAAGTACTTCACTGA 578
 65 CGTTTCTGAGTGAAGTGGCTGAAAGGCGACAGTGAACAAAACCTTCAGGCA 124
 579 GTTCAGAGTGTGGGAGAGGTGTTTGGGGAGGTATGTGCGCTGAGTGAAGAAAC 638
 125 ATACGAGTCTGGGCAAGGTGGCTTTGGAGGTGTGCTGCGCTGCAAGGTGGGCGAC 184
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 185 AGGTAAATGATGCTCTGCAAGAGCTGAGAAAGGAGATCAAGAAAGCGAAAGGGA 244
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 305 CTGGGCTTACGCTTATGAGAGCAAGAGCGCTGTGCTGCTGACATGATGAGCG 364
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 QY 939 CTATCGGACATGAAGCTGAGATGTGTTCTGATGACCTTGGCAATGCGAGTTATC 998
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 QY 1119 CTGGTTTGCATGGGATGACGATTTATGAATGTGTTGCTGAGACAAACCATTTAAGA 1178
 Db 662 CTGGTGGGCGCTGGCTGCTCTGTGACGAGATGATGCGAGCGCAGTGGCCTTCCAGA 721
 QY 1179 TTACAAGAAAAGGTCA 1195
 Db 722 GAGCAAGAAAAGAAATCA 738

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 DEFINITION genomic survey sequence.
 VERSION AY406082.1 GI:39762056
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1721)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 AUTHORS 2 (bases 1 to 1721)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
 Todd,M.A., Tanenbaum,D.M., Civeille,D.R., Lu,F., Murphy,B.,
 Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
 Adams,M.D. and Cargill,M.

TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
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ORIGIN

Query Match 17.8%; Score 295; DB 29; Length 1721;
 Best Local Similarity 49.0%; Pred. NO. 3e-56;
 Matches 553; Conservative 0; Mismatches 567; Indels 9; Gaps 3;
 QY 469 TTCTTGCAAGAGAGAGCCTTTAAGATTCTGTGACGAGCGCCTTTACAGCAAGTTCTG 528

Db 402 TACTTGAAGGAGACCCCTTCCAGAGTACCTGATAGCATGATTTTACCGTTTCTG 461
 QY 529 CAGTGGAAATCTTGGAGATGCAACAGTGTGACGAAGTACTTCACTGATTCAGATG 588
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 QY 589 CTGGGAGAAAGTGTGTTTGGGAGGTATGTGCTCCAGGTGAAAAACCTGGAGATG 648
 Db 522 NNN 581
 QY 649 TATGCTGTGAAGAACTGGAACAAGCGGCTGAGAAAGAAAGTGGGAGAAAGTGGCT 708
 Db 582 TATGCTGTGAAGCTTGTGAGAGAAAGAGATCAAAAGAGAAAGGGAATCCATGCA 641
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 QY 769 GCCTTGAAGAGAGACCCATCTCTGCTGTGATGACCTGATGATGATGAGAGACCTC 828
 Db 702 GCTATGAAACCAAGATGACATATGCTGTGCTTGTGACCATTTATGATGTGTGACCTG 761
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 QY 1546 GATGAGCAGAGAAATTAAGAAACGAGACTGTTGAGAGACTGAATG 1594

insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-GDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

	Query Match	16.9%	Score 280.6	DB 13	Length 903
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Db	273	TATCTCTGCAACCGCTTGGAGAAAGAGGATCAAAAAGAAAGAAAGGGAGATTCATGGCC	332		
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QY	769	GCCTTTAAGAGCAAGACCCATCTCTGCCCTGTGATGAGCTGATGATGGGAGACCTC	828		
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Db	633	TTGGCTGTAAAGATCCCCAGAGGAGACCTGATCCGGGCGGGGTGGGCACTGTTGGTAC	692		
QY	1069	ATGGCTCTGAGATCTCTAATGGAAGAAAGGTAAATTCTTATCTGTGACTGTGTTGTC	1128		
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VERSION	BM794145.1				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				

ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
	Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
REFERENCE	1 (bases 1 to 560)
AUTHORS	Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.I.

TITLE	21C Frontier Korean EST Project 2001
JOURNAL	Unpublished (2002)
COMMENT	Contact: Kim YS

Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel : +82-42-860-4470
Fax : +82-42-860-4409
Email: yongsung@gmail.kr, yb.kr
Plate: 37 row: D column: 08
High quality sequence stop: 560.

FEATURES
SOURCE

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Soares Laboratory and it was constructed as described by
Donald, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested
cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park J.G. et al.
(1990), Cancer Res 50: 2773-2780."

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	Query Match	16.4%	Score 272.24	DB 124	Length 501
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QY	646	ATGTATGCTGTAAAGAACTGGAACAAAGAGCGGCTTGAAAGAAAGGTGCGAAGAAATG	705		
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QY	706	GCTCTCTTTGGAAAAAGGAATCTTGGAAAGAGTCAAGACCCCTTTCATTGTCTCTGCGGC	765		
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GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NH_MGC
Library."

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ORIGIN

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Query Match      16.4%; Score 272.2; DB 13; Length 1017;
Best Local Similarity 58.8%; Pred. No. 3.7e-51;
Matches 526; Conservative 0; Mismatches 359; Indels 9; Gaps 3;

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EST.
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)

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REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strauberg, Ph.D.
Email: c9apbs@emall.nih.gov
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IMAGE Consortium (info@image.llnl.gov) for further information.
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FEATURES

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libraries (fetal lung NBH19W, testis NHT, and B-cell
NCI CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."

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ORIGIN

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Query Match      16.3%; Score 270.6; DB 9; Length 815;
Best Local Similarity 62.3%; Pred. No. 7.5e-51;
Matches 439; Conservative 0; Mismatches 263; Indels 3; Gaps 1;

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 ; APPLICANT: Walke, D. Wade
 ; APPLICANT: Wilgowski, Nathaniel L.
 ; APPLICANT: Turner, C. Alexander Jr.
 ; TITLE OF INVENTION: No. 644456el Human G-Coupled Protein Receptor Kinases and Polymu
 ; TITLE OF INVENTION: Encoding the Same
 ; FILE REFERENCE: LEX-0147-USA
 ; CURRENT APPLICATION NUMBER: US/09/802,117
 ; PRIOR FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: US 60/188,449
 ; PRIORITY FILING DATE: 2000-03-10
 ; NUMBER OF SEQ ID NOS: 5
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; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: C000636
; CURRENT APPLICATION NUMBER: US/09/738,894A
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-09-738-894A-1

Query Match 99.7%; Score 1654.2; DB 4; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1656; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGTGAGAGAGTGTGACAGAGGCTTCACTGAGTTCAAGTCTGAGAGAGC 60
Db 1 ATGTGAGAGAGTGTGACAGAGGCTTCACTGAGTTCAAGTCTGAGAGAGC 60
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Db 541 TTGAGATGCAACGAGTGTGACAGAGGCTTCACTGAGTTCAAGTCTGAGAGAGC 600

Db 541 TTGAGATGCAACCAAGTGTGACAGCAAGTACTTCACTAGTTCAGAGTGTGAGGAAAGGT 600
QY 601 GGTGTTGGGAGGATATGTGCTTCCAGGTGAAACCACTGGGAAATGTATGCTGTAG 660
Db 601 GGTGTTGGGAGGATATGTGCTTCCAGGTGAAACCACTGGGAAATGTATGCTGTAG 660
QY 661 AAATGGAACCAAGAAAGGCTGAAAGAAAGGAGGAGAAATGATGGCTCTTGGAAAG 720
Db 661 AAATGGAACCAAGAAAGGCTGAAAGAAAGGAGGAGAAATGATGGCTCTTGGAAAG 720
QY 721 GAAATCTTGAGAAAGTACAGACCCCTTCAATGCTCTCTGCTGCTTATGCTTGAAGC 780
Db 721 GAAATCTTGAGAAAGTACAGACCCCTTCAATGCTCTCTGCTGCTTATGCTTGAAGC 780
QY 781 AAGACCATCTGCTGCTTGTGATGAGCTTGAATGAGGAGGAGACCTTCAATGCTTGAAGC 840
Db 781 AAGACCATCTGCTGCTTGTGATGAGCTTGAATGAGGAGGAGACCTTCAATGCTTGAAGC 840
QY 841 TACAACGTTGGGAGGAGGCTGCTGAGCAATGAGGAGGAGGCTTCAATGCTTGAAGC 900
Db 841 TACAACGTTGGGAGGAGGCTGCTGAGCAATGAGGAGGAGGCTTCAATGCTTGAAGC 900
QY 901 GCCTGTGGAGTGTGCACTCTCATGATGCTGCAATGCTGCAATGCTGCAATGCTGCA 960
Db 901 GCCTGTGGAGTGTGCACTCTCATGATGCTGCAATGCTGCAATGCTGCAATGCTGCA 960
QY 961 AATGCTCTTGTGATGATCTGCGCACTGCGCACTGCGCACTGCGCACTGCGCACTGCG 1020
Db 961 AATGCTCTTGTGATGATCTGCGCACTGCGCACTGCGCACTGCGCACTGCGCACTGCG 1020
QY 1021 ATGAGGATGAGCAAGCCATCACCAGAGGCTGGAACCAATGTTATGATGCTGCTGAG 1080
Db 1021 ATGAGGATGAGCAAGCCATCACCAGAGGCTGGAACCAATGTTATGATGCTGCTGAG 1080
QY 1081 ATCTTATGAGAAAGTATGATGATGCTTATGCTGATGCTGCTGCTGCTGCTGCTGAG 1140
Db 1081 ATCTTATGAGAAAGTATGATGATGCTTATGCTGATGCTGCTGCTGCTGCTGCTGAG 1140
QY 1141 ATTTATGAAATGTTGCTGAGCAAGCAATTCATTAAGTAAAGAAAGTAAAGTAAAG 1200
Db 1141 ATTTATGAAATGTTGCTGAGCAAGCAATTCATTAAGTAAAGAAAGTAAAGTAAAG 1200
QY 1201 GAGGATCTGAGCAAGCAATCTGCAAGCAAGGCTCAATTCAGATGATGATGATGATGAG 1260
Db 1201 GAGGATCTGAGCAAGCAATCTGCAAGCAAGGCTCAATTCAGATGATGATGATGATGAG 1260
QY 1261 GAGGAGCAAAAGATATTTGAGGCTCTTCTTGTGTAAGAAACAGAGCAAGCTTGAAG 1320
Db 1261 GAGGAGCAAAAGATATTTGAGGCTCTTCTTGTGTAAGAAACAGAGCAAGCTTGAAG 1320
QY 1321 AGCAGAGAAAGTCTGATGATGCTTCAAGAAATCTTCTTAAAGCAATGATGATGATGATG 1380
Db 1321 AGCAGAGAAAGTCTGATGATGCTTCAAGAAATCTTCTTAAAGCAATGATGATGATGATG 1380
QY 1381 CGCCTGGAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
Db 1381 CGCCTGGAAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
QY 1441 AAAGACATGCTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
Db 1441 AAAGACATGCTGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
QY 1501 GATAGAGATGCTTCAAAACCTTGGAGCAAGGCTGCTGCTTCAAGCAATGATGATGATGATG 1560
Db 1501 GATAGAGATGCTTCAAAACCTTGGAGCAAGGCTGCTGCTTCAAGCAATGATGATGATGATG 1560
QY 1561 ATTATGAAACGAGCTGTTGAGGAACTGATGATGATGATGATGATGATGATGATGATGATG 1620
Db 1561 ATTATGAAACGAGCTGTTGAGGAACTGATGATGATGATGATGATGATGATGATGATGATG 1620
QY 1621 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1659
Db 1621 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1659

RESULT 4
US-09-964-469-1
; Sequence 1, Application US/09964469
; Patent No. 6579709
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636DIV
; CURRENT FILING DATE: US/09/964,469
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO. 1
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-09-964-469-1

Query Match 99.7% Score 1654.2; DB 4; Length 1662;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1656; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGTGAGCAATGAGGAGGCTTGGAGCAATGATGCTGCAACCGCTTACCTGCAAGGCTGCG 60
Db 1 ATGTGAGCAATGAGGAGGCTTGGAGCAATGATGCTGCAACCGCTTACCTGCAAGGCTGCG 60
QY 61 AAGCCTCTGCACTGCGCAAGCAAGAGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCG 120
Db 61 AAGCCTCTGCACTGCGCAAGCAAGAGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCG 120
QY 121 GAGGCTGCAAGGAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCG 180
Db 121 GAGGCTGCAAGGAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCG 180
QY 181 GAGGAGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCG 240
Db 181 GAGGAGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCG 240
QY 241 GCGAAGGCTGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCG 300
Db 241 GCGAAGGCTGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCG 300
QY 301 ACCAAGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCG 360
Db 301 ACCAAGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCG 360
QY 361 AACCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCG 420
Db 361 AACCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCG 420
QY 421 GAGGAGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCG 480
Db 421 GAGGAGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCGCAAGGCTGCG 480
QY 481 CAGCCCTTAAAGATTTGCTGCAAGGCTTCTGCAAGGCTTCTGCAAGGCTTCTGCAAGGCTTCTGCAAGGCTTCTG 540
Db 481 CAGCCCTTAAAGATTTGCTGCAAGGCTTCTGCAAGGCTTCTGCAAGGCTTCTGCAAGGCTTCTGCAAGGCTTCTG 540
QY 541 TTGAGATGCAACCAAGTGTGCAAGCAAGTATCTTCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTG 600
Db 541 TTGAGATGCAACCAAGTGTGCAAGCAAGTATCTTCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTGCAAGTGTG 600
QY 601 GGTGTTGGGAGGATATGTGCTTCCAGGTGAAACCACTGGGAAATGTATGCTGTAG 660
Db 601 GGTGTTGGGAGGATATGTGCTTCCAGGTGAAACCACTGGGAAATGTATGCTGTAG 660

QY	661	AAATGSAACAAGACCGCTGMAAGAAAGGTGGAGAAATGCTCTCTGGAAAAG	720
Db	661	AAATGSAACAAGACCGCTGMAAGAAAGGTGGAGAAATGCTCTCTGGAAAAG	720
QY	721	GAATCTTGGAAAGTTCAGACCCCTTTCATGTCTCTCTGAGCTATCCCTTTGAGAGC	780
Db	721	GAATCTTGGAAAGTTCAGACCCCTTTCATGTCTCTCTGAGCTATCCCTTTGAGAGC	780
QY	781	AAGACCCATCTGCTCTTGATGAGCTGATGAATGGGGAGACCTCAAGTTCCACATC	840
Db	781	AAGACCCATCTGCTCTTGATGAGCTGATGAATGGGGAGACCTCAAGTTCCACATC	840
QY	841	TACAGGTGGAGACGCGCTGGCTGGACATGAGCGGGGTGATCTTTTACTGGCCCAATG	900
Db	841	TACAGGTGGAGACGCGCTGGCTGGACATGAGCGGGGTGATCTTTTACTGGCCCAATG	900
QY	901	GCCGTGGAGATCTGCACTCCCATGAATCGGGCATGCTCTACGGGACATGAGCTCGAG	960
Db	901	GCCGTGGAGATCTGCACTCCCATGAATCTGGGATGTCTATCGGAGCATGAGCTCGAG	960
QY	961	AATGTCTTCTGATGACTCTCGCAACTGCAAGTTATCTGACTGGGGCTGGCGTGGAG	1020
Db	961	AATGTCTTCTGATGACTCTCGCAACTGCAAGTTATCTGACTGGGGCTGGCGTGGAG	1020
QY	1021	ATGAAAGGTGGAGACCCATCAACCCAGGGGCTGGAAACCATGGTTACTATGGCTCTGAG	1080
Db	1021	ATGAAAGGTGGAGACCCATCAACCCAGGGGCTGGAAACCATGGTTACTATGGCTCTGAG	1080
QY	1081	ATCTCTATGAGAAAGGTGATGTTATTCATCTCTGTGACTGTGTTGCCATGGATGAGC	1140
Db	1081	ATCTCTATGAGAAAGGTGATGTTATTCATCTCTGTGACTGTGTTGCCATGGATGAGC	1140
QY	1141	ATTATGAAATGCTTGTCTGACGACACACTTAAAGATTACAAGAAAAGGTCAATGAA	1200
Db	1141	ATTATGAAATGCTTGTCTGACGACACACTTAAAGATTACAAGAAAAGGTCAATGAA	1200
QY	1201	GAGGATCTGAGACAAAGAACTCTGCAAGAGAGTCAAAATCCAGCAATATTACTTCACA	1260
Db	1201	GAGGATCTGAGACAAAGAACTCTGCAAGAGAGTCAAAATCCAGCAATATTACTTCACA	1260
QY	1261	GAGGAGCAAAAGATATTTGCAAGCTCTTCTGGCTAAGAAACCAAGCAAGCTTTAGCA	1320
Db	1261	GAGGAGCAAAAGATATTTGCAAGCTCTTCTGGCTAAGAAACCAAGCAAGCTTTAGCA	1320
QY	1321	AGCAGAGAAAGTCTGATGATCCCAAGAAACATGATTTCTTTAAACCATCACTTTCT	1380
Db	1321	AGCAGAGAAAGTCTGATGATCCCAAGAAACATGATTTCTTTAAACCATCACTTTCT	1380
QY	1381	CGCTGGAAGCTGCGCTCAATGAACTCCCATTTGTGCAAGCTTCCTCACTGTTTATGCG	1440
Db	1381	CGCTGGAAGCTGCGCTCAATGAACTCCCATTTGTGCAAGCTTCCTCACTGTTTATGCG	1440
QY	1441	AAAGACATGCTGAATATGATGATTTCTTGAGGTTGGGGGGGTGAAATTTGATCAAA	1500
Db	1441	AAAGACATGCTGAATATGATGATTTCTTGAGGTTGGGGGGGTGAAATTTGATCAAA	1500
QY	1501	GATPACAGATCTTCAAAAATTGTCGACAGGTGCTGTTCTCTATPACATGCGCAAGAAAG	1560
Db	1501	GATPACAGATCTTCAAAAATTGTCGACAGGTGCTGTTCTCTATPACATGCGCAAGAAAG	1560
QY	1561	ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACTTACGGGTTGAG	1620
Db	1561	ATTATAGAAACGGGACTGTTTGAAGAACTGAATGACCCCAACAGACTTACGGGTTGAG	1620
QY	1621	GAGGATATTAATCAAGCTCGGCTGTGTTGTGTTATG	1659
Db	1621	GAGGATATTAATCAAGCTCGGCTGTGTTGTGTTATG	1659

```

? Patent No. 6444456
? GENERAL INFORMATION:
?
? APPLICANT: Walke, D. Wade
? APPLICANT: Wilgowski, Nathaniel L.
? APPLICANT: Turner, C. Alexander Jr.
? TITLE OF INVENTION: No. 6444456el Human G-Coupled Protein Receptor Kinases and Polymu
? TITLE OF INVENTION: Encoding the Same
? FILE REFERENCE: LEX-0147-USA
? CURRENT APPLICATION NUMBER: US/09/802.117
? CURRENT FILING DATE: 2001-03-08
? PRIOR APPLICATION NUMBER: US 60/188,449
? PRIOR FILING DATE: 2000-03-10
? NUMBER OF SEQ ID NOS: 5
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 3
? LENGTH: 1062
?
? TYPE: DNA
? ORGANISM: homo sapiens
?
? US-09-802-117-3

```

Query Match	63.1%	Score 1046.8	DB 4	Length 1062	
Best Local Similarity	99.8%	Pred. No. 5.3e-249			
Matches 1048	Conservative 0	Mismatches 2	Indels 0	Gaps 0	
QY	1	ATGTGGAATATGAGGAGCCCTGGACACAACTCATATGCGCAACACCGCTACACTGACAGGCCG	60		
Db	1	ATGTGTGAAATATGAGGAGCCCTGGACAACTCATATGCGCAACACCGCTACACTGAGGCCG	60		
QY	61	AAGCCTTCGGAATCTGCAACAGCAAAGAGTGTACAGCGCGCGCGGTGAGCTTGACCTTGTCC	120		
Db	61	AAGCCTTCGGAATCTGCAACAGCAAAGAGTGTACACACGCGCGCGCGGTGAGCTTGACCTTGTCC	120		
QY	121	GAGGTCAAGAGGTCTCGCGAGGTCCGCGCAAACTGTCCCTTGAACTTTCACACAGCTGTGT	180		
Db	121	GAGGTCAAGAGGTCTCGCGAGGTCTCGCGCAAACTGTCCCTTGAACTTTCACACAGCTGTGT	180		
QY	181	GAGGACAGACCCATCGGTGACCGCTCTTCCTGTGACTTCTGAGCAAGTGTGCCACGTTT	240		
Db	181	GAGGACAGACCCATCGGTGACCGCTCTTCCTGTGACTTCTGAGCAAGTGTGCCACGTTT	240		
QY	241	CGCAAGGCGGCACACTTCTTGAGAGATGTTCAGAACTGTGGAGCTGGCCGAGAGAGACCC	300		
Db	241	CGCAAGGCGGCACACTTCTTGAGAGATGTTCAGAACTGTGGAGCTGGCCGAGAGAGACCC	300		
QY	301	ACCAAGAAGAGGCGCTGAGAGGCGCTGTGTGGCCATCTGTGTGAGATGCCCTGCCCCGGG	360		
Db	301	ACCAAGAAGAGGCGCTGAGAGGCGCTGTGTGGCCATCTGTGTGAGATGCCCTGCCCCGGG	360		
QY	361	AACCCGAAACCTTCTTCAGGCCAGGCGGTGTGACCAAGTGTCCAAACAGACCAACTGAG	420		
Db	361	AACCCGAAACCTTCTTCAGGCCAGGCGGTGTGACCAAGTGTCCAAACAGACCAACTGAG	420		
QY	421	GAAAGCGAGTGTCTGTGAGTACGTGTGTGTGTGAGGCTGAGGCTCATGCTTTCTTGAAG	480		
Db	421	GAAAGCGAGTGTCTGTGAGTACGTGTGTGTGTGAGGCTGAGGCTCATGCTTTCTTGAAG	480		
QY	481	CAGCGCTTTAAGATTTTGTGTACAGGCGCTTGTACACAAATTTTGTGAGTGAATATC	540		
Db	481	CAGCGCTTTAAGATTTTGTGTACAGGCGCTTGTACACAAATTTTGTGAGTGAATATC	540		
QY	541	TTTGAGATGCAACAGTGTCAACAATTTCTTCACTGAGTTCAAGATGTGTGGAGAAAGT	600		
Db	541	TTTGAGATGCAACAGTGTCAACAATTTCTTCACTGAGTTCAAGATGTGTGGAGAAAGT	600		
QY	601	GGTTTTGGAGAGTATGTGTCTCAAGTGAATTAACAATGTGAGTCTGTGAAG	660		
Db	601	GGTTTTGGAGAGTATGTGTCTCAAGTGAATTAACAATGTGAGTCTGTGAAG	660		
QY	661	AAATCGAACAAGAGCGGTGAAAGAAAGAGTGTGTGAGAGTGTGTGCTTGTGAAAG	720		
Db	661	AAATCGAACAAGAGCGGTGAAAGAAAGAGTGTGTGAGAGTGTGTGCTTGTGAAAG	720		
QY	721	GAATATCTTGAGAGGTGACGAGCCCTTTCATGTCTCTGTGAGCTATGACCTTTGAGAC	780		

Db 721 GAATCTTGAGAGAGGTCAGACAGCCCTTCACTCTCTCTGCTTACGCTTTAGAGAC 780
Qy 781 AAGACCATCTCTGCTTCTGATGAGCTGATGATGAGAGAGACCTTAAGTTCCATC 840
Db 781 AAGACCATCTCTGCTTCTGATGAGCTGATGATGAGAGAGACCTTAAGTTCCATC 840
Qy 841 TACAGCTGAG 900
Db 841 TACAGCTGAG 900
Qy 901 GCCTGTGAG 960
Db 901 GCCTGTGAG 960
Qy 961 AAGTGTCTTCTGATGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 961 AAGTGTCTTCTGATGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Qy 1021 ATGAGAGTGGAG 1050
Db 1021 ATGAGAGTGGAG 1050

RESULT 6
US-09-738-894A-3
; Sequence 3, Application US/09738894A
; Patent No. 6331423
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636
; CURRENT APPLICATION NUMBER: US/09/738,894A
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 36651
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(36651)
; OTHER INFORMATION: n = A,T,C or G
US-09-738-894A-3

Query Match 37.2%; Score 617.4; DB 4; Length 36651;
Best Local Similarity 96.8%; Pred. No. 2.2e-142;
Matches 630; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ATGTGAGACATGAG 60
Db 2076 ATGTGAGACATGAG 2135
Qy 61 AAGCCCTGAG 120
Db 2136 AAGCCCTGAG 2195
Qy 121 GGGCTGAG 180
Db 2196 GGGCTGAG 2255
Qy 181 GAGGAG 240
Db 2256 GAGGAG 2315
Qy 241 CGAAG 300
Db 2316 CGAAG 2375
Qy 301 ACCAAG 360

Db 2376 ACCAAG 2435
Qy 361 AAGCCGAG 420
Db 2436 AAGCCGAG 2495
Qy 421 GAG 480
Db 2496 GAG 2555
Qy 481 CAGCCCTTTAAGAGATTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 2556 CAGCCCTTTAAGAGATTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2615
Qy 541 TTGAG 600
Db 2616 TTGAG 2675
Qy 601 GATTTTGGAG 651
Db 2676 GATTTTGGAG 2726

RESULT 7
US-09-964-469-3
; Sequence 3, Application US/09964469
; Patent No. 6579709
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000636DIY
; CURRENT APPLICATION NUMBER: US/09/964,469
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: 60/208,331
; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 09/738,894
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 36651
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(36651)
; OTHER INFORMATION: n = A,T,C or G
US-09-964-469-3

Query Match 37.2%; Score 617.4; DB 4; Length 36651;
Best Local Similarity 96.8%; Pred. No. 2.2e-142;
Matches 630; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 ATGTGAGACATGAG 60
Db 2076 ATGTGAGACATGAG 2135
Qy 61 AAGCCCTGAG 120
Db 2136 AAGCCCTGAG 2195
Qy 121 GGGCTGAG 180
Db 2196 GGGCTGAG 2255
Qy 181 GAGGAG 240
Db 2256 GAGGAG 2315
Qy 241 CGAAG 300

Db 2316 CGAAGGGGGGACCTTCTAGAGACGTGACAGACTGGAGCTGGCCGAGGAGGACCC 2375
 QY 301 ACCAAAGACAGCGGCTGACAGGAGGCTGGTGGCCACTTTGGAGAGGCCCTGGCCCGGAG 360
 Db 2376 ACCAAGACAGCGGCTGACAGGAGGCTGGTGGCCACTTTGGAGAGGCCCTGGCCCGGAG 2435
 QY 361 AACCCGCAACCTTCTCTAGAGAGGCGCTGGCCACCAAGTGGCAAGGACCACTGAG 420
 Db 2436 AACCCGCAACCTTCTCTAGAGAGGCGCTGGCCACCAAGTGGCAAGGACCACTGAG 2495
 QY 421 GAAGAGCAAGTGGCTGACAGTACCTGCGCAAGGCTGAGGCCATGCTTTCTTGGCAAG 480
 Db 2496 GAAGAGCAAGTGGCTGACAGTACCTGCGCAAGGCTGAGGCCATGCTTTCTTGGCAAG 2555
 QY 481 CAGCCCTTAAAGATTTCGTCACAGGCGCTTCACAGCAAGTTTCTGAGTGGAACTC 540
 Db 2556 CAGCCCTTAAAGATTTCGTCACAGGCGCTTCACAGCAAGTTTCTGAGTGGAACTC 2615
 QY 541 TTGAGATGCAACCAAGTGCAGACAACTTCACTGAGTTCAGAGTGTGGGAAAGGT 600
 Db 2616 TTGAGATGCAACCAAGTGCAGACAACTTCACTGAGTTCAGAGTGTGGGAAAGGT 2675
 QY 601 GGTGTTGGGAGGTATGTGCGCTCCAGGTGAAAAACACTGGAGAGATGTAT 651
 Db 2676 GGTGTTGGGAGGTATGTGCTCCAGTAGCCAGGCTAGAGAGTGAAGCAT 2726

RESULT 8

US-08-464-954A-2
 ; Sequence 2, Application US/08464954A
 ; Patent No. 6255069

GENERAL INFORMATION:

APPLICANT: BENOVIC, JEFFREY L.; GOMEZ, JORGE; KUNAPULI,

APPLICANT: PRIYA

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

TITLE OF INVENTION: MODULATING THE ACTIVITY OF G PROTEIN-COUPLED RECEPTOR

NUMBER OF SEQUENCES: 12

NUMBER OF SEQUENCES: 12

ADDRESS: JANE MASEY LICATA, ESQ.

STREET: WOODLAND FALLS CORPORATE PARK

STREET: 210 LAKE DRIVE EAST, SUITE 201

CITY: CHERRY HILL

STATE: NJ

COUNTRY: USA

ZIP: 08002

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/464,954A

FILING DATE: HEREWITH

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/076,084

FILING DATE: JUNE 11, 1993

ATTORNEY/AGENT INFORMATION:

NAME: JANE MASEY LICATA

REGISTRATION NUMBER: 32,257

REFERENCE/DOCKET NUMBER: JEFF-0118

TELECOMMUNICATION INFORMATION:

TELEPHONE: (609) 779-2400

TELEFAX: (609) 779-8488

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2848

TYPE: NUCLEIC ACID

STRANDEDNESS: SINGLE

TOPOLOGY: LINEAR

ANTI-SENSE: NO

US-08-464-954A-2

Query Match

25.3%; Score 419.8; DB 3; Length 2848;

Best Local Similarity 56.2%; Pred. No. 4.8e-94;

Matches 891; Conservative 0; Mismatches 682; Indels 12; Gaps 5;

QY 15 GGCCTGAGCAACTGATTCGCAACACCGCTTACTGACAGCCCGAAGCCCTGAGCTG 74
 Db 65 GGAAGCTGAGCAACTGATTCGCAACACCGCTTACTGACAGCCCGAAGCCCTGAGCTG 124
 QY 75 CGACGAAAG---AGCTGACGCGGCGGCTGATAGCTGAGCTGCGGCGCTGAGG 131
 Db 125 AAATGGAAGGCAAAAGCAAAATGCGGAGATGCTCAAGTTCCCTCAATCAAGCA 184
 QY 132 CTGCGGAGAGCTCGCCGCAAGAGCTGCTCTGAACCTTCAAGCTGTGTGAGAGAGAGCC 191
 Db 185 GTGCGAAGAGCTGCGGCTGAGCTTCAAGGTGATCAAGCTGTGTGAGAGAGAGCCG 244
 QY 192 CATGCTGCGGCTCTTCTGATCTTCTGACAGTGGCCAGTTCGCAAGGCGG 251
 Db 245 CATGCGGCGGCTCTTCTGATCTTCTGACAGTGGCCAGTTCGCAAGGCGGCTG 304
 QY 252 AACCTTCTAGAGAGCTGACAGAACTGGAGCTGGCCGAGAGAGAGCAACCAAGACG 311
 Db 305 CGCTTCTGAGATGGGAGTGGCGAGATGAGTGAACCCGGAATGACAGCGAAGGCAATG 364
 QY 312 CGGCTGACAGGAGGCTGAGGCACTTGTGAGTGGCCCTGCGCGGAGAACCCGCAACC 371
 Db 365 TGAGCGGCAAG---TACGCAAGATTTTGTGAGCAACAGGCTGACCTGATCTATCCCTG 421
 QY 372 CTTCCTGACCAAGGCGGCTGAGCAACAGTGGCCAGCAACCACTGAGAGAGAGCAAGT 431
 Db 422 GTTCCCGGCGAGCTGAGTGAAGAC-TGACACCGGCTGAGAGGCTGCGGCAAG 480
 QY 432 GGTGACAGTGAAGCTGCGCAAGGCTGAGGCACTGCTTTTTCAGAGAGAGAGCCCTTAA 491
 Db 481 ACCTTTTCAGAGACTACCGGCTGA--CCGACAGTACTGAGGCTGCGGCTTTTTC 538
 QY 492 GGAATTCGAGACAGGCGCTTACACAGCAAGTTTCTGAGTGAAGTCTTTCAGATGCA 551
 Db 539 GGAATTCGAGACAGGCGCTTACACAGCAAGTTTCTGAGTGAAGTCTTTCAGATGCA 598
 QY 552 ACCAGTGTGACAGAGTACTTCACTGAGTTCAGAGTCTGAGGAAAGGTGTTTGGGGA 611
 Db 599 GCGAGTGTGACAGAGTACTTCACTGAGTTCAGAGTCTGAGGAAAGGTGTTTGGGGA 658
 QY 612 GGTATGTGCGCTGAGTGAAGAAACCTGGGAAGTGTATGCTGTAGAGAACTGAGCA 671
 Db 659 GGTATGTGCGCTGAGTGAAGAAACCTGGGAAGTGTATGCTGTAGAGAACTGAGCA 718
 QY 718 GAAAGTGAACAGTATGTTGATGAGCTTGGCTTACGCTTACAGCAACAGAGCGGCT 838
 Db 778 GAAAGTGAACAGTATGTTGATGAGCTTGGCTTACGCTTACAGCAACAGAGCGGCT 898
 QY 792 CTGCTTGTGATGAGCTTGAAGTGAAGTGGGAGACCTCAAGTCAATCTCAAGCGG 851
 Db 839 GTGCTGTGATGAGCTTGAAGTGAAGTGGGAGACCTCAAGTCAATCTCAAGCGG 898
 QY 852 CACCGTGTGCTGAGCATGAGCGGCTGATCTTCTTCAAGTGGGCTGAGGAT 911
 Db 899 CACCGTGTGCTGAGCATGAGCGGCTGATCTTCTTCAAGTGGGCTGAGGAT 958
 QY 912 GCTGACCTTCATGAATCTGAGATGCTTATGAGGACATGAGAGTGTGCTTCT 971
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RESULT 9 US-08-221-817-12

; Sequence 12, Application US/08221817
 ; Patent No. 5532151
 ; GENERAL INFORMATION:
 ; APPLICANT: Chanity, David
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Hoekstra, Merle F.
 ; TITLE OF INVENTION: A No. 5532151el G Protein-coupled Receptor
 ; TITLE OF INVENTION: Kinase GRK6
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/221,817
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/123,932
 ; FILING DATE: 17 SEP 1993

ATTORNEY/AGENT INFORMATION:
 NAME: No. 5532151and, Greta F.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 31981
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2204 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 31..1758
 US-08-221-817-12

Query Match 25.2% Score 418.2; DB 1; Length 2204;
 Best Local Similarity 56.2%; Pred. No. 1.1e-93;
 Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;

QY 15 GAGCCCTGACCAACGATGCGCAACACCCCTACTGACAGCCCGAGAGCCTCTGAGACTG 74
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Db 747 GAAAGTGAACAGAGGTTTGTATGAGCTTGGCTTACGCTATAGACCAAGAGCCCT 806
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Db 987 GATATACCAAGCCACATCCGATCTCTGACCTGGGAGGAGCTGTGATGTGCGGAGG 1046
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QY 1152 GGTGTGGGAGCAACCATCAAAATTTCAAGGAAAGGTCAAGTAAAGGATCTGAA 1211
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QY 1572 GAGACTTTTGAAGAACTGAATGAC 1596
Db 1584 CAGGTGCTTCCAGAGCTGATGTC 1608

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RESULT 10

US-08-454-439-12
 ; Sequence 12, Application US/08454439
 ; Patent No. 5591618

GENERAL INFORMATION:

APPLICANT: Chantry, David
 APPLICANT: Gray, Patrick W.
 APPLICANT: Hoekstra, Merle F.
 TITLE OF INVENTION: A No. 5591618el G Protein-Coupled Receptor
 TITLE OF INVENTION: Kinase GRK6
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

```

ADDRESSSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,439
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,817
FILING DATE: 31-MAR-1994
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5591618and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2204 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 31..1758
US-08-454-439-12
Query Match 25.2%; Score 418.2; DB 1; Length 2204;
Best Local Similarity 56.2%; Pred. No. 1.1e-93;
Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;
QY 15 GGCCTGGAACATCGATTCGCAACACGCGCTACCTGAGAGCCCGAGAGCCCTGCACTG 74
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 QY 1572 GGGACTGTTGAGAACTGAATGAC 1596
 Db 1584 CGAGTCTTCCAAAGAGCTGAATGTC 1608
 RESULT 11
 PCT-US94-10487-12
 ? Sequence 12, Application PC/TUS9410487
 ? GENERAL INFORMATION:
 ? APPLICANT: ICOS Corporation
 ? TITLE OF INVENTION: A Novel G Protein-Coupled Receptor
 ? NUMBER OF INVENTIONS: 24
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ? STREET: 6300 Sears Tower, 233 South Wacker Drive
 ? CITY: Chicago
 ? STATE: Illinois
 ? COUNTRY: USA
 ? ZIP: 60606
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent In Release #1.0, Version #1.25
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: PCT/US94/10487
 ? FILING DATE:
 ? CLASSIFICATION:
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 08/221,817
 ? FILING DATE: 31 MAR 1994
 ? CLASSIFICATION:
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 08/123,932
 ? FILING DATE: 17 SEP 1993
 ? CLASSIFICATION:
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Noland, Greta E.
 ? REGISTRATION NUMBER: 35,302
 ? REFERENCE/DOCKET NUMBER: 27866/11981
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (312) 474-6300
 ? TELEFAX: (312) 474-0448
 ? TELEX: 25-3856
 ? INFORMATION FOR SEQ ID NO: 12:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 2204 base pairs
 ? TYPE: nucleic acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: cDNA
 ? FEATURE:
 ? NAME/KEY: CDS
 ? LOCATION: 31..1758
 ? PCT-US94-10487-12
 Query Match 25.2%; Score 418.2; DB 5; Length 2204;
 Best Local Similarity 56.2%; Pred. No. 11e-93;
 Matches 890; Conservative 0; Mismatches 683; Indels 12; Gaps 5;

132 CTGGCGGAGCTCCGCCAAGAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGACCC 191
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RESULT 12
US-08-221-817-21
Sequence 21, Application US/08221817
Patent No. 5532151
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
APPLICANT: Hoekstra, Merle F.
TITLE OF INVENTION: A No. 5532151 G Protein-Coupled Receptor
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/221,817
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5532151and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 13..1740
US-08-221-817-21

Query Match 23.9%; Score 395.8; DB 1; Length 1983;
Best Local Similarity 55.3%; Pred. No. 3.5e-88;
Matches 876; Conservative 0; Mismatches 697; Indels 12; Gaps 5;

15 GGCCTGGAACAACCTGATGCGCAACACCGCTTACCTGACGCGCCGGAACCTTGTGAGCAGAGCC 74
15 GAGAGTCGGAACAACCTGATGCGCAACACCGCTTACCTGACGCGCCGGAACCTTGTGAGCAGAGCC 74
75 GAGAGTCGGAACAACCTGATGCGCAACACCGCTTACCTGACGCGCCGGAACCTTGTGAGCAGAGCC 131
75 GAGAGTCGGAACAACCTGATGCGCAACACCGCTTACCTGACGCGCCGGAACCTTGTGAGCAGAGCC 131
75 GAGAGTCGGAACAACCTGATGCGCAACACCGCTTACCTGACGCGCCGGAACCTTGTGAGCAGAGCC 134
132 CTGCGGAGAGCTCCGCAAGAGCTGCTGAACTTCCAGACCTGCTGTGAGCAGAGCC 191
135 GTGTGAAGAGCTCCGCGCTACCTTGAAGAGTGAACCTGCTGTGAGCAGAGCC 194
192 CATGCGTCCGCGCTCTTCCGTGACTTCTTGAACAGTCCGCAAGTCCGCAAGAGCC 251
195 CATGCGGCGCTCTTATATGATGATGCTGCGCTACGAGGCTGAGCTGACCGCTGTAC 254
252 AACCTTCTGAGAGAGAGTGCAGAACTGGAGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 311
255 TGCCTTCTGAGAGAGAGTGCAGAACTGGAGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 314
312 CGCGCTGAGAGAGAGTGCAGAACTGGAGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 371
315 TGGGCGCTC---GGCTAATGAGAGATTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 371
372 CTCTCTGAGAGAGAGTGCAGAACTGGAGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 431
372 AGTTCCCGCGAGAGTGCAGAACTGGAGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 430
432 GGTGAGAGAGAGTGCAGAACTGGAGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 491
431 ACCTTCTGAGAGAGAGTGCAGAACTGGAGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 488
492 GATTTCTGAGAGAGAGTGCAGAACTGGAGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 551
489 GATTTCTGAGAGAGAGTGCAGAACTGGAGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 548
552 ACCAGTGCAGAGAGAGTGCAGAACTGGAGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 611
549 GCGAGTGCAGAGAGAGTGCAGAACTGGAGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 608
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1032 CAGAGTCGAGAGAGAGTGCAGAACTGGAGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1091
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1092 AAGAGTGAATTTCTGATGCTGAG 1151
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1206 GCGAGTGCAGAGAGAGTGCAGAACTGGAGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1265
1272 AGATATTTGAGAGAGTGCAGAACTGGAGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1331
1266 ACTGCTTCTGAGAGAGTGCAGAACTGGAGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1325
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1452 TGAATGATGATTTCTGAGAGAGAGTGCAGAACTGGAGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAG 1511
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1572 GCGAGTGCAGAGAGTGCAGAACTGGAGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1596
1566 TGAATGCTGAGAGAGTGCAGAACTGGAGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1590

RESULT 13
US-08-439-21
Sequence 21, Application US/0845439
Patent No. 5591618
GENERAL INFORMATION:
APPLICANT: Chantry, David
APPLICANT: Gray, Patrick W.
APPLICANT: Hoekstra, Merle F.
TITLE OF INVENTION: A No. 5591618el G Protein-Coupled Receptor
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,439
FILING DATE: 30-MAY-1995

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/221,817
 FILING DATE: 31-MAR-1994
 APPLICATION NUMBER: 08/123,932
 FILING DATE: 17 SEP 1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 559161band, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 31981
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELE: 25-3856
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1983 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 13..1740
 US-08-454-439-21

Query Match 23.9%; Score 395.8; DB 1; Length 1983;
 Best Local Similarity 55.3%; Pred. No. 3.5e-88;
 Matches 876; Conservative 0; Mismatches 697; Indels 12; Gaps 5;

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 372 CTTCCTAGCCAGGCGCTGGCCACCAAGATGCAAGAGCCACCACTAGAGAGAGAGT 431
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 432 GGTGCAAGTACCTGGCGAAGCTGAGAGCCATGGCTTTCTTGAAGAGAGCCCTTAA 491
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 849 CAGGCTGCTTCTTCCCAAGAGAGTGTGTGTCTATGCTGCGAGAGTCTGTGTGTCT 908
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 909 GAGAGACTTACACCGGGAAGCATGCTGTGACAGGAGCCTTAAAGCCAGAGATATCTTCT 968
 972 GATGACCTCGGCAATGCAAGTATCTGAGTGTGGGCTGGCTGGAGAGAGAGGAGTGG 1031
 969 GATGACCAATGCGCACTTGAATCTCGACCTGGGCTGGCTGGAGATGTTCTGTAGGG 1028
 1032 CAAGCCATCAACCAAGAGGCTGGAACCAATGTTATCATGAGCTCTGAGATCTTATGGA 1091
 1029 CCAAGCATCAAAAGGCGGTGTGGGAGCTGTGGGCTATATGCTTCCAGAG--GTGGTGA 1085
 1092 AAAGTGAATTTCTATCTCTGTGAGCTGTTGGCAATGGAGTGCAGCATTTATGAAT 1151
 1086 GAATGAGCCCTTCAATCTGATCTGAGCTGGGAGGCTGAGCTCTCTGTCGAGAT 1145
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 1212 GCAAGAACTCTGCAAGAGAGTGAATTTCCAGCATGATTAATTTCAAGAGAGCAAA 1271
 1206 GCGCTGTGCAAGAGAGTGTGTGAGAGATGACAGACCGCTTCCCAAGAGAGAGCTG 1265
 1272 AGATATTCAGAGCTCTTCTTGGCTTAAAGAACAGAGCAAGCTTATGAGAGAGAAAA 1331
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 1332 GTCTGATGATCCCAAGAAACATCTTCTTAAACAGATGAATTTCCCTGCGCTGAAAG 1391
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 1446 GGAATTTGAAGCTTCTCAAGTAAAGTGTGATCTGAGACCCCAAGCAAGCAAGCTT 1505
 1512 CTGAAAACCTTGGGAGAGGTGCTTCTTATAGCAAGGAGAGAGAAATTTATGAAG 1571
 1506 CTACAGAGATTTGCAAGGAGTGTGTCTCAATCCCTTGGCAAGAGAGATGTGGAGAC 1565
 1572 GGGACTGTTTGAAGAACTGATGAC 1596
 1566 TGAATGCTTCCAGAGAACTAATATGTC 1590

RESULT 14
 PCT-US94-10487-21
 Sequence 21, Application PC/TUS9410487
 GENERAL INFORMATION:
 APPLICANT: ICOS Corporation
 TITLE OF INVENTION: A Novel G Protein-Coupled Receptor

TITLE OF INVENTION: Kinase GRK6
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10487
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/221,817
FILING DATE: 31 MAR 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31981
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1983 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 13..1740
PCT-US94-10487-21
Query Match 23.8%; Score 395.8; DB 5; Length 1983;
Best Local Similarity 55.3%; Pred. No. 3.5e-88;
Matches 876; Conservative 0; Mismatches 697; Indels 12; Gaps 5;

QY 15 GGCCCTGGCAACCTGATGCGCCACACCGGCTACCTGACAGGCGCGGAAGCCCTCGGACG 74
DB 15 GGAGCTCGAAGAACTGTCAGCAACACGGGCTACCTGAGGCGCGGAAGGCTGTCGCG 74
QY 75 CGACAGCAAG--AGCTGAGCGCGCGCGCTGAGCTGCGCTGCGCGCGCTGACGAG 131
DB 75 GAATGCTAAGGCAAGAGCAAGAAATGCGCGAGATGCTGCGAGTTCCCCACATACGCA 134
QY 132 CTGCGCGAGCTCGCGCAAGAGCTGCTCCGAACTTCCACAGCTGTGTGAGCAGCGC 191
DB 135 GTGTAAAGAGCTCGCGCTACCTTGAACGTGACTACCAACCTGTGTAGAGCTCAGTC 194
QY 192 CATCGTGCAGCGCTCTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 251
DB 195 CATGCGCGCTCTTAT 254
QY 252 AACCTTCTAGAGAGCTGAGCACTGAGAGCTGCGCGAGAGAGAGAGAGAGAGAGAGAG 311
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QY 312 CGCGCTGAGAGGCTGTGTGCTCACTTGTGAGAGTGCCTGCGCGGAGAGAGAGAGAGAG 371

DB 315 TGCGGCTC---GGCTATGACAGATTTTGTAGGCCACAGCGGCTCTGACCTGATCCCTGA 371
QY 372 CTTCCTAGCGCAGGCGCTGCGCCACCAAGTGTCCAGAGAGCCCACTGAGAGAGAGAGAGT 431
DB 372 AGTTCCTCCGACAGCTGTGTAGTAAAC--TGTCCTACGCGCTGAGCAGAGAGAGAGAGAG 430
QY 432 GCGTCAGTACAGCTGCGCAAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 491
DB 431 ACCTTCTCCAGAGAGCTGACCGGCTTACCTAGAGTACCTTACAGAGAGAGAGAGAGAG 488
QY 492 GAGATTTGTACAG 551
DB 489 GAGTACCTGACAG 548
QY 552 ACAGTGTACAG 611
DB 549 GCGAGTACCAAG 608
QY 612 GGTATGTCGCGCTCCAG 671
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QY 672 GAGCGGCTGAG 721
DB 669 GAAAGCAATTAAG 728
QY 723 GAGGTGAG 791
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DB 789 GTGCTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 848
QY 852 CAGCGTGCCTGAG 911
DB 849 CAGAGCTGCTTCCGAG 908
QY 912 GCTGCACTTCAG 971
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QY 972 GATGAGCTGCGCAAG 1031
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QY 1152 GGTGCTGAG 1211
DB 1146 GATGAG 1205
QY 1212 GCAAG 1271
DB 1206 GCGGCTGAG 1265
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DB 1326 TGCGGCTGAG 1385
QY 1392 TGCGCTATGAG 1451
DB 1386 TGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1445

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 DB 1446 GGACATGACAGTTTCCACAGTTAAAGGATGATCTGAGGCCACACAGACTT 1505
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 QY 1572 GGACCTTTGAGGAACTGATGAC 1596
 DB 1566 TGAATGCTTCCAGGAACTAATGTC 1590

RESULT 15

US-08-221-817-10

Sequence 10, Application US/08221817

Patent No. 5532151

GENERAL INFORMATION:

APPLICANT: Chantry, David

APPLICANT: Gray, Patrick W.

APPLICANT: Hoefta, Merle F.

TITLE OF INVENTION: A No. 5532151 G Protein-Coupled Receptor

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/221,817

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/123,932

FILING DATE: 17 SEP 1993

ATTORNEY/AGENT INFORMATION:

NAME: No. 5532151and, Greta E.

REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 31981

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 2206 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 31..1926

US-08-221-817-10

Query Match

Best Local Similarity

Matches 866; Conservative

23.5%; Score 389.4; DB 1; Length 2206;

Pred. No. 1.4e-86;

0; Mismatches 681; Indels 18; Gaps 5;

QY 15 GGCCCTGACCACTGATCGCAACGCGCTACCTGCAAGCCCGAAGCCCTCGACTG 74
 DB 33 GGAGCTCGAAGACATCTAGCAACGAGCTCTACTCAAGGCCCGGAGAGGTGGCGGTGG 92

QY 75 CGACAGCAAG---AGCTGCAAGCGGCGGCGGTAGCTGCGCCCTGCGGCGTGCAGGG 131
 DB 93 AAATCCCAAGGCAAAAGCAAAATGCGGAGATGCTTCAGTTCCCTCAATCAAGCCA 152
 QY 132 CTGCGGAGGCTCCCGCAGAGCTGCTTGAATTCACAGCTGCTGTGAGCAGAGCC 191
 DB 153 GTGGAAGAGCTGCGGCTCAGCTCGAGGTACTATCAAGCTGTGCGAGCGGACGG 212
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 DB 213 CATGGGCGGCTGCTGTTCCGAGAGTTCTGTGCCACAGGCGGAGCTGAGCCGCTGCG 272
 QY 252 AACCTTCTAAGAGAGTGCAGAACTGAGAGCTGCGGAGAGGAGCCACCAAGAG 311
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 QY 312 CGGCTGCAAGGAGCTGTGAGCTGTGAGGAGTGCAGGAGTGCAGGAGGAGGAGT 371
 DB 333 TGGCGGAGAG---TAAAGAGAAATTTCTAAGGCAAGCGGCTCTGAGCTTATCTGTA 389
 QY 372 CTTCTCAGCAGGCGGCTGAGCCACCAAGTGCAGGAGCAGCAGCAGCAGCAGCAGT 431
 DB 390 GGTGCGGAGAGCTGTGAGAGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGT 443
 QY 432 GGTGAGTGCAGCTGCGCAGAGGCTGAGGAGTGCAGGAGTGCAGGAGTGCAGGAG 491
 DB 444 AAAGACCTTTCTAAGAGAACTACCGGCTGAGCCAGAGTGCAGGAGTGCAGGAGT 503
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 QY 852 GGTGAGTGCAGGAGTGCAGGAGTGCAGGAGTGCAGGAGTGCAGGAGTGCAGGAG 911
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QY 1332 GTCCTG--ATGATCCAGAGAACATCATTTCTTAAGAGATCAAATTCTGCTGGA 1388
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QY 1389 AGCTGGCTTAATTAACCCCATTTGTGCGAGACCTTCAGTGTGTTATGCCAAGACAT 1448
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QY 1569 AAGCG 1573
Db 1581 GACCG 1585

Search completed: August 13, 2004, 18:45:37
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